

Table 42: Comparative Sequences relating to SAG 0764

SEQ ID NO. 4201: 2603 V/R STRAIN
 ATGGTAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGGAAATAAAGCTAACCTTTTC
 ACTGGATGGGCTGACGTAGATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGG
 AAATTAATTTCAAGCAGCAGGTATTGAGTTCCACCTTGCTTTTACATCAGTTCTTAAACGT
 GCCATCAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAA
 AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATAAAGCAGAA
 GCAGCTGAACAATTTGGTATGAGCAAGTTTATATTTGGCGTCGTTTATATGATGATTTG
 CCTCCAGATATGGCTAAAGATGATGAACATTCAGCACATACTGATCGTCGCTATGCTTCA
 CTAGATGATTTCTGTTATCCAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGTCTT
 CCTTTCTGGGAGATAAAAATGCTCCTGCTCTTAAAGATGTAATAAATGTTTGTGGT
 GCACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAAACAATTTGTCAGATGATGAA
 ATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTCGAATTTGATGAAAAATTA
 AACCTTGTTCAGAAATTAATTAAGTAA

SEQ ID NO. 4202: 090 STRAIN
 GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTG
 GAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGTA
 ATTGAGTTCCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAACA
 AACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
 AATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAAT
 AAAGCAGAGCAGCTGAACAATTTGGTATGAGCAAGTTTCAATTTGGCG
 TCGTTTATATGATGATTTGCTCCAGATATGGCTAAAGATGATGAACATTC
 CAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTTCTGTTATTCCAG
 ATGCAGAAAAACCTTAAAGTTACTTTAGAGCGTGTCTTCCCTTTCTGGGA
 GATGAGAAAAACCTTAAAGTTACTTTAGAGCGTGTCTTCCCTTTCTGGGA
 AGATAAAATGCTCCTGCTCTTAAAGATGGTAAAAATGTTTGTGGTGGT
 CACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAAACAATTTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTCGA
 CGAATTTGATGAAAAATTAACCTTGTTCAGAAATTAATTAAGTAA

SEQ ID NO. 4203: A909 STRAIN
 GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGTA
 TTGAGTTCCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
 ATCATGGCGCTTAAACGAACGTCATTACGGTGGATTGACAGGAAAAAATA
 AAGCAGAGCAGCTGAACAATTTGGTATGAGCAAGTTTCAATTTGGCGT
 CGTTTATATGATGATTTGCTCCAGATATGGCTAAAGATGATGAACATTC
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTTCTGTTATTCCAG
 ATGCAGAAAAACCTTAAAGTTACTTTAGAGCGTGTCTTCCCTTTCTGGGA
 GATGAAAAATGCTCCTGCTCTTAAAGATGGTAAAAATGTTTGTGGTGGT
 ACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAAACAATTTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTCGA
 GAATTTGATGAAAAATTAACCTTGTTCAGAAATTAATTAAGTAA

SEQ ID NO. 4204: H36B STRAIN
 GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
 TGGAAATTAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGTA
 GTATTGAGTTCCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
 AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATA
 AATAAGCAGAGCAGCTGAACAATTTGGTATGAGCAAGTTTCAATTTGGCGT
 CGTTTATATGATGATTTGCTCCAGATATGGCTAAAGATGATGAACA
 TTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTTCTGTTATTCCAG
 CAGATGCAGAAAAACCTTAAAGTTACTTTAGAGCGTGTCTTCCCTTTCTGGG
 GAAGATAAAATGCTCCTGCTCTTAAAGATGGTAAAAATGTTTGTGGTGGT
 TGCACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAAACAATTTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTCGA
 ATTTGATGAAAAATTAACCTTGTTCAGAAATTAATTAAGTAA

SEQ ID NO. 4205: 18RS21 STRAIN
 GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGTA
 TTGAGTTCCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
 ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAATA
 AAGCAGAGCAGCTGAACAATTTGGTATGAGCAAGTTTCAATTTGGCGT
 CGTTTATATGATGATTTGCTCCAGATATGGCTAAAGATGATGAACATTC
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTTCTGTTATTCCAG
 ATGCAGAAAAACCTTAAAGTTACTTTAGAGCGTGTCTTCCCTTTCTGGGAA
 GATAAAATGCTCCTGCTCTTAAAGATGGTAAAAATGTTTGTGGTGGT
 ACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAAACAATTTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTCGA
 ATTTGATGAAAAATTAACCTTGTTCAGAAATTAATTAAGTAA

SEQ ID NO. 4206: M732 STRAIN
 GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGTA

Table 42: Comparative Sequences relating to SAG 0764

TTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA
 ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGAAAAATA
 AAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGGCGT
 CGTTCATATGATGATTTGCCCTCCAGATATGGCTAAAGATGATGAACATTC
 AGCACAATCTGATCGTTCGCTATGCTTCACTAGATGATTCGTTATTCCAG
 ATGCAGAAAACTTAAAGTTACTTTAGAGCGTGTCTTCCCTTCTGGGAA
 GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGGTGC
 ACACGGTAACTCAATCCGTGCTCTTGTAAACATATCAACCAATTTGT CAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACCTCCACCACCTTGTTTC
 GAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4207: COH1 STRAIN

GTAAAAATTAGTATTTCGCACGCCACGG
 TGAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
 ATCTTTGAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAAT
 CAAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACG
 TGCCATCAAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
 ACAGGAAAAAATAAGCAGAGCAGCTGAACAATTTGGTGTGATGAGCAAGT
 TCATATTTGGCGTTCGTTTCATATGATGATTTGCCTCCAGATATGGCTAAAG
 ATGATGAACATTCAGCACATACTGATCGTTCGCTTCACTAGATGAT
 TCTGTTATTCCAGATGACAGAAAACTTAAAGTTACTTTAGAGCGTGTCTCT
 TCCCTTCTGGGAAGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATG
 TGTTTGTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATC
 AAACAATTTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACCTCC
 ACCACTTGTTTTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATT
 ACTTAGGTAAA

SEQ ID NO. 4208: CJB110 STRAIN

GTAAAAATTAGTATTTCGCACGCCACGG
 TGAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
 ATCTTTGAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAAT
 CAAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACG
 TGCCATCAAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
 ACAGGAAAAAATAAGCAGAGCAGCTGAACAATTTGGTGTGATGAGCAAGT
 TCATATTTGGCGTTCGTTTCATATGATGATTTGCCTCCAGATATGGCTAAAG
 ATGATGAACATTCAGCACATACTGATCGTTCGCTTCACTAGATGAT
 TCTGTTATTCCAGATGACAGAAAACTTAAAGTTACTTTAGAGCGTGTCTCT
 TCCCTTCTGGGAAGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATG
 TGTTTGTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATC
 AAACAATTTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACCTCC
 ACCACTTGTTTTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATT
 ACTTAGGTAAA

SEQ ID NO. 4209: 1169NT STRAIN

AGTATTTCGCACGCCACGGTGAATCTGAGTGGAAATAAGCTAACCTTTTCA
 CTGGATGGGCTGACGTAGATCTTTGAGAAAAAGGTACACAACAAGCTATT
 GATGCTGGGAAATTAATTCAGCAGCAGGTATTGAGTTCGACCTTGCTTT
 TACATCAGTTCTTAAACGTCGCCATCAAAACAACCTAACCTTGCCCTTGAAG
 CAGCTGATCAACTTTGGGTACCAGTTGAAAAATCATGGCGCTTGAACGAA
 CGTCAATTCGGTGGATTGACAGGAAAAATAAGCAGAGCAGCTGAACA
 ATTTGGTGTGATGAGCAAGTTCAATTTGGCGTTCGTTTCATATGATGATTTGC
 CTCCAGATATGGCTAAAGATGATGAACATTCAGCACATACTGATCGTCCG
 TATGCTTCACTAGATGATTTCTGTTATTCCAGATGACAGAAAACTTAAAGT
 TACTTTAGAGCGTGTCTTCTCCTTTCTGGGAAGATAAAATTTGCTCCTGCT
 TTAAGATGGTAAAAATGTTGTTGTTGGTGCACACGGTAACTCAATCCGT
 GCTCTGTAAAAACATATCAACAATTTGTCAGATGATGAAATCATGGACG
 TGAAATTCCTAACCTCCACCACCTTGTTTTCGATTTGATGAAAAATTA
 ACCCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4210: M781 STRAIN

GTAAAAATTAGTATTTCGCACGCCACGGT
 GAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
 TCTTTGAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTC
 AAGCAGCAGGTATTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACG
 GCCATCAAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
 ACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
 CAGGAAAAAATAAGCAGAGCAGCTGAACAATTTGGTGTGATGAGCAAGT
 CATATTTGGCGTTCGTTTCATATGATGATTTGCCTCCAGATATGGCTAAAG
 TGATGAACATTCAGCACATACTGATCGTTCGCTTCACTAGATGATTT
 CTGTTATTCCAGATGACAGAAAACTTAAAGTTACTTTAGAGCGTGTCTCT
 CCTTTCTGGGAAGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATG
 GTTTGTTGGTGCACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCA
 AAACAATTTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACCTCC
 CCACTTGTTTTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATT
 CTTAGGTAAA

SEQ ID NO. 4211: JM930013 STRAIN

GTAAAAATTAGTATTTCGCACGCCACGGTGAATCT
 GAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTT
 AGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAG

Table 42: Comparative Sequences relating to SAG 0764

CAGGTATTGAGTTGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATC
AAAACTAACCTTGCCTTGAAGCAGCTGATCAACTTTGGGTACCAGT
TGAAAAATCATGGCGCTTGAACGAACGTCCTTACGGTGGATTGACAGGAA
AAATAAAGCAGAAGCAGCTGAACAAATTTGGTGTAGCAGCAAGTTTCATATT
TGGCGTGGTTCATATGATGTATTGCCTCCAGATATGGCTAAAGATGATGA
ACATTCAGCACATACTGATCGTGCCTATGCTTCACTAGATGATTCTGTTA
TTCCAGATGCAGAAAACCTAAAGTTACTTTAGAGCGTCTCTTCCCTTTT
TGGGAAGATAAAAATGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGT
TGGTGCACACGGTAACTCAATCCGTGCTCTGTAAACATATCAAACAAT
TGTGATGATGAAATCATGGACGTTGAAATTCCTAACCTTCCACCACCTT
GTTTTCGAAATTTGATGAAAAATTAACCTTGTTTCAGAATATTACTTAGG
TAAA

PRETTY of: /biotmp/msa63264.2{*} March 10, 2003 09:30 ..

1 50
msa63264.2{110_090} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_1169NT} ----- -AGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_18RS21} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_2603} atggtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_CJB110} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_COH1} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_H36B} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_JM9130013} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_M732} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_M781} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_A909} ---gtaaaat TAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
Consensus *****

51 100
msa63264.2{110_090} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_1169NT} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_18RS21} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_2603} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_CJB110} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_COH1} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_H36B} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_JM9130013} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_M732} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_M781} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_A909} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
Consensus *****

101 150
msa63264.2{110_090} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_1169NT} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_18RS21} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_2603} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_CJB110} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_COH1} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_H36B} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_JM9130013} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_M732} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_M781} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_A909} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
Consensus *****

151 200
msa63264.2{110_090} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_1169NT} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_18RS21} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_2603} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_CJB110} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_COH1} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_H36B} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_JM9130013} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_M732} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_M781} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_A909} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
Consensus *****

201 250
msa63264.2{110_090} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_1169NT} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_18RS21} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_2603} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_CJB110} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_COH1} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_H36B} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_JM9130013} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_M732} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_M781} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
Consensus *****

Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_A909}	TGCCCTTGAA	GCAGCTGATC	AACTTTGGGT	ACCAGTTGAA	AAATCATGGC
Consensus	*****	*****	*****	*****	*****
251					
msa63264.2{110_090}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_1169NT}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_18RS21}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_2603}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_CJB110}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_COH1}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_H36B}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_JM9130013}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M732}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M781}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_A909}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
Consensus	****-****	*****	*****	*****	*****
301					
msa63264.2{110_090}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_1169NT}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_18RS21}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_2603}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_CJB110}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_COH1}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_H36B}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_JM9130013}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M732}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M781}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_A909}	GCAGCTGAAC	AAITTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
Consensus	*****	*****	*****	*****	*****
351					
msa63264.2{110_090}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_1169NT}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_18RS21}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_2603}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_CJB110}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_COH1}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_H36B}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_JM9130013}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M732}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M781}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_A909}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
Consensus	*****	*****	*****	*****	*****
401					
msa63264.2{110_090}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_1169NT}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_18RS21}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_2603}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_CJB110}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_COH1}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_H36B}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_JM9130013}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M732}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M781}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_A909}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
Consensus	*****	*****	*****	*****	*****
451					
msa63264.2{110_090}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_1169NT}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_18RS21}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_2603}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_CJB110}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_COH1}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_H36B}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_JM9130013}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M732}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M781}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_A909}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
Consensus	*****	*****	*****	*****	*****
501					
msa63264.2{110_090}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_1169NT}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_18RS21}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_2603}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_CJB110}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_COH1}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_H36B}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_JM9130013}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_M732}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA

Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_M781}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_A909}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
Consensus	*****	*****	*****	*****	*****
551					
msa63264.2{110_090}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_1169NT}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_18RS21}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_2603}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_CJB110}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_COH1}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_H36B}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_JM9130013}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_M732}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_M781}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_A909}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
Consensus	*****	*****	*****	*****	*****
601					
msa63264.2{110_090}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_1169NT}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_18RS21}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_2603}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_CJB110}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_COH1}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_H36B}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_JM9130013}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_M732}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_M781}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
msa63264.2{110_A909}	ATCATGGACG	TTGAAATTC	TAACTTCCCA	CCACTTGTIT	TCGAATTTGA
Consensus	*****	*****	*****	*****	*****
651					
msa63264.2{110_090}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_1169NT}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_18RS21}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_2603}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_CJB110}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_COH1}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_H36B}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_JM9130013}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_M732}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_M781}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_A909}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
Consensus	*****	*****	*****	*****	
SEQ ID NO. 4212: 2603 V/R STRAIN					
VKLVFARHGSEWKNANLFTGWADVLDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA					
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV					
PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLERLALPFWEDKIA PALKDKGNV FVGA					
HGNSIRALVKHI KQLSDDEIMDVEI PNFPPPLVFEFDEKLNLVSEYLLGK					
SEQ ID NO. 4213: 090 STRAIN					
VKLVFARHGSEWKNANLFTGWADVLDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA					
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV					
PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLERLALPFWEDKIA PALKDKGNV FVGA					
HGNSIRALVKHI KQLSDDEIMDVEI PNFPPPLVFEFDEKLNLVSEYLLGK					
SEQ ID NO. 4214: A909 STRAIN					
VKLVFARHGSEWKNANLFTGWADVLDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA					
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV					
PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLERLALPFWEDKIA PALKDKGNV FVGA					
HGNSIRALVKHI KQLSDDEIMDVEI PNFPPPLVFEFDEKLNLVSEYLLGK					
SEQ ID NO. 4215: H36B STRAIN					
VKLVFARHGSEWKNANLFTGWADVLDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA					
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV					
PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLERLALPFWEDKIA PALKDKGNV FVGA					
HGNSIRALVKHI KQLSDDEIMDVEI PNFPPPLVFEFDEKLNLVSEYLLGK					
SEQ ID NO. 4216: 18RS21 STRAIN					
VKLVFARHGSEWKNANLFTGWADVLDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA					
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV					
PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLERLALPFWEDKIA PALKDKGNV FVGA					
HGNSIRALVKHI KQLSDDEIMDVEI PNFPPPLVFEFDEKLNLVSEYLLGK					
SEQ ID NO. 4217: M732 STRAIN					
VKLVFARHGSEWKNANLFTGWADVLDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA					
IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV					
PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLERLALPFWEDKIA PALKDKGNV FVGA					
HGNSIRALVKHI KQLSDDEIMDVEI PNFPPPLVFEFDEKLNLVSEYLLGK					
SEQ ID NO. 4218: COH1 STRAIN					

Table 42: Comparative Sequences relating to SAG 0764

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGNVVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4219: CJB110 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGNVVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4220: 1169NT STRAIN

VFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRAIKT
TNLALAEAADQLWVVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
AKDDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGNVVFVGAHG
NSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4221: M781 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGNVVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4222: JM9130013 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
IKTTNLALEAADQLWVVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTLERALPFWEDKIAPALKDGNVVFVGA
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

PRETTY of: /biotmp/msa70722.2{*} March 10, 2003 09:33 ..

msa70722.2{110_090} 1
msa70722.2{110_18RS21} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD 50
msa70722.2{110_2603} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_A909} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_CJB110} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_COH1} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_H36B} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_JM9130013} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_M732} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_M781} vkLVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_1169NT} ---VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
Consensus ---*****

msa70722.2{110_090} 51
msa70722.2{110_18RS21} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE 100
msa70722.2{110_2603} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_A909} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_CJB110} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_COH1} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_H36B} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_JM9130013} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_M732} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_M781} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_1169NT} LAFTSVLKRA IKTTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
Consensus *****

msa70722.2{110_090} 101
msa70722.2{110_18RS21} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN 150
msa70722.2{110_2603} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_A909} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_CJB110} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_COH1} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_H36B} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_JM9130013} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_M732} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_M781} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_1169NT} AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN
Consensus *****

msa70722.2{110_090} 151
msa70722.2{110_18RS21} LKVTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI 200
msa70722.2{110_2603} LKVTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_A909} LKVTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_CJB110} LKVTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_COH1} LKVTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_H36B} LKVTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_JM9130013} LKVTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_M732} LKVTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI

Table 42: Comparative Sequences relating to SAG 0764

msa70722.2{110_M781}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
msa70722.2{110_1169NT}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
Consensus	*****	*****	*****	*****	*****
	201		229		
msa70722.2{110_090}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_18RS21}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_2603}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_A909}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_CJB110}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_COH1}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_H36B}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_JM9130013}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M732}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M781}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_1169NT}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
Consensus	*****	*****	*****		

Table 43: Comparative Sequences relating to SAG0079

TCAACCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTG
AAACTGTCAAACGTCGCCTGGACGTTAATATGCTCAAGGAGAACCTATTCCTGAACACT
ATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTG
CAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4308: H36B STRAIN (REVERSE COMPLEMENT)
CAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTTAGCTAAAA
GTTATATTGATAAAGGTGAATGGTTCCTGATGAAGTAACAAACGGGATTTGTAAGAGAGC
GCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTTACTTGTGATGGATATCCACGTA

SEQ ID NO. 4309: JM9130013 STRAIN (REVERSE COMPLEMENT)
AATCTTTTAAATTATGGGTTTGCCTGGTGTCTGGTAAAGGT
ACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTCTCACATCTCAACAGGGGATATG
TTCCGCGCCCGCAATGGCTAATCAAACCGAAATGGGACGTTTTAGCTAAAAAGTTATATTGAT

SEQ ID NO. 4310: M732 STRAIN (REVERSE COMPLEMENT)
CTTTTAAATTATGGGTTTGCCTGGTGTCTGGTAAAGGTACTCAAGCAGCTAAGATTTGTTGAA
GAATTTGGTGTGTTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAA
ACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTTGGTTCCTGATGAA

SEQ ID NO. 4311: M781 STRAIN (REVERSE COMPLEMENT)
AATCTTTTAAATTACGGGTTTGCCTGGTGTCTGGTAAAGGTACTCAA
GCAGCTAAGATTGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCG
GCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGT

MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa25038.2{*} April 17, 2002 08:53 ..
PRETTY of: /biotmp/msa252229.2{*} January 31, 2003 03:05 ..

1 50
msa252229.2{114_COH1} ----atcctt taattatggg tttgcctggg gctggtaaag gtactcaagc
msa252229.2{114_M732} -----cttt taattatggg tttgcctggg gctggtaaag gtactcaagc
msa252229.2{114_M781} ---Aatcctt taattacggg tttgcctggg gctggtaaag gtactcaagc
msa252229.2{114_A909} ---Aatcctt taattatggg tttgcctggg gctggtaaag gtactcaagc

51 100
msa252229.2{114_COH1} agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
msa252229.2{114_M732} agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA
msa252229.2{114_M781} agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA

Table 43: Comparative Sequences relating to SAG0079

Consensus		-----	-----	-----	-----	-----	*****
		101					150
msa252229.2	{114_COH1}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_M732}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_M781}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_A909}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_JM9130013}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_CJB110}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_090}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_2603}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_H36B}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_18RS21}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2	{114_1169NT}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
	Consensus	*****	*****	*****	*****	*****	*****
		151					200
msa252229.2	{114_COH1}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_M732}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_M781}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_A909}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_JM9130013}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_CJB110}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_090}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_2603}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_H36B}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_18RS21}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2	{114_1169NT}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
	Consensus	*****	*****	*****	*****	*****	*****
		201					250
msa252229.2	{114_COH1}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_M732}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_M781}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_A909}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_JM9130013}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_CJB110}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_090}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_2603}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_H36B}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_18RS21}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
msa252229.2	{114_1169NT}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTTAC	
	Consensus	*****	*****	*****	*****	*****	*****
		251					300
msa252229.2	{114_COH1}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_M732}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_M781}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_A909}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_JM9130013}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_CJB110}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_090}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_2603}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_H36B}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_18RS21}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2	{114_1169NT}	TTGATGGaTA	TCCACGTACT	ATTGAgCAAG	CACACGCCTT	AGATGCTACG	
	Consensus	*****	*****	*****	*****	*****	*****
		301					350
msa252229.2	{114_COH1}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_M732}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_M781}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_A909}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_JM9130013}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_CJB110}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_090}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_2603}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_H36B}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_18RS21}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
msa252229.2	{114_1169NT}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TTAAAGTGGA	
	Consensus	*****	*****	*****	*****	*****	*****
		351					400
msa252229.2	{114_COH1}	TCCaCaCATGc	CTTATAGAGC	GTTTGAGTgG	cCGTATTATC	AATCGTAAAA	
msa252229.2	{114_M732}	TCCaCaCATGc	CTTATAGAGC	GTTTGAGTgG	cCGTATTATC	AATCGTAAAA	
msa252229.2	{114_M781}	TCCaCaCATGc	CTTATAGAGC	GTTTGAGTgG	cCGTATTATC	AATCGTAAAA	
msa252229.2	{114_A909}	TCCaTcATGt	CTTATAGAGC	GTTTGAGTgG	tCGTATTATC	AATCGTAAAA	
msa252229.2	{114_JM9130013}	TCCaTcATGt	CTTATAGAGC	GTTTGAGTgG	tCGTATTATC	AATCGTAAAA	
msa252229.2	{114_CJB110}	TCCaTcATGt	CTTATAGAGC	GTTTGAGTgG	tCGTATTATC	AATCGTAAAA	
msa252229.2	{114_090}	TCCaTcATGt	CTTATAGAGC	GTTTGAGTgG	tCGTATTATC	AATCGTAAAA	
msa252229.2	{114_2603}	TCCaTcATGt	CTTATAGAGC	GTTTGAGTgG	tCGTATTATC	AATCGTAAAA	
msa252229.2	{114_H36B}	TCCaTcATGt	CTTATAGAGC	GTTTGAGTgG	tCGTATTATC	AATCGTAAAA	
msa252229.2	{114_18RS21}	TCCaTcATGt	CTTATAGAGC	GTTTGAGTgG	tCGTATTATC	AATCGTAAAA	

Table 43: Comparative Sequences relating to SAG0079

msa252229.2{114_1169NT}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA
Consensus	****_****_	*****	*****-	-*****	*****
	401				450
msa252229.2{114_COH1}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M732}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M781}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_A909}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_JM9130013}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_CJB110}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_090}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_2603}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_H36B}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_18RS21}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_1169NT}	CTGGTGAAC	TTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa252229.2{114_COH1}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_M732}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_M781}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_A909}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_JM9130013}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_CJB110}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_090}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_2603}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_H36B}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_18RS21}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_1169NT}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
Consensus	*****	*****	*****	*****	*-*****
	501				550
msa252229.2{114_COH1}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M732}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M781}	CTTGGACGTT	aATATTGCTC	AA-----	-----	-----
msa252229.2{114_A909}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgaa
msa252229.2{114_JM9130013}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactataaaa
msa252229.2{114_CJB110}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatag--
msa252229.2{114_090}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_2603}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_H36B}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_18RS21}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_1169NT}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatagta
Consensus	*****	*****	*****	*****	-----
	551				600
msa252229.2{114_COH1}	agcttggctc	tgttacagat	attgaaggtg	atcaagaaat	aacagaagtt
msa252229.2{114_M732}	agcttggctc	tgttacagat	attgaaggtg	atcaagaaat	aacagaagtt
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	agcttggctc	tgttacagat	attgaaggtg	a-----	-----
msa252229.2{114_JM9130013}	agcttggctc	tgttacagat	attgaaggtg	atca-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	agcttggctc	tgttacagat	attgaaggtg	atcaagaaat	aacagaagtt
msa252229.2{114_2603}	agcttggctc	tgttacagat	attgaaggtg	atcaagaaat	aacagaagtt
msa252229.2{114_H36B}	agcttggctc	tgttacagat	attgaaggtg	atcaagaaat	aacagaagtt
msa252229.2{114_18RS21}	agcttggctc	tgttacagat	attgaaggtg	atcaagaaat	aacagaagtt
msa252229.2{114_1169NT}	agcttggcct	tgttacagat	attgaaggtg	atcaagaaat	aa-----
Consensus	-----	-----	-----	-----	-----
	601				636
msa252229.2{114_COH1}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M732}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	-----	-----	-----	-----	-----
msa252229.2{114_JM9130013}	-----	-----	-----	-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_2603}	tttgcagatg	ttgaaaaagc	gttgctagaa	ctcaaa	-----
msa252229.2{114_H36B}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_18RS21}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_1169NT}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
Consensus	-----	-----	-----*****	*****	-----

SEQ ID NO. 4312: 2603 V/R STRAIN
MNLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVP
DEVINGVKERLAEDDIAEKGFLLDGYPRTEIQAHALDATALBELGLRLDGVINIKVDPSC
LIERLSKRIINRKTGETFHKVFNPVVDYKBEEDYQREDDKPEVTKRRLDVNIAQGEPILE
HYRKLGLVTDIEGNQETEVFADVEKALLELK

SEQ ID NO. 4313: 090 STRAIN
NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRTEIQAHALDATALBELGLRLDGVINIKVDPSC
IERLSGRIINRKTGETFHKVFNPVVDYKBEEDYQREDDKPEVTKRRLDVNIAQGEPILEH

Table 43: Comparative Sequences relating to SAG0079

YRKLGLVTDIEGNQEI TEVFADVEKALLELK

SEQ ID NO. 4314: 1169NT STRAIN
GKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDPQVTNGIVKER
LAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPSCLIERLSGRI IN
RKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVHIAQGEPILEHYSKLGLVTDI
EGNQEI

SEQ ID NO. 4315: 18RS21 STRAIN
NLLTTGSPGAGKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDP
EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPSCL
IERLSGRI INRKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVNIAQGEPILEH
YRKLGLVTDIEGNQEI TEVFADVEKALLE

SEQ ID NO. 4316: A909 STRAIN
NLLIMGLPGAGKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDP
EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPSCL
IERLSGRI INRKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVNIAQGESILEH
YRKLGLVTDIEG

SEQ ID NO. 4317: A909 STRAIN
NLLIMGLPGAGKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDP
EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPSCL
IERLSGRI INRKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVNIAQGESILEH
YRKLGLVTDIEG

SEQ ID NO. 4318: CJB110 STRAIN
NLLTTGLLGAGKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDP
EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPSCL
IERLSGRI INRKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVNIAQGEPILEH
Y

SEQ ID NO. 4319: COH1 STRAIN
LLIMGLPGAGKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDPDE
VTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPTCLI
ERLSGRI INRKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVNIAQGEPILEHY
RKLGLVTDIEGNQEI TEVFADVEKALLE

SEQ ID NO. 4320: H36B STRAIN
GDMFRAAMANQTEMGRLA KSYIDKGELVDPDEVTNGIVKERLAEDDIAEKGFLLDGYPR TIE
QAHALDATLEELGLRLDGVINI KVDPSCLIERLSGRI INRKTGETFHKVFNPPVDYKEE
DYQREDDKPE TVKRRRLDVNIAQGESILEHYRKLGLVTDIEGNQEI TEVFADVEKALLE

SEQ ID NO. 4321: JM9130013 STRAIN
NLLIMGLPGAGKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDP
EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPSCL
IERLSGRI INRKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVNIAQGEPILEH
YKKGVLVTDIEGN

SEQ ID NO. 4322: M732 STRAIN
LLIMGLPGAGKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDPDE
VTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPTCLI
ERLSGRI INRKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVNIAQGEPILEHY
RKLGLVTDIEGNQEI TEVFADVEKALLELK

SEQ ID NO. 4323: M781 STRAIN
NLLITGLPGAGKGTQAAKIVEEFGVAHI STGDMFRAAMANQTEMGRLA KSYIDKGELVDP
EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINI KVDPTCL
IERLSGRI INRKTGETFHKVFNPPVDYKEEDYYQREDDKPE TVKRRRLDVNIAQ

MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa32357.2{*} April 17, 2002 09:17 ..

Table with 5 columns: Accession, Position 1, Position 50, Position 100, Position 150. Rows include sequences for 18RS21, M781, CJB110, A909, 1169NT, M732, COH1, H36B, and a Consensus line.

Table with 5 columns: Accession, Position 51, Position 100, Position 150, Position 200. Rows include sequences for 18RS21, M781, and CJB110.

Table 43: Comparative Sequences relating to SAG0079

msa252352.2{114_090}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_JM9130013}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_A909}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_1169NT}	SYIDKGELVP	DqVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_2603}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_COH1}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_M732}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_H36B}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
Consensus	*****	*..*****	*****	*****	*****
	101				150
msa252352.2{114_18RS21}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_M781}	LEELGLRLDG	VINIKVDpTC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_CJB110}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_090}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_JM9130013}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_A909}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_1169NT}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_2603}	LEELGLRLDG	VINIKVDPsC	LIERLSxRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_COH1}	LEELGLRLDG	VINIKVDpTC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_M732}	LEELGLRLDG	VINIKVDpTC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_H36B}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
Consensus	*****	*****	*****	*****	*****
	151				200
msa252352.2{114_18RS21}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M781}	EDYYQREDDK	PETVKRRLDV	nIAQ-----	-----	-----
msa252352.2{114_CJB110}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hy-----	-----
msa252352.2{114_090}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_JM9130013}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hykklglvtd	iegn-----
msa252352.2{114_A909}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	ieg-----
msa252352.2{114_1169NT}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hysklglvtd	iegnqei---
msa252352.2{114_2603}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_COH1}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M732}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_H36B}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	iegnqeitev
Consensus	*****	*****	*****	*****	*****
	201				212
msa252352.2{114_18RS21}	fadvekalle	--			
msa252352.2{114_M781}	-----	--			
msa252352.2{114_CJB110}	-----	--			
msa252352.2{114_090}	fadvekalle	LK			
msa252352.2{114_JM9130013}	-----	--			
msa252352.2{114_A909}	-----	--			
msa252352.2{114_1169NT}	-----	--			
msa252352.2{114_2603}	fadvekalle	LK			
msa252352.2{114_COH1}	fadvekall-	--			
msa252352.2{114_M732}	fadvekalle	LK			
msa252352.2{114_H36B}	fadvekal--	--			
Consensus	-----	**			

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SEQ ID NO. 4401
STRAIN 2603
 GTGGATAAACATCACTCAAAAAGGCTATTTTAAAGTTAACA
 CTTATAACAACCTAGTATTTTATTATGTCATAGCAATCAAGTGAATGCAGAGGAGCAAGAA
 TTAATAAACCAAGAGCAATCACCTGTAATTTGCTCAACAGCCATCGCCATCG
 GTAACCTACTAATCTGTTGAAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGCG
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATATTAGAAAGAG
 TTATCTAAAAACCTTGATACGCTTAATTTGGGGGCTGATCTTGAAGAAAGAAATATCCCTCT
 AAACCCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAATGCTTCACTGCAATA
 GCACAGAAAGTTCCTCAGCATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGCT
 GTTCTTGATACATCTAAAATAACAAAAATTAACAAGCCATAACCAAGAGGAAAGGGAAAT
 GTAGTAGCTATTATGATACCTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATAGC
 CCAAAAGATGATAAGCACAGCTTTAAAACCTAAGACAGAAATTTGAGGAATTAAGAAAGCAAAA
 CATAATATCACTTATGGGAAATGGGTTAACGATAAGATTTGTTTTGACATAACTACGCC
 AACATACAGAAACCGTGGCTGATATTCAGCAGCTATGAAAGATGGTTATGGTTAGAA
 GCAAAAGAAATATTTCCGATGGTACACAGCTTGTGGTATTTTGTAGGTAATAGTAAACGT
 CCAGCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAAATG
 CGTATTCAGATAAAATTTGATTTCGGACAAAATTTGGTGAAGCATATGCTAAAAGCAATCACA
 GACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAGTATTTGAAAAACAGCTGATTTCT
 TTAATGCTCTCAATGATAAAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAAGGGCGTT
 GCAGTTGTTGCTGCGCGAAATGAAGCGCATTTGGTATGGATATAGCAAAACCAATTA
 TCAACTAATCCTGACTACGGTAAATAGTCCAGCTATTTCTGAAGATACCTTTGAGT
 GTTGCTAGCTATGAACTCACTTAAAACCTATCAGTGAGGTGCTGAACAACCTATTGAAGGT
 AAGTTAGTTAAGTTGCCGATTTGTACTTCTAAACCTTTTGACAAAAGGTAAAGCCCTACGAT
 GTGGTTTATGCCAATTTATGGTGCAAAAAAGACTTTGAAGTTAAGGACTTTAAAGGTAAG
 ATTGCATTAATTTGAGCGTGGTGGTGGACTTGATTTATGACTAAAATCACTCATGTCTACA
 AATGCAGGTGTTGTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGAAATTTCTTA
 ATTCTTACCGTGAATCACCTGTGGGATTTATAGTAAAGTAGATGGCAGCGTATAAAA
 AATACTTCAAGTCAGTTAAACATTTAACCCAGAGTTTGAAGTAGTTGATAGCCAAAGTGGT
 AATCGTATGCTGGAACAATCAAGTTGGGGCGTGCAGCTGAAGGAGCAATCAAGCCCTGAT
 GTAACAGCTTCTGGCTTTGAAATTTATTTCTTCAACCTATAAATAATCAATCAAAACAATG
 TCTGGTACAAAGTATGGCTTACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCAT
 TTGGCTGAGAAATATAAAGGGATGAATTTAGATTTCAAAAAATTTGCTAGAAATTTCTAAA
 AACATCCTCATGAGCTCAGCAACAGCATTAATAGTGAAGAGGATAAGGCGTTTATTCA
 CCACGTCAGCAAGTGGCAGGTGATGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTAT
 ATTACTGGAACCATGGCAAGCTAAAATTAATCTCAAAACCAATGGGAGATAAATTTGAT
 ATCACAGTTACAATTTATAAACTTTGTAGAAGGTGTTCAAAGAAATTTGATTTATCAAGCTAAT
 GTAGCAACGAAACAGTAAATTAAGGTAATTTGCCCTTAAACCAAGCCCTTGTCTAGAT
 ACTAATTTGGCAGAAAGTAATTTCTCGTATAAAGAAACCAAGTTGATTTACTATTGAT
 GCTAGTCAATTTAGTCAAGAAATTAAGAAACAGATGGCAATGGTTATTTCTTAGAAGGT
 TTTGATCGTTTAAAGAAAGCAAGGATAGTAAATCAGGAGTTAATGAGTATTCCTTTTGTGA
 GGATTTAATGGTATTTTGGCAACTTACAAGCACTTGAACACCCGATTTATAAGAGCGCTT
 TCTAAAGGTAGTTTCTACTATAACCAATGATACAATCATAAAGACCAATTTGGAGTAC
 AATGAATCAGCTCCTTTTGAAGCAACAACCTATACTGCTTGTTAACAACAATCGCTCT
 TGGGGCTATGTTGATTTATGTCAAAATGGTGGGAGTTAGAAATAGCACCCGAGAGTCCA
 AAAAGAAATTTTGGAACTTTTGGAAATTAAGTTGAGGATAAACAACATTCATCTTTTG
 GAAAGAGATGCAGCGAATAATCCATATTTGCCATTTCTCCAATAAAGATGGAATAGG
 GACGAAATCACTCCCGAGCAACTTTCTTAAGAAATTTAAGGATATTTCTGCTCAAGTT
 CTAGATCAAAATGGAAATGTTATTTGGCAAGTAAAGTTTACCATCTTATCGTAAAT
 TTCCATTAATTAATCCAAGCAAGTGTGGTCAATTCATCGTATGGATGCTTCTCAGTGGAGT
 GGTATGATTAAGGATGGCAAGTTGTAGCAGATGGTTTTATACTTATCGCTTACGTTAC
 ACACAGTAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTAAAGTACAAGTAAGTACT
 AAGTCAACCAATCTTCTTACAGCTCAGTTTGTATGAACTAATCGAACATAAAGCTTA
 GCCATGCTAAGGAAAGTAGTTATGTTTCTACATATCGTTTACAAATAGTATTTATCTCAT
 GTTGTAAAAGATGAAGAAATATGGGATGAGACTTCTTACCATTATTTCCATATAGATCAA
 GAAGTTAAGGTGACACTTCTTAAACCGTTAAGATAGGAGAGAGTGAAGTTGCGGTAGAC
 CCTAAGGCCTTGACACTTGTGTTGGAAGATAAGCTGTAATTTGCAACCGTAAAATTTG
 TCGATCTCTGAAATAGGCAAGTATCAGAGAAAAGAAACGCTATAGTAAATTTCTAAC
 AGTTTCAAAATATTTGATAACTTGAATAAAGAACTATGTTTATTTCTAAAAAGAAAA
 GTAGTAAACAAGAAATCTAGAAGAAATTAATTTAGTTAAGCCGCAACTACAGTTACTACT
 CAATCATTTCTAAAGAAATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTCAACAAC
 AATAATAGTACAGAGTAGCTAAGATCATATCACTAACAATAACGGGGATTTCTGTTAAC
 CATACTTACCTAGTACATCAGATAGAGCAACCAATGGTCTATTTGTTGGTACTTTGGCA
 TTGTTATCTAGTTTACTTCTTTATTTGAAACCCAAAAGACTAAAAATAATAGTAAA

SEQ ID NO. 4402
STRAIN 090
 GAGGAGCAAGAAATTAATAAACCAAGAGCAATCACCTGTAATTGCT
 AATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATGTTGAAAA
 AACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGTGAAGAAATGGGTG
 ATACATCTGTAAAAAATGACAAAACAGAAGATGAATATTAGAAAGATTA
 TCTAAAAACCTTGATACGCTTAATTTGGGGGCTGATCTTGAAGAAAGATA
 TCCCTTAAACCCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAA
 ATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCGTATGAAGAGGTG
 AAGCCAGAAAGCAAGTCATCGCTTGTCTTTTGTATACATCTAAAATAAC
 AAAATGCAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGCTATTA
 TTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATAGCCCA
 AAAGATGATAAGCACAGCTTTAAAACCTAAGCAGAAATTCGAGGAAATTA
 AGCAAAACATAATCACTTATGGGAAATGGGTAAACGATAAGATTGTTT
 TTGCACATAACTACGCCAACAAATACAGAAACGGTGGCTGATATTGCAGCA
 GCTATGAAAGATGGTTATGGGTGAGAAAGCAAGAAATTTTCGCATGGTAC
 ACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTTCCAGCAATCAATG
 GTCTTCTTTTAGAAGGTGCAGCGCAATGCTCAAGTCTTATTAAATGGCT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATTCCAGATAAAAATTGATTCCGACAAAATTGGAGAAGCATATGCTAAAGC
AATCAGCAGACCGTGTAACTTAGGAGCAAAAaCGATTAATATGAGCCCTTG
GAAAAACAGCAGATTCTTTAAAttGCaCTCAATGATAAAGTTAAATTAGCA
CTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGAAA
TGAAGGTGCATTTGGTATGGATTATAGCAAACCATATCAACTAAATcCTG
ACTACGGTACGGTTAAATAGTCCAGCTATTTCTGAAGATACTLTGAGTGT
GCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACAACAT
TGaaGGTAAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTTtGACA
AAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGCAaaaaAAGAC
TTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATtGAGCGTGGtGG
TGGACTTGAATTTTATGACTAAaatCACTcATGCTACAAATGCAGGTGTTG
tTGGTATCGTtATtTtTAACgAtCAAGAaaAACGtGGAATTTTcTAAT
CCTTACCCTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGGCGAGCG
TATAAAAAATACTTCAAGTCAGTTAACATTTAACAGAGTTTtGAAAGTAG
TTGATAGCCAAGGTGGCAATCGTATGCTGGAAACATCAAGTTGGGGCGTG
ACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAAT
TTATTTCTCAACCTATAATAATCAATACCAAAACATGTCTGGTACAAGTA
TGGCTTACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCATTTG
GCTGAGAAATATAAAGGGATGAATTTAGATTCTTAAAAAATGTCTAGAAAT
GTCTAaaAACATCCTCATGAGCTCAGCaCAGCATTATATAGTgAAGAgG
ATAAGGCGTtTtATtCaCCAGTCAGCAAGGtGCAGGtGTAGTTGATGCT
GAAAAAGCTATCCAAGCTCAATATTTATGTTACTGGAAACGATGGCAAAGC
TAAAAITAACTCAAAACGAGTGGGAGATAAAATTTGATATCACAGTTACAA
TTCATAAACTTGTAGAAGGTGTCAAAGAAATGTATATCAAGCTAATGTA
GCAACAGAACaAGTAAATAAAGGTAATTTGCCCTTAAACCAACAAGCctT
GCTAGATACTAATTGGCAGaaAGTAATTTCTtCGTGATAAAGAAACACAAG
TTcGATTTACTATTTGATGCTAGTCAATTTAGTCAGAAATTTAAAGAAACAG
ATGGCAAATGGTTATTTCTTAgAAGGTTTGTACGTTTAAAGAAGCCAA
GGATAGtAAATCAGGAGTTAaTGAGTATTCCTTTGTAGGATtLAATGGTG
ATTTTGGCAACTTACAAGCACTTGAACACCGATTTATAAGACGCTTTCT
AAAGGTAGTTTCTACTATAAACCAAAATGATACAACCTATAAAGCCAAAT
GGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACGCTCTGT
TAACCAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATGGTGGG
GAGTTAGAAATTAGCACCGGAgAGTcCAAAAAGAATTTATTTTAgGAACTTT
TGAGAATAAAGGTTGAGGATAAAAACAATTCATCTTTTGGAAAGAGATGCAG
CgAATAATCCATATTTGCCATTTCTCCAAATAAAGATGGAATAAGGGAT
GAATCACTCCCAGGCACTTTCTTAAGAATGTTAAGGATATTTCTGCG
TCAAGTTCTAGATCAAAATGGAATGTTATTTGGCAAAGTAAGGTTTTAC
CATCTTATCGTAAAAATTTCCATAAATCAAAAGCAAAGTGATGGTCAT
TATCGTATGGATGCCTTTTCAGTGGAGTGGTTTAGATAAGGATGGCAAAGT
TGTAGCAGATGGTTTTTATACCTTATCGCCTACGTTACACACAGTAGCAG
AAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAAG
TCACCAATCTTCTTTACTAGCTCAGTTTGTATGAACTAATCGAACATTT
AAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTTCTTACATATCGTTTTAC
AATTAGTTTTATCTCATGTTGTAAAAAGATGAAGAATATGGGGATGAGACT
TCTTACCATTATTTCCATATAGATCAAGAAGGTAAGTGCACTTCCTTAA
AACGGTTAAGATAGGAGAGAGTGGGTTGCAGTAGACCTTAAGGCCATTTGA
CACTGTTGTGGAAAGATAAGCTGGTAATTTTGCACCGGTAATTTGTCT
GACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATAGTAAT
TTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAGAATCTATGTTTA
TTTTCTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAAATAACATTA
GTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGCTAAAGAATAAAC
TAAATCAGGAAATGAGAAAGTCTCTCACTTCTACAAACAATAATAGTAGCA
GAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCAT
ACC

SEQ ID NO. 4403

STRAIN A909

GAGGAGCAAGAAITAAAAAACAAGAGCAAT
CACCTGTAATTTGCTAAATGTTGCTCAACAGCCATCGCCATCGGTAACACT
AATACTGTTGAAAAAACAATCTGTAAACATCTGCTTCTGCTAGTAATAACAGC
GAAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAAT
TATTAGAAGAGTTATCTAAAAACCTTGATACGTCATAATTTGGGGCTGAT
CTTGAAGAAGAATATCCCTCTAAACAGAGACAACCAACAATAAAGAAG
CAATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTCCCTCAG
CATATGAAGAGTGAAGCCAGAAAGCAAGTCATCACTTGTGTTCTTGTAT
ACATCTAAAATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAA
TGATGAGCTATTTGATGACTGGCTTTGATATTAACCATGATATTTTTC
GTTTAGATAGCCCAAAAGATgaTAAGCACAGCTTTAAaACTAAGGCAGAA
TTTGAGGAATTAAGCAAAACATAATATCACTTATGGGAAATGGGTTAA
CGATAAGATTGtTTTTGCACATAACTACGCCaaCAATACAGAAACGGTGG
CTGATATTGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAT
ATTTCCGATGGTACACAGTGTGCTGGTATTTTGTAGGTAATAGTAAAGC
TCCAGCAATCAATGGTCTTCTTTAGAAGGTGCAGCGCAAAATGCTCAAG
CTTATTAATGCGTATTTCCAGATAAAAATTGATTCGGCAAAAATTTGGTGAA
GCATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGAT
TAATATGAGCCTTGGAAAAACAGCAGATTCTTTAATTGCTCTCAATGATA
AAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTT
GTGGCTGCCGAAATGAAGGTGCATTTGGTATGGATTATAGCAAACCAT
ATCAAATACTCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAG
ATACTTTGAGTGTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTC
GTTGAAACAACATTTGAAGGTAAGTATAGTTAAGTTGCCGATTGTGACTTC
TAAACCTTTTGACAAAGGTAAGCCCTACGATGTGGTTTATGCCAATTATG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GTGCAAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATT
AAITGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTA
CAAATGCAGGTGTTGTTGGTATCGTTAATTTTAAACGATCAAGAAAAACGT
GGAATTTTCTAATTCCTTACCGTGAATACCTGTGGGGTTATAGTAA
AGTAGATGGCGAGCGTATAAAAAATACCTCAAGTCAGTTAACATTTAAC
AGAGTTTTGAAGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAACAA
TCAAGTTGGGGCGTACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGC
TTCTGGCTTTGAAATTTATTTCTCAACCTATAATAATCAATACCAACAA
TGTCCTGGTACAGTATGGCTTACCACATGTGTCAGGATTAATGACAAATG
CTTCAAAGTCATTTGGCTGAGAAATAAAGGATGAATTTAGATTCTAA
AAAATTGCTAGaATTGTCTAAAACATcCTCATGAGCTCAGCAACAGCAT
TATATAGTGAAGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGTGCA
GGTGTAGTTGATGCTGAAAAAGCTATCCAAGCTCAATATATGTTACTGG
AAACGATGGCAAAGCTAAAATTAATCTCAAACGAGTGGGAGATAAATTTG
ATATCACAGTTACAATTCATAAATTTGTAAGAGGTGTCAAAGAAATTTGAT
TATCAAGCTAATGTAGCAACAGAACAGTAAATAAAGGTAATTTGCCTT
TaAACCaCAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTGCTG
ATAAAGAAACACAAGTTCCGATTACATATGATTCTAGTCAATTTAGTCAG
AAATTAAGAAACAGATGGCAATGTTATTTCTTAGAAGGTTTTGTACGG
TTTTAAAGAAAGCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTG
TAGGATTTAATGGTATTTTGGCACTTACAAGCACTTGAACACCGGATT
TATAAGAGCCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAAC
TCATAAAGACCAATTTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACA
ACTATATGCTCTGTAAACACAATCAGCGCTTTGGGGCTATGTTGATTAT
GTCAAAAATGGTGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAAAT
TATTTTAGGAACCTTTGAGAATAAGGTTGAGGATAAAAACAAATTCATCTTT
TGGAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCCCAAATAAA
GATGAAATAGGGATGAAATCACTCCCAGGCAACTTTCTAAGAAATGT
TAAGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAATGTTATTTGGC
AAAGTAAGGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAG
CAAAGTGATGGTCATTTATCGTATGGATGCCCTTCAGTGGAGTGGTTAGA
TAAGGATGGCAAAGTTGTAGCAGATGGTTTTTATACTTATCGTTACGTT
ACACACCGTAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTAAGGTT
CAAGTAAGTACTFAAGTCACCAAACTTCTCCTCAGGAGCTCAGTTGATGA
AACTAATCGAACATTAAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTT
CTACATATCGTCTACAATTAGTTTATCTCATGTTGTAAGAAAGTAGAGAA
TATGAGATGAGAGCTTCTTACCATTAATTTCCATATAGATCGAGAAGTAA
AGTGACACTTCTTAAACAGTAAAGTAGGAGAGAGTGGGTTGAGTAG
ACCCTAAGACCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTCCGA
ACGGTAAAATTTGCTGACCTCTGGAATAAGGCAGTAGTATCAGAGAAAGA
AAACGCTATAGTAATTTCTAACAAATTTCAAATATTTTGATAACTTGAAA
AAGAACCTATGTTTATTTCTAAAAGAAAGAAAGTAGTAACCAAGAACTA
GAAGAAATAGCATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCAT
GTCTAAGAAATAAATCAATCAGGAAATGAGAAAGTCTCACTTCTACAA
ACAATAATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGG
GATTTCTGTTAACCATACC

SEQ ID NO. 4404

STRAIN H36B

GAGGAGCAAGAATTA AAAAACAAGAGCAATCACCTGTAATTGC
TAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATACTGTTGAAA
AAACATCTGTAAACATCTGCTTCTGCTAGTAATACAGCGAAAGAAATGGGT
GATACATCTGTAAAAATGACAAAACAGAAAGATGAATTTATGAAAGATT
ATCTAAAAACCTTGATACGTCATAATTTGGGGCTGATCTTGAAGAAGAAAT
ATCCCCTCAAAACAGAGACAAACCAATAAAGAAAGCAATGTAGTAACA
AATGCTTCAACTGCAATAGCACAGAAaGTTCCTCAGCATGAAAGAGGT
GAAGCCAGAAGCAAGTCATCACTTGTGTTCTTGATACATCTAAAATAA
CAAATTTGCAAGCCATAACCCAAAGAGGAAAGCGAAATCTAGTAGCTAAT
ATTGATACTGGCTTTGATATTAACCATGATAATTTTCGTTTAGATAGCCC
AAAAGATGATAAGCACAGCTTTAAAACTAAGGCAGAAATTTGAGGAATTA
AAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAAGATTGTT
TTTTGCATAACTACGCCAAaCAATACAGAAACGGTGGCTGATATTGCAGC
AGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAATATTTGCGATGGTA
CACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAGCAATCAAT
GGTCTTCTTTAGAAGGTGACAGCGCAAAATGCTCAAGTCTTATTAATGCG
TATTTCCAGATAAAAATGATTCGGCAAAATTTGGTGAAGCATATGCTAAAAG
CAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAGCCTT
GSAAAAACAGCAGATTCTTTAATTGCTCTCAATGATAAAGTTAAATTAGC
ACTTAAATTAGCTTCTGAGAAGGGCTTGCAGTTGTTGGCTGCGCGAA
ATGAAGGTGCATTTGGTATGGATTATAGCAAACCAATATCACTAATCCT
GACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGTACTTTGAGTGT
TGCTAGCTATGAATCACTTAAAACATCAGTGAGGTCGTTGAAAACACTPA
TTGAAGGTAAAGTTAGTTAAGTTGCCGATTGTGACTCTAAAACCTTTGAC
AAAGGTAAGGCCTACGATGTGGTTATGCCAATTAATGGTCAAAAAAAGA
CTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCGTGGT
GTGGACTTGAATTTATGACTAAAAATCACTCATGCTACAAATGCAGGTGTT
GTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGAAATTTCTAAT
TCTTACCCTGAATTAACCTGTGGGGGTTATAGTAAGTAGATGGCGAGC
GTATAAAAATACTTCAAGTCAGTTAACATTTAACAGAGTTTGAAGTA
GTTGATAGCCAAAGGTGGCAATCGTATGCTGGAACCAATCAAGTTGGGGCGT
GACAGCTGAAGGAGCAATCAAGCCTGATGTAAACGCTTCTGGCTTTGAAA
TTTATTTCTCAACCTATAATAATCAATACCAACCAATGTCTGGTACAGT
ATGGCTTCAACCATGTTGAGGATTAATGACAATGCTTCAAAGTCATTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGCTGAGAAATAFAAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAAT
 TGCTFAAAAACATCCCTCATGAGCTCAGCAACAGCATTATATAGTGAAGAG
 GATAAGGCGTTTTATTCCACCACGTCAGCAAGGTGCAGGTGATGTTGATGC
 TGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAAG
 CTAATAATTAATCTCAAACGAGTGGGAGATAAATTTGATATCACAGTTACA
 ATTCATAAACTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGT
 AGCAACGAAACAGTAAATAAAGGTAATTTGCCCTTAAACCcAAGCCT
 TGCTAGATACTAATTTGGCAGAAAGTAAATCTTCGTGATAAAGAAACACAA
 GTTCGATTTACTATTGATTTAGTCAATTTAGTCAGAAATTTAAAAGACA
 GATGGCAAATGGTTATTTCTTAGAAGGTTTGTACGTTTAAAGAAGCCA
 AGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATTTAATGGT
 GATTTTGGCAACTTACAAGCACTGAAACCCGATTTATAAGACGCTTTC
 TAAAGTAGTITTTACTATAAACCAAATGATACAACTATAAAGACCAAT
 TGGAGTACAATGAATCAGCTCCTTTTGAAGCAACCACTTACTGCCCTG
 TTAACCAATCAGCGCTCTGGGGCTATGTTGATTAATGTCAAAAATGGTGG
 GGAGTTAgAATTAgCACCCGAGAGTCCAAAAGAATTATTTAGGAACCTT
 TTGAGAAATAGGTTGAGGATAAAAACAATTCATCTTTGGAAAGAGATGCA
 CGGAATAATCCATATTTGCCATTTCTCAAATAAAGATGGAAATAGGGA
 TGAATCACTCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTG
 CTCAGTTCTAGATCAAAATGGAATGTTAATTTGGCAAAGTAAGGTTTAA
 CCATCTTATCGTAAAAAATTTCCATAATAATCCAAAGCAAAGTGTGGTCA
 TTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAGATAAGGATGGCAAAG
 TTGTAGCAGATGGTTTTTATACTTATCGTTTACGTTACACACCACTAGCA
 GAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAA
 GTCACCAAATCTCCTTCAAGGCTCAGTTTGTGAACTAATCGAACAT
 TAAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTTCTACATATCGTCTA
 CAATAGTTTATCTCATGTTTGTAAAAGATGAAGAATATGGAGATGAGAC
 TTCTTACCATTAATTTCCATATAGATCAAGAAGGTAAAGTGACACTTCTTA
 AAACAGTTAAGATAGGAGAGAGTGGGTTGCACTAGACCCCTAAGACCTTG
 ACACCTGTTTGGAAAGATAAAGCTGGTAATTTTCGCAACCGTAAAAATGTC
 TGACCTTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATAGTAA
 TTTCTAACAATTTCAAATATTTGATAACTTGAATAAAGAACCTATGTTTT
 ATTTCTAAAGAAGGAAAAGTAGTAAACAAGAACTAGAGAATAATGCAAT
 AGTTAAGCCGCAACTACAGTTACTACTCAATCATTTGTCTAAAGAATAAA
 CTCATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAGTAGC
 AGAGTAGCTAAGATCATATCACCTAAAACATAACGGGGATTTCTGTTAACCA
 TACC

SEQ ID NO. 4405

STRAIN 18RS21

GAGGAGCAAGAAATAAAAAACCAAGAGCAATCACC
 TGTAAATGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACTAATA
 CTGTTGAAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAACTACAGCGAAA
 GAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTAAT
 AGAAGAGTTATCTAAAAACCTTGATACGTTCTAATTTGGGGGCTGATCTTG
 AAGAAGATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAAT
 GTAGTAACAAATGCTTCAAATGCAATAGCACAGAAAGTTCCCTCAGCATA
 TGAAGAGGTGAAGCCAGAAAGCAAGTCACTCGCTTGTGTTCTTGATACAT
 CTAATAATACAAAAATTACAAGCCATTAACCAAGAGGAAAGGAAATGTA
 GTAGCTATTAATGATACTGGCTTTGATATTAAACATGATATTTTCGTTT
 AGATAGCCCAAAGATGATAAGCAAGCTTTAAAACTAAGACAGAATTTG
 AGGAATTAAGCAAAAACATAATATCACTTATGGGAAATGGGTTAACGAT
 AAGATTGTTTTGACATAAATACGCAACAATAACAGAAACCGTGGCTGA
 TATTGACGAGCTATGAAAGATGGTTATGTTTCAAGCAAGAAATATTT
 CGCATGGTACACAGCTTGTGTTATTTTGTAGGTAATAGTAAACGTTCCA
 GCAATCAATGTTCTTTTAGAAGGTGACAGCCCAATGCTCAAGTCTT
 ATTAATGCGTATTCAGATAAAATGATTCCGCAAAATTTGGTGAAGCAT
 ATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAAT
 ATGAGTATTTGAAAAACAGCTGATTTCTTAATGCTCTCAATGATAAAGT
 TAAATTAGCACTTAAATTAGCTTCTGAGAAGGGGCTGCAAGTTGTTGGG
 CTGCCGAAATGAAGGCGCATTTGGTATGGATATAGCAACCAATATCA
 ACTAATCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATAC
 TTTGAGTGTGCTAGCTATGAATCACTTAAAACTACAGTGAAGTCTGTTG
 AAACAACATATTGAAGGTAAGTTAGTTAAGTTGCCGATTTGACTTTCTAAA
 CCTTTTGACAAAGGTAAGGCTACGATGTTGTTATGCCAATATGGTGC
 AAAAAAGACTTTGAAGGTAAGGACTTTAAGGTAAGATGCAATTAATG
 AGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAT
 GCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGGAA
 TTTTCTAATTTCTTACCCTGAATTAACCTGTGGGATTTATAgTAAAGTAG
 ATGGCGAGCGTATAAAAAATCACTCAAGTCAAGTAAACATTAAACAGAGT
 TTTGAAGTAgTTGATAGCCAGGTGGTAACTCGTATGCTGGAACAATCAAG
 TTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTG
 GCTTTGAAATTTATTTCTCAACCTATAATAATCAATACCAaCAATGTTCT
 GGTACAAGTATGGCTTCAACACATTTGACAGGATTAATGACAATGCTTCA
 AAGTCATTTGGCTGAGAAATATAAAGGATGAATTTAGATTTCTAAAAAAT
 TGCTAGAATTGTTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATAT
 AGTGAAGAGGATAAGGCGTTTTATTCACCAGCTCAGCAAGGTGAGGTTGT
 AGTTGATGCTGAAAAAGCTATCCAAGCTCAATATATATTTACTGAAACG
 ATGGCAaAGCTAAAAATTAATCTCAAACGAAATGGGAGATAAATTTGATATC
 ACAGTTACAATTCATaAACTTGTAGAAGGTGTCAAAGAATTGTATTATCA
 AGCTAATGTAGCAACAGAAACAAGTAAATAAAGGTAATTTGCCCTTaaAC
 CACAAGCCTTGTAGATACATAATTTGGCAGAAGTAATTTCTTcGTGATAAA
 GAAACCAAGTTCCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AAAAGAACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTA
AAGAAGCCAAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGA
TTTAATGGTGATTTTGCGAACCTTACAAGCACTTGAACAACCGATTATAA
GACGATTTCTAAAGGTAGTTTCTACTATAAACCAAAATGATACAACCTATA
AAGACCAATGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATAT
ACTGCCTTGTAAACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAA
AAATGGTGGGGAGTTAGAAATAGCaCCGGAGAGTCCAAAAAGAAATTTT
TAGGAACTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTGGAA
AGAGATGCAGCGAATAATCCATATTTGGCAATTTCTCCAAATAAGATGG
AAATAGGGACGAATCACTCCCAGGCAACLTCTTAAGAAATGTTAAGG
ATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGT
AAGGTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAG
TGATGGTCATTATCGTATGGATGCTCTCAGTGGAGTGGTTAGATAAGG
ATGGCAAAGTTGTAGCAGATGGTTTTTATACCTTATCGCTTACGTTACACA
CCAGTAGCAGAAGGAGCAATAGTCAAGGAGTCAAGCTTTAAAGTACAAGT
AAGTACTAAGTCAACCAATCTTCTTCAAGAGCTCAGTTTGTGAACTA
ATCGAACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACA
TATCGTTTACAATTAGTTTATCTCATGTTGTAAGATGAAGAAATAGG
GGATGAGACTTCTACCATTTTCCATATAGATCAAGAAGGTAAGTGA
CACTTCTAAAACGGTTAAGATAGGAGAGAGTGAAGTTGCGGTAGACCCT
AAGCCCTTGACACTTGTGTGGAAGATAAAGCTGGTAAATTCGCAACGGT
AAAAATGTCTGATCTCTGAATAAGGCAGTAGTATCAGAGAAGAAAACG
CTATAGTAAATTTCTAACAGTTTCAAATATTTTGATAACTTGA AAAAAGAA
CCTATGTTTATTTCTAAAAAAGAAAAGTAGTAAACAAGAACTAGAGA
AATAATATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTTCTA
AAGAAATACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAAT
AATAGTAGCAGAGTAGCTAAGATCATATCACTTAAACATAACGGGATTC
TGTTAACCATACC

SEQ ID NO. 4406

STRAIN M732

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCT
GTAATTTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACTAATAT
TGTTGAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGTGAAG
AAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTA
GAAGAGTTATCTAAAAACCTTGATACGCTAATTTGGGGCTGATCTTGA
AGAAGAAATATCCCTCTAAACCAAGAGCAACCAACAATAAAGAAGCAATG
TAGTAACAAATGCTTCAACTGCAATAGCACAGAAGTCCCTCAGCATAT
GAAGAGGTGAAGTCAAGAAGCAAGTCACTCGCTTGCTGTTCTTGATACATC
TAAATAACAAAAATFACAAGCCACAACCCAAGAGGAAAGGAAATGTAG
TAGCTATTTATGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTA
GATAGCCCAAAGATGATAAGCAAGCTTTAAAACCTAAGGCAAGAAATTA
GGAATTAAGAACAACATAATATCACTTATGGGAAATGGGTTAACGATA
AGATTGTTTTTGCACATAACTACGCCCAACAATACAGAACCGTGGCTGAT
ATTGCAGCAGCTATGAAAGATGGTTATGGGTCAAGAAGCAAGAAATATTTT
GCATGGTACACAGCTTGTCTGGTATTTTGTAGGTAATAGTAAACGCTCCAG
CAATCAATAGTCTTCTTTAGAAAGGTGCAGCCCAAAATGCTCAAGTCTTA
TTAATGCGTATFCCAGATAAAATGATTCGGACAAATTTGGAGAAGCATA
TGCTPAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATA
TGAGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTT
AAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTGTTGGC
TGCCGAAATGAAGGTGCATTTGGTATGGATTATAGCAAACCATTTATCAA
CTAATCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAAGTACT
TTGAGTGTGCTAGCTATGAATCACTTAAAACCTATCAGTGAAGTCTGTTGA
AACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTTGTGACTTCTAAAC
CTTTGACAAAGGTAAGGCTTACGATGTGGTTTATGCCAATTTAGGTTGCA
AAAAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTTGAG
CGTGTGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGC
AGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGAAATTT
TCTAATTTCTTACCGTGAATTAACCTGTGGGGGTTATTAGTAAAGTAGAT
GGCAGCGGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCCAGAGTTT
TGAAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAAACAATCAAGTT
GGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGC
TTTGAAATTTATTTCTCAACCTATAATAATCAATACTAAACAATGCTCTGG
TACAAGTATGGCTTACCACATGTTGCAGGATTAATGACAAATGCTTCAA
GTCAATTTGGCTGAGAAATAAAAAGGATGAATTTAGATTCTAAAAAATGG
CTAGAAATGCTTAAAAACATCTCATGAGCTCAGCAACAGCATTATATAG
TGAAGAGGATAAGGCGTTTATTCACCACCTCAGCAAGGTGCAGGTGTAG
TTGATGCTGAAAAAGCTATCCAAGCTCAATATTTACTGGAACCGAT
GGCAAAGTTAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCAC
AGTTACAATTCATaAACTTGTAGAAGGTGTCAAAGAAATTTGATATCAAG
CTAATGTAGCAACAGAAaCAAGTAAATAAAGGTAATTTGCCCTTAAACCA
CAAGCCTTGCTAGATACTAATTTGGCAGAAAGTAATTTCTCGTATAAAGA
AACCAAGTTTCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTA
AAGACAGATGGCAAATGGTTATTTCTTAGAAGGTTTGTACGTTTAAA
GAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGAT
TAATGGTGAATTTGCGAACCTTCAAGCACTTGAACAaCCGATTTATAAGA
CGCTTTCTAAAGGTAGTTTCTACTATAAACCAAAATGATACAACCTATAAA
GACCAATTTGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATAC
TGCTTTGTTAACCAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAA
ATGGTGGGGAGTTAGAAATTAGCACCGGAGAGTCCAAAAAGAAATTTATTA
GGAACTTTTGAAGAAATAGGTTGAGGATAAAACAATTCATCTTTTGAAG
AGATGCAGCGAAATAATCCATATTTTGCATTTCTCCAATAAAGATGGAA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATAGGGACGAAATCACTCCCAGGCACTTTCTTAAGAAATGTTAAGGAT
A11TTC1GCTCAAGTTC1TAGATCAAATGGAAATGTTATTGGCAAAGTAA
GGTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAGCAAAGTG
ATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGAT
GGCAAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTACACACC
AGTAGCAGAAGGAGCaAATAGTCAGGAGTCAGACTTTAAAGTTCAGATAA
GTACTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGTAGAACTAAT
CGAACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATA
TCGTTTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGGG
ATGAGACTTCTTACCATTAATTCATATAGATCAAGAAGGTAAGGTGACA
CTTCCTAAAACGGTTAAGATAGGAGAGAGTGGGTTGCGGTAGACCTAA
GGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCAACGGTAA
AATTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCT
ATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAAGACC
TATGTTTATTCTTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAA
TAACATTAGTTAAGCCTCAAACACTCAGTTACTACTCAATCATGTCTAAA
GAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTCAAAACAATAA
TAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTG
TTAACCATACC

SEQ ID NO. 4407

STRAIN COH1

GAGGAGCAAGAATTA AAAAACCAGGCAATCACCTGT
AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAaACTACTAATATTG
TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA
ATGGGcGATACATCTGTA AAAAATGACAAAACAGAAGATGAATATTAGA
AGAGTTATCTAAAAACCTTGATACGCTCAAATTTGGGGGCTGATCTTGAAG
AAGAATATCCCTCTAAACCAGAGaCAACCAACAATAAAGAAGCAATGTA
GTAACAATGCTTCACTGCAATAGCACAGAAAGTTCCTCAGCATATGA
AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGTCTTGTGATACATCTA
AAATAACAAAATTACAAGCCCAACCCAAAGAGGAAAGGGAAATGTAGTA
GCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGA
TAGCCCAAAAGATGATAAGCACAGCTTTAAAACCTAAGGCAGAAATTTGAGG
AACTAAAGCAAAAACATAAATATCACTTATGGGAATGGTTAACGATAAG
ATTGTTTTGACATAACTACGCCaCAATACAGAAACGGTGGCTGATAT
TGACAGAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAATAATTTTGC
ATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAGCA
ATCAATAGTCTTCTTTAGAGGTTGACAGCCCAATAGCTCAAGTCTTATT
AATGCGTATTCCAGATAAAAATGATTCGGACAATAATGGAGAAGCATATG
CTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAAATATG
AGCCTGGGAAAAACGGCTGATTCTTTAATTTGCTCTCAATGATAAAGTTAA
ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTGTGGCTG
CCGGAATGAAGGTGCATTGGGTATGGATTATAGCAAACCTTATCAACT
AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACFTT
GAGTGTGCTAGCTATGAATCACTTAAAACCTATCAGTGGGTGCTTGAAG
CAACTATTGAAGGTAAGTTAGTTAAGTTGCGGATTTGACTTCTAAACCT
TcTGACAAGGTAAGGCCTACGATGTGGTTTATGCCAATTTATGGTGCAAA
AAAGATTTTGAAGTAAGGACTTTAAAGGTAAGATGTCATTAAATGAGCG
TGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGCAAG
GTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAACCTGGAAATTTT
CTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGATGG
CGAGCGTATAAAAATACTTCAAGTCAGTTAAACATTTAAACAGAGTTTGTG
AAGTAGTTGATAGCCAAGTGGCAATCGTATGCTGGAACAATCAAGTTGG
GGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT
TGAAaTTTATCTTCAACCTATAATAATCAATACTAAACAATGTCTGGTA
CAAGTATGGCTTCAACCATGTTGCAGGATTAATGACAATGCTTCAAAGT
CAITTTGGCTGAGAAATATAAGGGATGAATTTAGATTCTAaAAAATTTGCT
AGaTTGCTCTAaAaACATCCTCATGAGCTCAGCAACAGCATTTATATAGT
AAGAGGATAAGGCGTTTTATTCCACCGTCAGCAAGGTGCAGGTGTAGTT
GATGCTGAAAAAGCTATCCAAAGCTCAATATATGTTACTGGAAACGATGG
CAAAGTTAAAATTAATCTCAAAACGAGAGGGAGATAAATTTGATATCACAG
TTACAATTCATaAACTTGTAAGAAGGTGTCRAAGAAATGATATATCAAGCT
AATGTAGCAaCAGAACAAGTAAATAAAGGTAATTTGCCCTTAAACCA
AGCCTTGCTAGATACTAATTTGGCAGAAAGTAAATTTCTcGTGATAAGAAA
CACAAGTTCGATTTACTAATTTGATGCTAGTCAATTTAGTCAGAAATTA AAA
GAACAGATGGCAAAATGGTTATTTCTTAGAAGGTTTGTACGTTTTTAAAGA
AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA
ATGGTGAATTTGCGAACTTACAAGCACTTGAACACCCGATTTATAAGAGC
CTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAATCTATAAAGA
CCAATTTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACTG
CCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTAATGTCAAAAAT
GGTGGGGAGTTAGAAATAGCACCGGAGAGTCCAAAAAGAAATTTATTTAGG
aACTTTTGAAGATAAGGTTGAGGATAAAAACAATTCATCTTTTGGAAAAG
ATGCAGCGAAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAAT
AGGACGAAATCACTCCCAGGCaACTTTCTTAAGAAATGTTAAGGATAT
TTCTGCTCAAGTCTTAGATCAAATGGAAATGTTAATTTGGCAAAGTAAGG
TTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAGCAAAAGTATG
GGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTAGATAAAGGATGG
CAAAGTTGTAgCAGATGGTTTTTATACTTATCGCTTACGTTACACACCAG
TAGCAGAAGGAGCAAAATAGTACAGGAGTCAGACTTTaAAGTTCAAGTAAGT
AcTAAGTCACCAAATCTTCCTTCACGAGCTCAGTTTGTAGaAACTAATCG
AAATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATATC
GTTTCAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTTAAAGTGACACT
TCCTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCTAAGG
CCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA
TTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT
AGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAGAAAGAACCTA
TGTTTTATTTCTAAAGAAGGAAAAGTAGTAAACAGAATCTAGAAGAAATA
ACATTAGTTAAGCCTCAAACACAGTTACTACTCAATCATTTGCTAAAAGA
AATAACTAAATCAGGAAATGAGAAAGTCCCTCACTTCTACAAACAATAATA
GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT
AACCATACC

SEQ ID NO. 4408

STRAIN M781

GAGGAGCAAGAAITFAAAAAACCAAGAGCAATCACCTGT
AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATTG
TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA
ATGGGTGATACACTCTGTAATAAATGACAAAACAGAGATGAATTTATAGA
AGAGTTATCTAAAACCTTGATACGTTCAATTTGGGGCTGATCTTGAAG
AAGAAATATCCCTCTAAACAGAGACAAACCAATAAAGAAAGCAATGTA
GTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGA
AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGTCTTCTTGATACATCTA
AAATAACAAAAATTAACAGCCACAACCCAAAGAGGAAAGGGAATGTAGTA
GCTATTATTGATACTGGCTTTGATATTAACCAATGATATTTTCGTTTAGA
TAGCCCAAAGATGATAAGCACAGCTTAAAACCTAAGGCAGAAATTTGAGG
AATTAAGCAAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAG
ATTGTTTTGACATTAACCTACGCCAAACAAATACAGAAACGGTGGCTGATAT
TGCAGCAGCTATGAAAGATGGTTATGGTTCAGAAAGCAAGAAATTTTGC
ATGGTACACACCTTGTCTGGTATTTTGTAGGTAATAGTAACCGTCCAGCA
ATCAATAGTCTTCTTTAGAAGGTGCAGGCCAAAATGCTCAAGTCTTATT
AATGCGTATTTCCAGATAAAATTTGATTTCGGAACAATTTGGAGAAGCATATG
CTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATG
AGCCTGGGAAAAACGGCTGATTTCTTAATTTGCTCAATGATAAAGTTAA
ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTGTTGGCTG
CCGGAATGAAGGTGCAATTTGGTATGGATTATAGCAAACCATTTATCAACT
AATCCTGACTACGGTACGGTAAATAGTCCAGCTATTTCTGAAGATACTTT
GAGTGTGCTAGCTATGAATCACTTAAAACCTATCAGTGAGGTGGTTGAAA
CAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTCTCAACCT
TTTGACAAAGGTAAGCCCTACGATGTGGTTTTATGCCAATTTATGGTGCAAA
AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTTGAGCG
TGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAAATCAG
GTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGAAATTTT
CTAATTCCTTACCGTGAATTAACCTGTGGGGTTATTAGTAAAGTATAGATG
CGAGCGTATAAAAAATCACTTCAAGTCAAGTTAACATTTAACACAGATTTTg
AAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGG
GGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTTCTGGCTT
TGAAATTTATCTTCAACCTATAAATCAATTAACCAATGCTCTGGTA
CAAGTATGGCTTCAACCATGTGTCAGGATTAATGACAATGCTTCAAAGT
CATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTTGCT
AGAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTTATATAGTG
AAGAGGATAAGCGTTTTTATTCACCACGTCAAGCAAGGTGCAGGTGTAGTT
GATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGAAACCGATGG
CAAAGTTAAAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCACAG
TTACAATTCATaaACTTGTAGAGGTGTCAAAGAATTGTATTATCAAGCT
AATGTAGCaaCAGAACAAGTAAATAaAGGTAATTTGCCCTTaaCCaCa
AGCCTTGTCTAGATACTAATTTGGCAGaaGtaATTCTTcGTGATAAAGAAA
CACAAGTTCgAATTTACTaTGTATGCTAGTCAATTTAGTCAGAAATTA AAA
GAACAGATGGCAAAATGGTTATTTCTTAGAAGGTTTGTACGTTTTTAAAGA
AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA
ATGGTGATTTTGGCAACTLACAAGCACTTGAACACCCGATTTATAAGACG
CTTTCTAAAGGTAGTTTCTACTATAAAcCAAATGATACAACTCATAAAGA
CCAATTTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACTG
CCTTGTAAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAT
GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAGAAATTTTATAGG
AACTTTTGAGAATAAGGTTGAGGATAAAAACAAATTCATCTTTGGAAAGAG
ATGCAGCGAAATAATCCATATTTTGCCATTTCTCCAATTAAGATGGAAT
AGGGACGaaATCACTCCCAGGCaActTCTTAAGAAATGTTAAGGATAT
TTCTGCTCAAGTCTTAGATCAAAATGGAATGTTATTTGGCAAAGTAAAG
TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAAGCAAAGTGAT
GGTCATTTATCGTATGGATGCTCTTCAAGTGGAGTGGTTTAGATAAAGGATG
CAAAGTTGATAGCAGATGGTTTTATACTTATCGCTTACGTTACACACCAG
TAGCAGAAAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCAAAGTAAAGT
ACTAAGTCACCAAATCTTCCCTCAGGAGCTCAGTTTATGATAAACTAATCG
AACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACATATC
GTTTACAATTAGTTTTATCTCATGTTGTAAGAATGAAGAATATGGGGAT
GAGACTTCTTACCATTAATTTCCATATAGATCAAGAAGGTAAGTGAACACT
TCCTAAAACGGTTAAGATAGGAGAGAGTGGGTTGCGGTAGACCCTAAGG
CCTTGACACTTGTGTGGAAGATAAAGCTGGTAAATTTGCAACGGTAAAA
TTGTGACCTTCTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT
AGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAGAAAGAACCTA
TGTTTTATTTCTAAAGAAGGAAAAGTAGTAAACAGAATCTAGAAGAAATA
ACATTAGTTAAGCCTCAAACACAGTTACTACTCAATCATTTGCTAAAAGA
AATAACTAAATCAGGAAATGAGAAAGTCCCTCACTTCTACAAACAATAATA
GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AACCATACC

SEQ ID NO. 4409

STRAIN CJB110

GAGGAGCAAGAATTAAAAACCAAGCAATCACCTGTAA
 TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACTAATATTTGTT
 GAAAAACATCTGTAnCAGCTGCTTCTGCTAGTAATACAGCGAAAGAAAT
 GGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTTATAGAAG
 AGTTATCTAAAAACCTTGATACGCTCTAATWGGGGGCTGATCTTGAGAAA
 GAATATCCCTCTAAACCAGAGACAAACCAATTAAGAAAAGCAATGTAGT
 AACAAATGCTTCAACTGCAATAGCACAGAAAAGTTCCCTCAGCGTATGAAG
 AGGTGaaGCCAGAAAGCAAGTCATCGCTTGCTGTTTTTGATACATCTAAA
 ATAACAAAATTCGAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGC
 TATTATTGATACTGGCTTTGATATTAAACCATGATATTTTCGTTTAGATA
 GCCAAAAGATGATAAGCACAGCTTTAAACTAAAGCAGAATTTCGAGGAA
 tTAAAGCAAAAACATAATATCACTTATGGGAATGGGTTAACGATAAGAT
 TGTTTTGCACATAACTACGCCAAACATACAGAAAACGGTGGCTGATATTG
 CAGCAGCTATGAAAGATGTTTATGGGTGAGAACAAAGAAATATTTCCGAT
 GGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCACGCAAT
 CAATGGTCTTCTTTTAGAAGGTGACGCGCAATGCTCAAGTCTTATFAA
 TGCTTATCCAGATAAAATGATTCGGACAAATTTGGAGAAGCATATGCT
 AAAGCAATCACAGACGCTCTTAATCTAGSAGCAAAAACGATTAATATGAG
 CCTTGAAAAAACAGCAGATTCTTTAATTGCACCTCAATGATAAAAGTTAAAT
 TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTGTGTTGTTGGCTGCC
 GGAATGAAGGTGCATTTGGTATGGATTATAgCAAACCTTATCAACTAA
 TcCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGA
 GTGTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTCGTTGaaACA
 ACTATTGAAAGGTAAGTTAGTTAAGTTGCCGATTTGTGACTTCTAAACCTTT
 TGACAAAGGTAAAGCCTACGATGTGGTTTATGCCAATTAATGGTGCAAAAA
 AAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTTAGCGT
 GGTGGTGGACTTGAATTTATGACTAAAATCACTCATGCTACAAATGCAGG
 TGTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGAAATTTTc
 TAATTCCTTACCGTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGGC
 GAGCGTATAAAAAATACITCAAGTCAGTTAACATTTAACCAgAGTTTGA
 AGTAgTTGATAGCCAAgGTGGCAATCGTATGCTGGAACAATCAAGTcGGG
 CGGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT
 GAAATTTTATTCTTCAACCTATAATAATCAATACCAAACAATGCTGGTAC
 AAGTATGGCTTCAACACATGcTGCAGGATTAATGACAAATGCTTCAAATC
 ATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTTGTA
 GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA
 AGAGGATAAGGCGTTTTATTCACCAGCTCAGCAAGGTcGCAGGTGTAGTTG
 ATGCTGAAAAAGCTATCCAAGCTCAATATTTATGTTACTGGAACCGATGGC
 AAAGCTAAAAATTAATCTCAAACGAGTGGGAGATAAATTTGATATCACAGT
 TACAATTCATAAACCCTGTAGAAGGTGTCAAAGAAATGTATTTATCAAGCTA
 ATGTAGCAACAGAAcAAGTAAATAAAGTAAATTTGCCCTTaaAACCAAA
 GCCTTGCTAGATACTAATTTGGCAGAAAGTAATTTCTcGTGATAAAGAAAC
 ACAAGTTCGATTTACTAeTGATGCTAGTCAATTTAgTCAGAAATTAAGAG
 AACAGATGGCAAATGGTATTTCTTAGAAGGTTTTGTACGTTTTAAAGAA
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTAA
 TGGTGTATTTGCCAACTLACAGCACTTGAACACCGGATTTATAAGACGC
 TTTCTAAAGGTAGTcTCTACTATAAACCAATGATACAACTCATAAAGAC
 CAATTTGGAGTACAATGAATCAGCTCctTTTGAAGCAACAACCTATACTGC
 CTTGTTAACCAATCAGCGTCTTGGGGCTATGTTGATTTATGTCAAATAATG
 GTGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAGAATTTATTTTAGGA
 ACTTTTGAGAATAAGGTTGAGGATAAAAACAAATCACTTTTGGAAAGAGA
 TGCAGCGAATAATCCATATTTTGCCATTTCTCCAATAAAGATGGAATA
 GGGATGaaATCACTCCCAGGCACCTTCTTAAGAAATGTTAAGGATATT
 TCTGCTCAAGTTCTAGATCAAATGGAATGTTATTTGGCAAAGTAAGGT
 TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG
 GTCAATTTCTGATGGATGCCCTTTCAGTGGAGTGGTTAgATAAgGATGGC
 AAAGTTGTAGCAGATGGTTTTTATACTTATCGCCTACGTTACACACCAGT
 AGCAGAAgGAGCAATAGTCAAGGAGTCAgACTTTAAAGTTCAAGTAAGTA
 CTAAGTCACCAAATCTTCTTTACTAGCTCAGTTTGTGAAACTAATCGA
 ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACATATCG
 TTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGATG
 AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAGTGACACTT
 CCTAAAAACGGTTAAGATAGGAGAGAGTGGGTTGAGTACGCTTAAAGGC
 CTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAT
 TGTCTGACCTCTTGAaTAAgCAGTAGTATCAGAGAAAAGAAAACGCTATA
 GTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAAGAACTAT
 GTTTATTTCTAAAAGAAAGAAAAGTAGTAAAACAAGAACTAGAAGAATAA
 CATTAGTTAAGCCGaaACTACAGTTACTACTCAATCATTTGTCTAAAGAA
 ATAACTAAATCAGGAAATGAGAAAGTCCCTCACTTCTACAAAACAAATAG
 TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA
 ACCATACC

SEQ ID NO. 4410

STRAIN 1169NT

GAGGAGCAGAATTAAAAACCAAGCAATC
 ACCTGTAATTTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACTA
 ATATTTGTTGAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGCG
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAAT
 ATTAGAAGAGTTATCTAAAAACCTTGATACGCTCTAATATGGGGCTGATC

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

TTGAAGAAGAAATATCCCTCTAAACCAGAGACAACCAACAATAAGGAAAGC
AATGTAGTAAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGC
ATATGAAGAGGTGAAGCCAAAAGCAAGTCAATCGCTTGGCTGTTCTTGATA
CATCTAAAATAACAAAATGCAAGCCATAACCCAAAGAGGAAAGGAAAT
GTAGTAGCTATATTTGATACTGGCTTTGATATTAACCATGATATTTTTCG
TTTATAGTAGCCAAAAGATGATAAGCACAGCTTTAAAAATAAGGCAGAAAT
TCGAGGAATTTAAAGCAAACATAATATCACTTATGGGAAATGGTAAAC
GATAAGATTTGTTTTGACATAAAGTACGCCAACATAACAGAAACGGTGGC
TGATATTGCAGCAGCTATGAAAGATGGTTATGGTTGAGAAAGCAAAAGATA
TTTCGCATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGT
CCAGCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGT
CTTATTATGCGGTATTCAGATAAAAATGATTCGGACAAATTCGGAGAAG
CATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCTAAAACGATT
AATATGAGTATTTGAAAAACAGCTGATTTCTTAAATGCTCTCAATGATAA
AGTTAAATTAAGCACTTAAATAGCTTCTGAGAAGGGCGTTGCAAGTTGTTG
TGGCTGCcCGAAATGAAGCGCATTTGGTATGGATTATAGCAAACCGTTA
TCAACTAATcCTGACTACGGtACGGtTAATAGTCCAGCTATTTCTGAGA
TACTTTGAGTGTGCTAGCTATGAATCACTTAAACATACAGTGAAGTGG
TTGAAACAACATTTGAAGGTAAAGTTAGTTAAGTtCGCCGATTGtGACTTCT
AAACCTTtGACAAAGGTAAGCCCTACGATGGGTTTATGCCAATTAAGG
TGCAAAAAGAGACTTTGAAGGTAAAGGACTTTAAAGGTAAGATTGCATTAA
TTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACA
AATGCAGGTGTTGTTGGTATCGTTATTTTTAACGATCAAGAAAACGTTGG
AAATTTTCTAATTCCTTACCCTGAATTACCCTGGGGGTTATTAGTAAAG
TAGATGGCGAGCGTATAAAAaATACTTCAAGTCAGTTAACATTTAAACCAg
AGATTTGAAGTAGTTGATAGCCAAgGTGGCAATCGTATGCTGGAAcAAATC
aAGTtGGGGCGTACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTT
CTGGCTTCGaAATTTATTTCTTcCaCCTATAATAATCAATACCAAACAATG
TCTGGTACAAGTATGGCTTCAACCACTGTTGCGAGGATTAATGACAATGCT
TCAAAGTCAATTTGGCTGAGaAATAATAAGGGATGAATTTAGATTCTAAaA
AATTTGCTAGAATTTCTAAAAACATCCCTCATGAGCTCAGCAACAGCATT
TATAGTGAAGAGGATAAGGCGTTTTATTCACCACGTCAGCAAGGtGCAGG
TGTAGTTGATGCTGAAAAGCTATCCAAGCTCAATATTATGTTACTGGAA
ACGATGGCAAAGCTAAAATTAATCTCAAACGAGTGGGAGATAAATTTGAT
ATCAGCTTACATTCATAAACTTGTAGAAGGTGTCAAAAGAAATGATTTA
TCAAGCTAATGTAGCAACAGAAACAGTAAATAAAGGTAATTTGCCCTTA
AACCACAAGCCTTGTAGATACTAATTTGGCAGAAAGTAATTTCTtCGTAT
AAAGAAACACAAGTTCGATTTACTATTGATGCTAGTCAATTTAgtCAGAA
ATTAAAAGAACAGATGGCAAATGGTTAATTTCTTAgAAGGTTTTGTACGTT
TTAAAGAAGCTAAGGATAGTAAATCAGGAGTTAATGAGTATTCCTTTTGT
GGAATTTAATGGTGAATTTTGGAGCTTACAAGCACTTGAACACCGATTTA
TAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACCT
ATAAAGCAACATTTGGAGTATAATGAATCAGCTCCTTTTGAAAGCAACAAC
TATACTGCCCTTGTAAACACAATCAGCGTCTTGGGGCTATGTTGATATGT
CaAAAATGGTGGGAGTTAGAATTAGCACCCGGAGAGTcCAAAAAGAAATTA
TTTTAGGAACTTTTGAGAATAAGGTTGAGGATAAAAACAATTCATCTTTTG
GAAAGAGATGCAGCGAATAATCCATATTTGCCATTTCTCCAATAAAGA
TGGAAATAGGGATGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTA
AGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAA
AGTAAGGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCAAAGCA
GATGATGGTCAATATCGTATGGATGCCCTTCAGTGGAGTGGTTAgATA
AGGATGGCAAAGTTGTAGCAGATGGTTTTTATCTTATCGCTTACGTTAC
ACACCAGTAGCAGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTTCA
AGTAAGTACTAAGTCAACCAATCTTCTTCAAGCTCAGTTTGTAGTGAaA
CTAATCGAAcATTAAAGCTTAGCCATGCCTAAGGGAAAGTAGTTATGTTCT
ATATATCGCTACAATAGTTTTATCTCATGTTGTAAGAATGAAGAATA
TGGAGATGAGACTTCTTACTATTTCCATATAGATCAAGAAGGTAAAG
CGACACTTCTTAAAACGGTTAAGATAGGAGAGAGTGAAGTTGCAGTAGAC
CCTAAGGCCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTCCGAaC
GGTAAAATTTGCTGACCTTGAATAAGGCAGTAGTATCAGAGAAGGAAA
ACGCTATAGTAAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAA
GAACCTATGTTTATTTCTAAAAAAGAAAAGTAGTAAACAAGAAATCTAGA
AGAAATAAATATTAGTTAAGCCGCAcACTACAGTTACTACTCAaTCAATGT
CTAAAGAAATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAAC
ATAAATAGTAGTAGTAGCTAAAATCATATCACCTAAAACATAATGGGAA
TTCTGTTAACCATACC

SEQ ID NO. 4411
STRAIN JM9130013
GAGGAGCAAGAATTA AAAAACCAGGCAATCACCTGTAA
TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATACTGTT
GAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAAATACAGCGAAAAGAAAT
GGGTGATACATCTGTAAAAAATGACAAAACAGAAAGTAAATATTAGAAg
AGTTATCTAAAAACCTTGATACGTCTAATTTGGGGCTGATCTTGAAGAA
GAATATCCCTTAAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGT
AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGAAG
AGGTGAAGCCAGAAAGCAAGTCATCGCTTGGCTGTTCTTGATACATCTAAA
ATAACAAAATTAACAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGC
TATTTATGATACGGCTTTGATATTAACCATGATATTTTTCGTTTAGATA
GCCAAAAGATGATAAGCACAGCTTTAAAACCTAAGACAGAAATTTGAGGAA
TTAAAAGCAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGAT
TGTTTTTGCACATAACTACGCCAACATAACAGAAACGGTGGCTGATATTG
CAGCAGCTATGAAGATGGTTATGGTTCAAGCAAGCAAGAAATATTTCGCAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGTACACACGTTGCTGGTATTTTTGTAGGTAATAGTAAACGTCAGCAAT
CAATGGTCTCTTTTGAAGGTCAGCGCCAAATGCTCAAGTCTTATTA
TGCGTATCCAGATAAAATTTGATTCGGACAAATTTGGTGAAGCATATGCT
AAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATGAG
TATTGGAAAAACAGCTGATTCTTTAATTTGCTCTCAATGATAAAGTTAAAT
TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGGCTGCC
GGAAATGAAGGGCAATTTGGTATGGATTATAGCAAAACCATATCAACTAA
TCCTGACTACGGTACGGTTAATAGTCCAGCTATTCTGAAGATACTTTGA
GTGTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTCGTTGAAACA
ACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTT
TGACAAAAGTAAgGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA
AAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATGAGCGT
GGTGGTGGACTTGATTTATGACTAAAATCACTCATGCTACAAAATGCAGG
TGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTTC
TAATTCCTTACCCTGAATTACCTGTGGGGATTATTAGTAAAGTAGATGCC
GAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCCAGAGTTTGA
AGTAGTTGATAGCCAAGGTCGTAATCGTATGCTGGAACAATCAAGTTGGG
GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTT
GAAATTTATCTTCAACCTATAATAATCAATACCAAAACATGTCTGGTAC
AAGTATGGCTTCCACCATGTTGCAGGATTAATGACAATGCTTCAAAGTC
ATTTGGCTGAGAATATAAAGGGaTGAATTTAGATTCTTAAAAAATTGCTA
GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA
AGAGGATAAGGCGTTTATTCAACCAGTCAGCAAGGTGCAGGTTAGTTG
ATGCTGAAAAAGCTATCCAAGCTCaATATTATATTACTGGAAACGATGGC
AAAGCTAAAATTAATCTCAAACGAATGGGAGATAAAATTTGATATCACAGT
TACAATTCATaAACTTGTAGAAGGTGTCAAAGAAATGTATTATCAAGCTA
ATGTAGCAACAGAAACAGTAAATAAAGGTAATTTGCCCTTAAACCAAA
GCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTTGTGATAAAGAAC
ACAAGTTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAGAG
AACAGATGGCAAATGGTTAATTTCTTAGAAGGTTTGTACGTTTAAAGAA
GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTAA
TGGTATTTTGGCACTTACAAGCACTTGAACACCCGATTATAAGAGCGC
TTTCTAAAGGTAGTTTCTACTATAAACCAATGATCAACTCATAAAGAC
CAATTTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATACTACTGC
CTTGTAAACAAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATG
GTGGGGAGTTAGAATTAGCACCCGGAGAGTCCAAAAAGAAATTTATTTAGGA
ACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTGGAAGAGA
TGCAGCGAATAATCCATATTTGCCAATTTCTCCAAATAAGATGGAAATA
GGACGAAATCACTCCCAGGCAACTTCTTAAAGAAATGTTAAGGATATT
TCTGCTCAAGTTCTAGATCAAAAATGGAATGTTATTTGGCAAAGTAAGGT
TTTACCATTCTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG
GTCAATTATCGTATGGATGCTCCTCAGTGGAGTGGTTTAGATAAGGATGGC
AAAGTTGTAGCAGATGGTTTATACTTATCGCTTACGTTACACACCCAGT
AGCAGAAAGGAGCAAATAGTCAGGAGTCAGACTTTAAAGTACAAGTAAGTA
CTAAGTCACCAATCTTCTTCCAGAGCTCAGTTTGTGAAACTAATCGA
ACATTAAGCTTAGCCATGCCAAGGAAAGTAGTTATGTTCTACATATCG
TTTACAATTAGTTTATCTCATGTTGTAAGATGAAGAAATATGGGGATG
AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAGTGAACCTT
CCTAAAAACGGTTAAGATAGGAGAGAGTGGGTTGCGGTAGACCCCTAAGGC
CTTGACACTTGTGTGAAGATAAAGCTGGTAATTTCCGAaCGGTAAAAAT
TGTCTGATCTCTGAATAAGGCAGTATATCAGAGAAAGAAACCGCTATA
GTAATTTCTaACAGTTCAAATATTTGATAACTTGA AAAAAGAACCTAT
GTTTATTTCTAAAAAGAAAAGTAGTAAACAGAATCTAGAAGAAATAA
TATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAAGAA
ATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAAACAAATAAG
TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA
ACCATACC

PRETTY of: /biotmp/msa183564.2{*} May 13, 2003 03:28 ..

Table with 5 columns: sequence identifier, position 1, position 50, position 51, position 100. Rows include various sequence identifiers like msa183564.2{147_COH1} and a consensus line.

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_A909}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_H36B}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_1169NT}	-----	-----	-----	-----	GAGGAGCAAG
Consensus	*****	*****	*****	*****	*****
101					
msa183564.2{147_COH1}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_M732}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_M781}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_2603}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_JM9130013}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_18RS21}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_090}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_CJB110}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_A909}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_H36B}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
msa183564.2{147_1169NT}	AATTA	CAAGAG	TCACCT	TTGCTA	TGCTCA
Consensus	*****	*****	*****	*****	*****
151					
msa183564.2{147_COH1}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_M732}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_M781}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_2603}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_JM9130013}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_18RS21}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_090}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_CJB110}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_A909}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_H36B}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_1169NT}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
Consensus	*****	*****	*****	*****	*****
151					
msa183564.2{147_COH1}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_M732}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_M781}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_2603}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_JM9130013}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_18RS21}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_090}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_CJB110}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_A909}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_H36B}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
msa183564.2{147_1169NT}	CCATCG	CGGTA	TAATA	GAAAA	CTGTAA
Consensus	*****	*****	*****	*****	*****
201					
msa183564.2{147_COH1}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_M732}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_M781}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_2603}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_JM9130013}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_18RS21}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_090}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_CJB110}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_A909}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_H36B}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_1169NT}	TGCTT	AGTA	tGAA	GGGT	TCTG
Consensus	*****	*****	*****	*****	*****
201					
msa183564.2{147_COH1}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_M732}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_M781}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_2603}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_JM9130013}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_18RS21}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_090}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_CJB110}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_A909}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_H36B}	TGCTT	AGTA	tGAA	GGGT	TCTG
msa183564.2{147_1169NT}	TGCTT	AGTA	tGAA	GGGT	TCTG
Consensus	*****	*****	*****	*****	*****
251					
msa183564.2{147_COH1}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_M732}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_M781}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_2603}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_JM9130013}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_18RS21}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_090}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_CJB110}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_A909}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_H36B}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_1169NT}	ATGAC	AGA	TTAT	AGT	AAAC
Consensus	*****	*****	*****	*****	*****
251					
msa183564.2{147_COH1}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_M732}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_M781}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_2603}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_JM9130013}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_18RS21}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_090}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_CJB110}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_A909}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_H36B}	ATGAC	AGA	TTAT	AGT	AAAC
msa183564.2{147_1169NT}	ATGAC	AGA	TTAT	AGT	AAAC
Consensus	*****	*****	*****	*****	*****
301					
msa183564.2{147_COH1}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_M732}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_M781}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_2603}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_JM9130013}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_18RS21}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_090}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_CJB110}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_A909}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_H36B}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_1169NT}	ACGT	TGG	TCT	GA	GAAT
Consensus	*****	*****	*****	*****	*****
301					
msa183564.2{147_COH1}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_M732}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_M781}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_2603}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_JM9130013}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_18RS21}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_090}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_CJB110}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_A909}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_H36B}	ACGT	TGG	TCT	GA	GAAT
msa183564.2{147_1169NT}	ACGT	TGG	TCT	GA	GAAT
Consensus	*****	*****	*****	*****	*****
351					
msa183564.2{147_COH1}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_M732}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_M781}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_2603}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_JM9130013}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_18RS21}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_090}	GACA	AATA	GCA	AAT	TCA
Consensus	*****	*****	*****	*****	*****
351					
msa183564.2{147_COH1}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_M732}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_M781}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_2603}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_JM9130013}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_18RS21}	GACA	AATA	GCA	AAT	TCA
msa183564.2{147_090}	GACA	AATA	GCA	AAT	TCA
Consensus	*****	*****	*****	*****	*****

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_CJB110}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_A909}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_H36B}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_1169NT}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
Consensus	*****	*****	*****	*****	*****
401					
msa183564.2{147_COH1}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG
msa183564.2{147_M732}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG
msa183564.2{147_M781}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG
msa183564.2{147_2603}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_JM9130013}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_18RS21}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_090}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_CJB110}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_A909}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_H36B}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_1169NT}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
Consensus	*****	*****	**-*****	*****-*	*-*****
451					
msa183564.2{147_COH1}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_M732}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_M781}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_2603}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_JM9130013}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_18RS21}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_090}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_CJB110}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_A909}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_H36B}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_1169NT}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
Consensus	*****	*****	*****	*****	*-*****
501					
msa183564.2{147_COH1}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_M732}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_M781}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_2603}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_JM9130013}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_18RS21}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_090}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_CJB110}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_A909}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_H36B}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
msa183564.2{147_1169NT}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCITTG
Consensus	*****	*****	*****	*****	*****
551					
msa183564.2{147_COH1}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_M732}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_M781}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_2603}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_JM9130013}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_18RS21}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_090}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_CJB110}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_A909}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_H36B}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
msa183564.2{147_1169NT}	ATATTAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAGA	TGATAAGCAC
Consensus	*****	*****	*****	*****	*****
601					
msa183564.2{147_COH1}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_M732}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_M781}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_2603}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_JM9130013}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_18RS21}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_090}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_CJB110}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_A909}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_H36B}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_1169NT}	AGCTTTAAAA	aTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
Consensus	*****	-***-****	***-*****	*****	*****
651					
msa183564.2{147_COH1}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_M732}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_M781}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_2603}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_JM9130013}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_18RS21}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_090}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_CJB110}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_A909}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_H36B}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_1169NT}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
Consensus	*****	*****	*****	*****	*****
	701			750	
msa183564.2{147_COH1}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M732}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M781}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_2603}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_JM9130013}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_18RS21}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_090}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_CJB110}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_A909}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_H36B}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_1169NT}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
Consensus	*****	*****	*****	*****	*****
	751			800	
msa183564.2{147_COH1}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_M732}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_M781}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_2603}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_JM9130013}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_18RS21}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_090}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_CJB110}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_A909}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_H36B}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_1169NT}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TTGCTGGTAT
Consensus	*****	*****	*****	*****	*****
	801			850	
msa183564.2{147_COH1}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_M732}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_M781}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_2603}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_JM9130013}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_18RS21}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_090}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_CJB110}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_A909}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_H36B}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
msa183564.2{147_1169NT}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCTT	CTTTTAGAAG
Consensus	*****	*****	*****	*****	*****
	851			900	
msa183564.2{147_COH1}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_M732}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_M781}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_2603}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_JM9130013}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_18RS21}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_090}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_CJB110}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_A909}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_H36B}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
msa183564.2{147_1169NT}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAAAT
Consensus	*****	*****	*****	*****	*****
	901			950	
msa183564.2{147_COH1}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_M732}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_M781}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_2603}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_JM9130013}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_18RS21}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_090}	GATTCGGACA	AATTTGGaGa	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_CJB110}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_A909}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_H36B}	GATTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_1169NT}	GATTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
Consensus	*****	*****	*****	*****	*****
	951			1000	
msa183564.2{147_COH1}	TAATCTAGGA	GcAAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_M732}	TAATCTAGGA	GcAAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_M781}	TAATCTAGGA	GcAAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_2603}	TAATCTAGGA	GcAAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTGATT
msa183564.2{147_JM9130013}	TAATCTAGGA	GcAAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTGATT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_18RS21}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	taTtGGAAAA	ACaGcTGATT
msa183564.2{147_090}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAgATT
msa183564.2{147_CJB110}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAgATT
msa183564.2{147_A909}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAgATT
msa183564.2{147_H36B}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAgATT
msa183564.2{147_1169NT}	TAATCTAGGA	GCTAAAACGA	TAAATATGAG	taTtGGAAAA	ACaGcTGATT
Consensus	*****	**_*****	*****	--*_*****	**_*_*_*_*
1001					
msa183564.2{147_COH1}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M732}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M781}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_2603}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_JM9130013}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_18RS21}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_090}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_CJB110}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_A909}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_H36B}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_1169NT}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
Consensus	*****	-*****	*****	*****	*****
1051					
msa183564.2{147_COH1}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_M732}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_M781}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_2603}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGG
msa183564.2{147_JM9130013}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGG
msa183564.2{147_18RS21}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_090}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_CJB110}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_A909}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_H36B}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_1169NT}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGG
Consensus	*****	*****	*****	*****	*_*****
1101					
msa183564.2{147_COH1}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M732}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M781}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_2603}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_JM9130013}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_18RS21}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_090}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_CJB110}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_A909}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_H36B}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_1169NT}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
Consensus	*****	*****_*	*****	*****	*****
1151					
msa183564.2{147_COH1}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_M732}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_M781}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_2603}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_JM9130013}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_18RS21}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_090}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_CJB110}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_A909}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_H36B}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
msa183564.2{147_1169NT}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CIATGAATCA
Consensus	*****	*****	*****	*****	*****
1201					
msa183564.2{147_COH1}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M732}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M781}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_2603}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_JM9130013}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_18RS21}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_090}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_CJB110}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_A909}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_H36B}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_1169NT}	CTTAAAACCTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
Consensus	*****	*****	*****	*****	*****
1251					
msa183564.2{147_COH1}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M732}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M781}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_2603}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_JM9130013}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_18RS21}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_090}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_CJB110}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_A909}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_H36B}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_1169NT}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
Consensus	*****	*****	*****	*****	*****
1301					
msa183564.2{147_COH1}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_M732}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_M781}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_2603}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_JM9130013}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_18RS21}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_090}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_CJB110}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_A909}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_H36B}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_1169NT}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
Consensus	*****	*****	*****	*****	*****
1351					
msa183564.2{147_COH1}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_M732}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_M781}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_2603}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_JM9130013}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_18RS21}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_090}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_CJB110}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_A909}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_H36B}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
msa183564.2{147_1169NT}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGG	CTTGATTTTA
Consensus	*****	*****	*****	*****	*****
1401					
msa183564.2{147_COH1}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_M732}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_M781}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_2603}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_JM9130013}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_18RS21}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_090}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_CJB110}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_A909}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_H36B}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_1169NT}	TGACTAAAAT	CACTCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
Consensus	*****	*****	*****	*****	*****
1451					
msa183564.2{147_COH1}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M732}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M781}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_2603}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_JM9130013}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_18RS21}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_090}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_CJB110}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_A909}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_H36B}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_1169NT}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
Consensus	*****	*****	*****	*****	*****
1501					
msa183564.2{147_COH1}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_M732}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_M781}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_2603}	ACCTGTGGGG	aTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_JM9130013}	ACCTGTGGGG	aTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_18RS21}	ACCTGTGGGG	aTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_090}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_CJB110}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_A909}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_H36B}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
msa183564.2{147_1169NT}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAAFACTT
Consensus	*****	*****	*****	*****	*****
1551					
msa183564.2{147_COH1}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M732}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M781}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_2603}	CAAGTCAGTT AACATTTAAC CAGAGcTTTG AAGTAGTTGA TAGCCAAGGT
msa183564.2{147_JM9130013}	CAAGTCAGTT AACATTTAAC CAGAGcTTTG AAGTAGTTGA TAGCCAAGGT
msa183564.2{147_18RS21}	CAAGTCAGTT AACATTTAAC CAGAGcTTTG AAGTAGTTGA TAGCCAAGGT
msa183564.2{147_090}	CAAGTCAGTT AACATTTAAC CAGAGcTTTG AAGTAGTTGA TAGCCAAGGT
msa183564.2{147_CJB110}	CAAGTCAGTT AACATTTAAC CAGAGcTTTG AAGTAGTTGA TAGCCAAGGT
msa183564.2{147_A909}	CAAGTCAGTT AACATTTAAC CAGAGcTTTG AAGTAGTTGA TAGCCAAGGT
msa183564.2{147_H36B}	CAAGTCAGTT AACATTTAAC CAGAGcTTTG AAGTAGTTGA TAGCCAAGGT
msa183564.2{147_1169NT}	CAAGTCAGTT AACATTTAAC CAGAGcTTTG AAGTAGTTGA TAGCCAAGGT
Consensus	*****-*****
1601	
msa183564.2{147_COH1}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_M732}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_M781}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_2603}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_JM9130013}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_18RS21}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_090}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_CJB110}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_A909}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_H36B}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
msa183564.2{147_1169NT}	GGcAATCGTA TGCTGGAACA ATCAAGTTGG GGCcTGACAG CTGAAGGAGC
Consensus	*****
1650	
msa183564.2{147_COH1}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_M732}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_M781}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_2603}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_JM9130013}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_18RS21}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_090}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_CJB110}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_A909}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_H36B}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
msa183564.2{147_1169NT}	AATCAAGcCTT GATGTAACAG CTTCTGGcCTT tGAAATTTAT TCTTCAACCT
Consensus	*****-*****
1651	
msa183564.2{147_COH1}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_M732}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_M781}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_2603}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_JM9130013}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_18RS21}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_090}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_CJB110}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_A909}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_H36B}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
msa183564.2{147_1169NT}	ATAATAATCA ATAcLAAACA ATGcTcTGgTA CAAGTATGGC TTCACcCAT
Consensus	*****-*****
1701	
msa183564.2{147_COH1}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_M732}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_M781}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_2603}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_JM9130013}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_18RS21}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_090}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_CJB110}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_A909}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_H36B}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
msa183564.2{147_1169NT}	GTTGcAGGAT TAATGAcAAT GcTTcAAAgT cATTtGGcCTG AGAAATATAA
Consensus	*****-*****
1751	
msa183564.2{147_COH1}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_M732}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_M781}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_2603}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_JM9130013}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_18RS21}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_090}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_CJB110}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_A909}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_H36B}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
msa183564.2{147_1169NT}	AGGgATGAAT TTAGATTTcTA AAAAAATTGcT AGAATTGcTcT AAAAAcATcc
Consensus	*****
1801	
msa183564.2{147_COH1}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
msa183564.2{147_M732}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
msa183564.2{147_18RS21}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
msa183564.2{147_090}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
msa183564.2{147_CJB110}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
msa183564.2{147_A909}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
msa183564.2{147_H36B}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
msa183564.2{147_1169NT}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
Consensus	*****
1851	
msa183564.2{147_COH1}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT
msa183564.2{147_M732}	TCATGAGcTc AGCAAcAGCA TTATATAGTG AAGAGGATAA GGCgTTTTAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M781}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_2603}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_JM9130013}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_18RS21}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_090}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_CJB110}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_A909}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_H36B}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_1169NT}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
Consensus	*****	*****	*****	*****	*****
1901					
msa183564.2{147_COH1}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M732}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M781}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_2603}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_JM9130013}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_18RS21}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_090}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_CJB110}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_A909}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_H36B}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_1169NT}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
Consensus	*****	*****	*****	*****	*****
1951					
msa183564.2{147_COH1}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M732}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M781}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_2603}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGcTAAA	ATTAATCTCA
msa183564.2{147_JM9130013}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGcTAAA	ATTAATCTCA
msa183564.2{147_18RS21}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGcTAAA	ATTAATCTCA
msa183564.2{147_090}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_CJB110}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_A909}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_H36B}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_1169NT}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
Consensus	*****	***-*****	*****	*****-****	*****
2001					
msa183564.2{147_COH1}	AACGAgagGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M732}	AACGAgagGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M781}	AACGAgagGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_2603}	AACGAatGGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_JM9130013}	AACGAatGGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_18RS21}	AACGAatGGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_090}	AACGAggtGGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_CJB110}	AACGAggtGGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_A909}	AACGAggtGGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_H36B}	AACGAggtGGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_1169NT}	AACGAggtGGG	AGATAAAATTT	GATATCACAG	TTACAATTCA	TAAACTTGTA
Consensus	*****-****	*****	*****	*****	*****
2051					
msa183564.2{147_COH1}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M732}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M781}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_2603}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_JM9130013}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_18RS21}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_090}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_CJB110}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_A909}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_H36B}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_1169NT}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
Consensus	*****	*****	*****	*****	*****
2101					
msa183564.2{147_COH1}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M732}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M781}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_2603}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_JM9130013}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_18RS21}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_090}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_CJB110}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_A909}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_H36B}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_1169NT}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
Consensus	*****	*****	*****	*****	*****
2151					
msa183564.2{147_COH1}	GGCAGAAAGT	AATTCCTCGT	GATAAAGAAA	CACAAGTTCG	ATTTACTIATT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M732}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_M781}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_2603}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_JM9130013}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_18RS21}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_090}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_CJB110}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_A909}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_H36B}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_1169NT}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
Consensus	*****	*****
	2201	2250
msa183564.2{147_COH1}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_M732}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_M781}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_2603}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_JM9130013}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_18RS21}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_090}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_CJB110}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_A909}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_H36B}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_1169NT}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
Consensus	***_*****	*****
	2251	2300
msa183564.2{147_COH1}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_M732}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_M781}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_2603}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_JM9130013}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_18RS21}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_090}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_CJB110}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_A909}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_H36B}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
msa183564.2{147_1169NT}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcaAGGAT AGTAATCAGG	
Consensus	*****	***_*****
	2301	2350
msa183564.2{147_COH1}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_M732}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_M781}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_2603}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_JM9130013}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_18RS21}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_090}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_CJB110}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_A909}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_H36B}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_1169NT}	AGTTAATGAG TATTCCITTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
Consensus	*****	*****_****
	2351	2400
msa183564.2{147_COH1}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_M732}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_M781}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_2603}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_JM9130013}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_18RS21}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_090}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_CJB110}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_A909}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_H36B}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_1169NT}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
Consensus	*****	*****
	2401	2450
msa183564.2{147_COH1}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_M732}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_M781}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_2603}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_JM9130013}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_18RS21}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_090}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_CJB110}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_A909}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_H36B}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_1169NT}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
Consensus	*****	***_*****

2451

2500

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_COH1}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_M732}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_M781}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_2603}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_JM9130013}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_18RS21}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_090}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_CJB110}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_A909}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_H36B}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_1169NT}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
Consensus	*****	*****	*****	*****	*****
2501					
msa183564.2{147_COH1}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M732}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M781}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_2603}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_JM9130013}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_18RS21}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_090}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_CJB110}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_A909}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_H36B}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_1169NT}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
Consensus	*****	*****	*****	*****	*****
2551					
msa183564.2{147_COH1}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_M732}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_M781}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_2603}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_JM9130013}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_18RS21}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_090}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_CJB110}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_A909}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_H36B}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_1169NT}	ACCGGAGAGT	CCAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
Consensus	*****	*****	*****	*****	*****
2601					
msa183564.2{147_COH1}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M732}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M781}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_2603}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_JM9130013}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_18RS21}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_090}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_CJB110}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_A909}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_H36B}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_1169NT}	AGGATAAAAC	AAATTCATCTT	TTGGAAGAG	ATGCAGCGAA	TAATCCATAT
Consensus	*****	*****	*****	*****	*****
2651					
msa183564.2{147_COH1}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_M732}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_M781}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_2603}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_JM9130013}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_18RS21}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_090}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_CJB110}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_A909}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_H36B}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_1169NT}	TTTGCCATTT	CTCCAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
Consensus	*****	*****	*****	*****	*****
2701					
msa183564.2{147_COH1}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M732}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M781}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_2603}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_JM9130013}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_18RS21}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_090}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_CJB110}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_A909}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_H36B}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_1169NT}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
Consensus	*****	*****	*****	*****	*****
2750					
msa183564.2{147_COH1}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M732}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M781}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_2603}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_JM9130013}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_18RS21}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_090}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_CJB110}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_A909}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_H36B}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_1169NT}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
Consensus	*****	*****	*****	*****	*****

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	2751		2800
msa183564.2{147_COH1}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_M732}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_M781}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_2603}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_JM9130013}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_18RS21}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_090}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_CJB110}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_A909}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_H36B}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
msa183564.2{147_1169NT}	AAAATGGAAA TGTATTGG	CAAAGTAAGG TTTTACCATC	TTATCGTAAA
Consensus	*****	*****	*****
	2801		2850
msa183564.2{147_COH1}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_M732}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_M781}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_2603}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_JM9130013}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_18RS21}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_090}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_CJB110}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_A909}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_H36B}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
msa183564.2{147_1169NT}	AAITTCATA ATAATCCAAA	GCAaAGTGAT GGTCAATTATC	GTATGGATGC
Consensus	*****	***-*****	*****
	2851		2900
msa183564.2{147_COH1}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_M732}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_M781}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_2603}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_JM9130013}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_18RS21}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_090}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_CJB110}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_A909}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_H36B}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_1169NT}	ctTTCAGTGG AGTGGTTAG	ATAAGGATGG CAAAGTTGTA	GCAGATGGTT
Consensus	*****	*****	*****
	2901		2950
msa183564.2{147_COH1}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_M732}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_M781}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_2603}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_JM9130013}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_18RS21}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_090}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_CJB110}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_A909}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_H36B}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_1169NT}	TTTATACTTA TCGctTACGT	TACACACCAG TAGCAGAAGG	AGCAAATAGT
Consensus	*****	***-*****	*****
	2951		3000
msa183564.2{147_COH1}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_M732}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_M781}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_2603}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_JM9130013}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_18RS21}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_090}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_CJB110}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_A909}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_H36B}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
msa183564.2{147_1169NT}	CAGGAGTCAG ACTTTAAAGT	tCAAGTAAGT ACTAAGTCAC	CAAATCTTCC
Consensus	*****	-*****	*****
	3001		3050
msa183564.2{147_COH1}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_M732}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_M781}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_2603}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_JM9130013}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_18RS21}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_090}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_CJB110}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_A909}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_H36B}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
msa183564.2{147_1169NT}	TTcAcgAGCT CAGTTTGATG	AAACTAATCG AACATTAAGC	TTAGCCATGC
Consensus	*****	*****	*****

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

		3051			3100	
msa183564.2	{147_COH1}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_M732}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_M781}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_2603}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_JM9130013}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_18RS21}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_090}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_CJB110}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_A909}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_H36B}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
msa183564.2	{147_1169NT}	CTAAGGaaAG	TAGTTATGTT	CCTACATATC	GTTTACAATT	AGTTTTATCT
	Consensus	*****-***	*****	***-*****	*-*****	*****
		3101			3150	
msa183564.2	{147_COH1}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_M732}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_M781}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_2603}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_JM9130013}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_18RS21}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_090}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_CJB110}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_A909}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_H36B}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_1169NT}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ActATTATTT
	Consensus	*****	*****	*****-***	*****	***-*****
		3151			3200	
msa183564.2	{147_COH1}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_M732}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_M781}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_2603}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_JM9130013}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_18RS21}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_090}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_CJB110}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_A909}	CCATATAGAT	CgAGAAGGTA	AAGtGACACT	TCCTAAAACa	GTTAAGATAG
msa183564.2	{147_H36B}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACa	GTTAAGATAG
msa183564.2	{147_1169NT}	CCATATAGAT	CaAGAAGGTA	AAGcGACACT	TCCTAAAACg	GTTAAGATAG
	Consensus	*****	*-*****	***-*****	*****-*	*****
		3201			3250	
msa183564.2	{147_COH1}	GAGAGAGTGA	GTTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_M732}	GAGAGAGTGA	GTTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_M781}	GAGAGAGTGA	GTTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_2603}	GAGAGAGTGA	GTTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_JM9130013}	GAGAGAGTGA	GTTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_18RS21}	GAGAGAGTGA	GTTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_090}	GAGAGAGTGA	GTTTGCcGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_CJB110}	GAGAGAGTGA	GTTTGCcGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_A909}	GAGAGAGTGA	GTTTGCcGTA	GACCCTAAGa	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_H36B}	GAGAGAGTGA	GTTTGCcGTA	GACCCTAAGa	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_1169NT}	GAGAGAGTGA	GTTTGCcGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
	Consensus	*****	*****-***	*****-*	*****	*****
		3251			3300	
msa183564.2	{147_COH1}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_M732}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_M781}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_2603}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_JM9130013}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_18RS21}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_090}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_CJB110}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_A909}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_H36B}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
msa183564.2	{147_1169NT}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TTGTCTGAcC	TCTTGAATAA
	Consensus	*****	*****-**	*****	*****-*	*****
		3301			3350	
msa183564.2	{147_COH1}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_M732}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_M781}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_2603}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_JM9130013}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_18RS21}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_090}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_CJB110}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_A909}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_H36B}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_1169NT}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

Consensus	*****	*****	*****	*****	****-*****
	3351				3400
msa183564.2{147_COH1}	AATATTTTGA	TAACCTGAAg	AAAGAacCTA	TGTTTATTTC	TAAAgAAGgA
msa183564.2{147_M732}	AATATTTTGA	TAACCTGAAg	AAAGAacCTA	TGTTTATTTC	TAAAgAAGgA
msa183564.2{147_M781}	AATATTTTGA	TAACCTGAAg	AAAGAacCTA	TGTTTATTTC	TAAAgAAGgA
msa183564.2{147_2603}	AATATTTTGA	TAACCTGAAa	AAAGAacCTA	TGTTTATTTC	TAAaaAAGaA
msa183564.2{147_JM9130013}	AATATTTTGA	TAACCTGAAa	AAAGAacCTA	TGTTTATTTC	TAAaaAAGaA
msa183564.2{147_18RS21}	AATATTTTGA	TAACCTGAAa	AAAGAacCTA	TGTTTATTTC	TAAaaAAGaA
msa183564.2{147_090}	AATATTTTGA	TAACCTGAAa	AAAGAacCTA	TGTTTATTTC	TAAAgAAGgA
msa183564.2{147_CJB110}	AATATTTTGA	TAACCTGAAa	AAAGAacCTA	TGTTTATTTC	TAAAgAAGgA
msa183564.2{147_A909}	AATATTTTGA	TAACCTGAAa	AAAGAacCTA	TGTTTATTTC	TAAAgAAGgA
msa183564.2{147_H36B}	AATATTTTGA	TAACCTGAAa	AAAGAacCTA	TGTTTATTTC	TAAAgAAGgA
msa183564.2{147_1169NT}	AATATTTTGA	TAACCTGAAa	AAAGAacCTA	TGTTTATTTC	TAAaaAAGaA
Consensus	*****	*****	*****	*****	****-*****
	3401				3450
msa183564.2{147_COH1}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAc
msa183564.2{147_M732}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAc
msa183564.2{147_M781}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAc
msa183564.2{147_2603}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	atATTAGTTA	AGCCcCAaAc
msa183564.2{147_JM9130013}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	atATTAGTTA	AGCCcCAaAc
msa183564.2{147_18RS21}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	atATTAGTTA	AGCCcCAaAc
msa183564.2{147_090}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAc
msa183564.2{147_CJB110}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAc
msa183564.2{147_A909}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	gcATTAGTTA	AGCCcCAaAc
msa183564.2{147_H36B}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	gcATTAGTTA	AGCCcCAaAc
msa183564.2{147_1169NT}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	atATTAGTTA	AGCCcCAcAc
Consensus	*****	*****	*****	*****	****-*****
	3451				3500
msa183564.2{147_COH1}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M732}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M781}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_2603}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_JM9130013}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_18RS21}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_090}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_CJB110}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_A909}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTcAA	TCAGGAAATG
msa183564.2{147_H36B}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTcAA	TCAGGAAATG
msa183564.2{147_1169NT}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
Consensus	*****	*****	*****	*****	*****
	3501				3550
msa183564.2{147_COH1}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_M732}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_M781}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_2603}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_JM9130013}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_18RS21}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_090}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_CJB110}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_A909}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_H36B}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAgATC
msa183564.2{147_1169NT}	AGAAAGTCCT	CACCTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAAaATC
Consensus	*****	*****	*****	*****	*****
	3551				3600
msa183564.2{147_COH1}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_M732}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_M781}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_2603}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_JM9130013}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_18RS21}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_090}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_CJB110}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_A909}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_H36B}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_1169NT}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
Consensus	*****	*****	*****	*****	*****
	3601				3650
msa183564.2{147_COH1}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_M732}	-----	-----	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----	-----	-----
msa183564.2{147_2603}	-----	-----	-----	-----	-----
msa183564.2{147_JM9130013}	-----	-----	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3651				3700
msa183564.2{147_COH1}	-----	-----	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----	-----	-----
msa183564.2{147_2603}	ctagtttact	tctttatttg	aaacccaaaa	agactaaaaa	taatagtaaa
msa183564.2{147_JM9130013}	-----	-----	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----	-----	-----
msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 4412

STRAIN 2603

VDKHHSKKA~~IL~~KLTLITTSILLMHSNQVNAEEQELKNQE~~Q~~SPVIANVAQQPSPSVTTNTIV
EKTSVTAASASNTAKEMGDTSVKNDKTEDELEELSKNLDTSNLGADLEEEYPSK~~P~~ETTN
NKESNVV~~T~~ASTAIAQKVPSAYEEV~~K~~PESSSLAVLDTSKIT~~K~~LQAITQRGKGNVVAIID
TGDFINHDI~~F~~RLD~~S~~PKDDKHSFKTKTEFEELKAKHNI~~T~~Y~~G~~KWVNDKI~~V~~FAHNYANN~~T~~ETV
ADIAAMKDG~~Y~~GEAKNI~~S~~HGTHVAGI~~F~~VGN~~S~~KRPAINGLLEGAAPNAQVLLMRI~~P~~DKI
DSDK~~F~~GEAYAKAITDAVNLGAKTINMSIGKTADSLIALNDKVKLAL~~K~~LASEKGVAVVVA
GNEGAFGMDY~~S~~KPLSTNPDYGTVNSPAISEDTLSVASYESL~~K~~TI~~S~~EVVET~~T~~IEGKLV~~K~~LP
IVTSKPF~~D~~KGKAYDVVYANGAK~~K~~DFEGKDFGKIALIERGGGLDFMTKI~~T~~HATNAGVVG
IVI~~F~~NDQEK~~R~~GNFLI~~P~~YREL~~P~~VGI~~I~~SKVDGERIKNTSSQLTFNQSP~~F~~VVDSQGGNRMLEQ
SSWGV~~T~~AEGAI~~K~~PDV~~T~~ASGF~~E~~IYSS~~T~~YNNQYQ~~T~~MSGTSMASPHVAGLMTMLQSHLAEKYK
GMNLD~~S~~KKLLELSKNILMSSATALYSEEDKAFYSPRQQGAGVVD~~A~~EKAIAQ~~A~~QYYITGNDG
KAKINLKR~~M~~GDKFDTIVTIIHKLVEGVKELYQANVATEQV~~N~~KGK~~F~~AL~~K~~PKQALLD~~T~~NWQKV
ILRD~~K~~ETQVRFTIDASQFSQ~~L~~KEQMANGYFLEGFVRFKEAKDSN~~Q~~ELMSIPFVGFNGDF
ANLQALE~~T~~PIYK~~T~~LSKGSFYYPNDTTHKDQLEYNESAPFESNNYTALLTQ~~S~~ASWGYVDY
VKNGGELELAPESPKRIILGT~~F~~ENKVEDKTIHLLERDAANNPYFAISPNK~~D~~GNRDEIT~~P~~Q
ATFLRN~~V~~KDISAQVLDQNGNVIWQSKVLP~~S~~YRKNFHN~~N~~PKQSDGHYRMDALQWSGLDKDG
KVVADGFY~~T~~YRLRYTPVAEGANSQESDFK~~V~~QVSTKSPNLPSRAQFDE~~T~~NR~~T~~LSLAMPKES
SYVPT~~R~~LQVLVSHVVKDEEYGD~~E~~TSYHYFHI~~D~~QEGK~~V~~TL~~P~~KTVKIGESEVAVDPKAL~~T~~L
VVEDKAGNFAT~~V~~KLSDLLNKAVVSEKENAIVISNS~~F~~KYFDNLKKEP~~M~~FI~~S~~KK~~E~~KV~~V~~NK~~N~~L
EEIILV~~K~~PQT~~T~~VTTQSL~~S~~KEITKSGNEK~~V~~L~~T~~STNN~~S~~SRVAKIISPKHNG~~D~~SVNHTL~~P~~ST
SDRATNGLFVGT~~L~~ALLSSLLLYL~~K~~PKKTK~~N~~NSK

SEQ ID NO. 4413

STRAIN A909

EEQELKNQE~~Q~~SPVIANVAQQPSPSVTTNTVEKTSVTSASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSK~~P~~ETTNKESNVV~~T~~ASTAIAQKVPSAYEEV~~K~~PESS
SSLAVLD~~T~~SKIT~~K~~LQAITQRGKGNVVAIIDTGDFINHDI~~F~~RLD~~S~~PKDDKHSFKTKAEFEE
LKAKHNI~~T~~Y~~G~~KWVNDKI~~V~~FAHNYANN~~T~~ETVADIAAMKDG~~Y~~GEAKNI~~S~~HGTHVAGI~~F~~VG
NSK~~R~~PAINGLLEGAAPNAQVLLMRI~~P~~DKIDSDK~~F~~GEAYAKAITDAVNLGAKTINMSLGK
TADSLIALNDKVKLAL~~K~~LASEKGVAVVVAAGNEGAFGMDY~~S~~KPLSTNPDYGTVNSPAISE
DTLSVASYESL~~K~~TI~~S~~EVVET~~T~~IEGKLV~~K~~LP~~I~~VTSKPF~~D~~KGKAYDVVYANGAK~~K~~RLR.R.G
L.R.DCIN.AWWT.FYD.NHSCYKCRCCWYR.YF.RSRKTWKFNSLP.ITCGGY.SRW
RAYK~~Y~~FKSVNI.PEF.SS.PRWQSYAGTIKLG~~R~~DS.RSNQA.CNSFWL.NLFFNL.S
IPNNV~~Y~~KYGF~~T~~TCCRINDNASKSFG.EI.RDEF~~R~~.KIARIV.KHPHELSNSI.RG.
GVLFTTSARCRCS.C.KSPSSILCYWKRWQS.N.SQTSGR.I.YHSYNS.TCRR~~C~~RIV
LSS.CSNRTSK.R.ICP.TTSLARY.LAESNSS.RNTSSIY.F.SI.SEIKRTD~~G~~KWL
FLRR~~F~~CTF.RSQQ.SGVNEYSFCRI.W.FCELTST.NTDL.DAF.R.FLL.TK.YNS.R
PIGVQ.ISSF.KQQLYCLVNTISVLGLC.LCQKWGVRI~~S~~TGESKKNYFRNF.E.G.G.N
NSSFGKRCSE.SIFCHFSK.RWK.G.NHSPGNFLKCC.GYFCSSSRK~~K~~W~~C~~YLAK.GFTI
LS.KFP.SKAK.WLSYGCPSVEWFR.GWQSCSRWFLYLSFTLHTSSRRSK.SGVRL.S
SSKY.VTKSSFTSSV.N.SNIKLSHA.GK.LCSYISTISFIS~~C~~CKR.RIWR.DFLPLF
PYRSRR.SDTS.NS.DRRE.GCSR.PDLTCCGR.SW.FRNGKIV.PLE.GSSIRERKRY
SNF.QQIF.LEKRTYVYF.RRKSSQESRRNSIS.AANYSYYSIIV.RNNSIRK.ESP
HFYKQ.QSS.DHIT.T.RGFC.PY

SEQ ID NO. 4414

STRAIN H36B

EEQELKNQE~~Q~~SPVIANVAQQPSPSVTTNTVEKTSVTSASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSK~~P~~ETTNKESNVV~~T~~ASTAIAQKVPSAYEEV~~K~~PESS
SSLAVLD~~T~~SKIT~~K~~LQAITQRGKGNVVAIIDTGDFINHDI~~F~~RLD~~S~~PKDDKHSFKTKAEFEE
LKAKHNI~~T~~Y~~G~~KWVNDKI~~V~~FAHNYANN~~T~~ETVADIAAMKDG~~Y~~GEAKNI~~S~~HGTHVAGI~~F~~VG
NSK~~R~~PAINGLLEGAAPNAQVLLMRI~~P~~DKIDSDK~~F~~GEAYAKAITDAVNLGAKTINMSLGK
TADSLIALNDKVKLAL~~K~~LASEKGVAVVVAAGNEGAFGMDY~~S~~KPLSTNPDYGTVNSPAISE
DTLSVASYESL~~K~~TI~~S~~EVVET~~T~~IEGKLV~~K~~LP~~I~~VTSKPF~~D~~KGKAYDVVYANGAK~~K~~DFEGK
FKGKIALIERGGGLDFMTKI~~T~~HATNAGVVGIVI~~F~~NDQEK~~R~~GNFLI~~P~~YREL~~P~~VGI~~I~~SKVDG
ERI~~K~~NTSSQLTFNQSP~~F~~VVDSQGGNRMLEQSSWGV~~T~~AEGAI~~K~~PDV~~T~~ASGF~~E~~IYSS~~T~~YNNQ
YQ~~T~~MSGTSMASPHVAGLMTMLQSHLAEKYKGMNLD~~S~~KKLLELSKNILMSSATALYSEEDK
AFYSPRQQGAGVVD~~A~~EKAIAQ~~A~~QYYITGNDGKAKINLKR~~V~~GDKFDTIVTIIHKLVEGVKELY
YQANVATEQV~~N~~KGK~~F~~AL~~K~~PKQALLD~~T~~NWQKVILRD~~K~~ETQVRFTIDSSQFSQ~~L~~KEQMANGY
FLEGFVRFKEAKDSN~~Q~~ELMSIPFVGFNGDFANLQALE~~T~~PIYK~~T~~LSKGSFYYPNDTTHKD
QLEYNESAPFESNNYTALLTQ~~S~~ASWGYVDYVKNGGELELAPESPKRIILGT~~F~~ENKVEDKTI
HLLERDAANNPYFAISPNK~~D~~GNRDEITPQATFLRN~~V~~KDISAQVLDQNGNVIWQSKVLP~~S~~
YRKNFHN~~N~~PKQSDGHYRMDALQWSGLDKGKVVADGFY~~T~~YRLRYTPVAEGANSQESDFK~~V~~
QVSTKSPNLPSRAQFDE~~T~~NR~~T~~LSLAMPKESSYVPT~~R~~LQVLVSHVVKDEEYGD~~E~~TSYHYF

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

HIDQEGKVTLPKTVKIGESEVAVDPKTLTLVVEDKAGNFATVKLSDLLNKAUVSEKENAI
VISNNFKYFDNLKKEPMFI SKKEGKVVNKNLEEEIALVKPQTTVTTQSLSKETIQSGNEKVL
TSTNNSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4415
STRAIN L8RS21

EEQELKNQEQSPVIANVAQQPSPSVTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPEPTNNKESNVVNSTAIAQKVPSAYEEVKPESK
SSLAVLDTSKITKLOATTQRGKGNVVAIIDTGFIDNHDI FRLDSPKDDKHSFKTKTEFEE
LKAKHNIYGGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGI FVG
NSKRPAINGLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAIDAVNLGAKTINMSGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLTKTISEVVETIIEGKLVKLP I VTSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDMTKITHTATNAGVVGIV I FNDQEKRGNFLLI PYRELPVGI I SKVDG
ERIKNTSSQLTFNQSEFVVDSDQGNRMLEQSSWCVTAEGA I KPDVTAASFBIYSSYTNNO
YQTMSTSMASPHVAGLMTMLQSHLAEKYKGMNLDKSKLLELSKNILMSSATALYSEBDK
AFYSPRQOQAGVVDKAKIAQAQYITGNDGKAKINLKRMGDKFDITVTIHKLVEGVKELY
YQANVATEQVNVKGFALKPQALLDTNWQKVLIRDKETQVRFIDASQFSQKLKQBQMANGY
FLEGFVRFKBAKDSNQLMSI PFVGFNGDFANLQALETPI YKTI SKGSFYKPNDDTHKD
QLEYNESAPFVSNVYIALLTQASASWGYVDVYKNGGELELAPESPRI I LGTFENKVEDKT
IHLLEDAANNPYFAISPKNKGNRDEITPQATFLRNVKDI SAQVLDQNGNVIWQSKVLP
YRKNPHNNPKQSDGHYRMDALQWGLDKDQKVVADGFYTYRLRYTPVAEGANSQESDPKV
QVSTKSPNLPSPRAQFPDETNRITLSLAMPKESYVPTYRLQVLSHVVDKDEEYGDSTSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNKAUVSEKENAI
VISNNFKYFDNLKKEPMFI SKKEGKVVNKNLEEEI ILVKPQTTVTTQSLSKETIKSGNEKVL
TSTNNSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4416
STRAIN M732

EEQELKNQEQSPVIANVAQQPSPSVTNI VEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPEPTNNKESNVVNSTAIAQKVPSAYEEVKSEK
SSLAVLDTSKITKLOATTQRGKGNVVAIIDTGFIDNHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNIYGGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGI FVG
NSKRPAINSLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAIDAVNLGAKTINMSGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLTKTISEVVETIIEGKLVKLP I VTSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQLVLSLFLTIKKNVEIF.FLTVNVLWGLLVK.MA
SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPII IN
TKQCLVQVWLHMLQD.QCFKVIWLRNIGK.I.ILKNC.NCLTSS.AQQQHYIVKRI
RFIHHVSKVQV.LMLKLSKLNIMLETMAKLLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNPLNHHKPC.ILIGRK.FFVKKKHFDDLLMLVNLVRN.KNRQWMI
S.KVLYVLLKPRIVIRS.VFLL.DLMVILRTYKHLKHFIRRFKVVSTINQMIQLIKT
NWSTNMQLLKATITLPC.HNQRGLAMLIMSKMVG.S.N.HRRVQKELF.ELLRIRLRKIQ
FIWKEMQRIIHLPLFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISII IQSKVMVI I VVWMLFSGVV.IRMAKL.QMVFILIAVYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELKSLMKLIEH.A.PCLRKVVMPFLHIVYN.FYLM.LKMKMGMRLLTII S
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKT.L.
.FLTVSNILIT.RKNLCLFLKKEK.TRI.KK.H.LSLKLQLLNLHCLLK.LNQEMRKSS
LQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4417
STRAIN COH1

EEQELKNQEQSPVIANVAQQPSPSVTNI VEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPEPTNNKESNVVNSTAIAQKVPSAYEEVKSEK
SSLAVLDTSKITKLOATTQRGKGNVVAIIDTGFIDNHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNIYGGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGI FVG
NSKRPAINSLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAIDAVNLGAKTINMSGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLTKTISEVVETIIEGKLVKLP I VTSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQLVLSLFLTIKKNVEIF.FLTVNVLWGLLVK.MA
SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPII IN
TKQCLVQVWLHMLQD.QCFKVIWLRNIGK.I.ILKNC.NCLTSS.AQQQHYIVKRI
RFIHHVSKVQV.LMLKLSKLNIMLETMAKLLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNPLNHHKPC.ILIGRK.FFVKKKHFDDLLMLVNLVRN.KNRQWMI
S.KVLYVLLKPRIVIRS.VFLL.DLMVILRTYKHLKHFIRRFKVVSTINQMIQLIKT
NWSTNMQLLKATITLPC.HNQRGLAMLIMSKMVG.S.N.HRRVQKELF.ELLRIRLRKIQ
FIWKEMQRIIHLPLFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISII IQSKVMVI I VVWMLFSGVV.IRMAKL.QMVFILIAVYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELKSLMKLIEH.A.PCLRKVVMPFLHIVYN.FYLM.LKMKMGMRLLTII S
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKT.L.
.FLTVSNILIT.RKNLCLFLKKEK.TRI.KK.H.LSLKLQLLNLHCLLK.LNQEMRKSS
LQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4418
STRAIN M781

EEQELKNQEQSPVIANVAQQPSPSVTNI VEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPEPTNNKESNVVNSTAIAQKVPSAYEEVKSEK
SSLAVLDTSKITKLOATTQRGKGNVVAIIDTGFIDNHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNIYGGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGI FVG
NSKRPAINSLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAIDAVNLGAKTINMSGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLTKTISEVVETIIEGKLVKLP I VTSKPFDKGKAYDVVYANYGAKKILKVRT
LKVRLH.LSVVVDLIL.LKSLMLQMQLVLSLFLTIKKNVEIF.FLTVNVLWGLLVK.MA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHMLQD..QCFKVIWLRNIKG.I.ILKNC.NCLKTSS.AQQOHYIVKRIR
RFIIHVSQVQV.LMLKLSKLNIMLLETMAKLLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNPLPLNHKPC.I.LIGRK.FFVIKHKFDLLLMLVNLVRN.KNRWQMI
S.KVLYVLKPRIVIRS.VFLL.DLMVILRTYKHLKRRFIRRFLKVVSTINQMIQLIKT
NWSTMNQLLKAATILPC.HNQLGAMLIMSKMVGS.N.HRRVQKELF.ELLRIRLRIKQ
FIFWKEMQRI.IHILPFLQIKMEIGTKSLPRQLS.EMLRI.FLLKF.I.KMEMLFGKVRFYHL
IVKISII.IQSKVMVI.IVWMLFSGVV.I.RMAKL.QMVFLIAYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHELMLKLIBH.A.PCLRKVMFLHIVYN.FYLM.L.KMKMGMRLLTIIS
I.IKKVK.HFLKRLR.EVRRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKTL.
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKQLLNLHCLKK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4419
STRAIN JM9130013

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPEPTTNNKESNVVTAASAI.AQKVP.SAYE.VE.VKPE.SK
SSLAVFDTSKITLQAI.TQRGKGNVVAI.IDTGF.DINHDI.FRLDS.PKDDKHS.FKTKAE.FEE
LKAKHNI.TYKQWVNDKI.VFAHNYANNTETVADIAAAMK.DGYGSEAKNI.SHGTHVAGI.FVG
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDKFGEAYAKA.ITDAVNLGAKTINMSLIGK
TADSLIALNDKVKLALKLAASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKITSEVVETIIEGKLVKLP.IVTSKPF.DKGGKAYD.VVYANYGAKKDFEGKD
FKGKIAL.IERGGGLDFMTKI.THATNAGVVG.IVI.FNDQEKRGNF.LI.PYREL.PVGI.SKVDG
ERIKNTSSQ.LTFNQSF.FEVVDSQGGNRMLEQ.SSWGVT.AEGA.IKPDV.TASGFEI.YSSTYNNQ
YQTM.SGT.SMASPHVAGL.MTML.QSHLAEKY.KGMNLD.SKLLLEL.SKNIL.MSSATAL.YSEEDK
AFYS.PRQQGAGV.VDAEKAI.QAQQY.ITGNDG.KAKINL.KRMDK.FDI.TVTI.HKLV.EGVKELY
YQANVATEQ.VNKGK.FALKP.QAL.LD.TNWQKV.I.LRD.KET.QVRFT.IDAS.QFSQ.LKQEMANGY
FLEG.FVR.FKEAKDS.NQELMSI.PFVGFNGD.FANL.QALETP.I.YKTL.SKGS.FYYK.PNDT.THKD
QLEYNESAP.PESNNY.TALLT.QSASWG.VYDVY.VKNGGELE.LAPES.PKRI.I.LGT.FENK.VEDKT
IHLLERDAANNPYFAI.SPNKDG.NRDEIT.PQAT.FLRNVKD.I.SAQVLD.QONGV.I.WQSKV.LPS
YRKN.FHNNP.KQSDGHYRMDAL.QWSGLD.KDKGVVADGF.YTYRL.RYTP.VAEGANS.QESDFKV
QVST.KSPNL.PLLAQ.FDETNRTL.SLAMP.KESSYV.PTYRLQL.VL.SHVVKDE.YGDETSYHYF
HIDQEGKVTL.PKTVKI.GESEVAVDP.KALTL.VVEDKAGNFAT.VKLSDL.LNKAVVSE.KENAI
VISNSFKY.FDNLK.KESMFI.SKEGKV.VNKNLEEBEITLVK.PQTTVTTQ.SLSKEIT.KSGNEKVL
TSTNNNSRVAKI.I.SPKHNGDSVNHT

SEQ ID NO. 4420
STRAIN 090

EEQELKNQEQSPVIANVAQQPSPSVTTNI VEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPEPTTNNKESNVVTAASAI.AQKVP.SAYE.VE.VKPE.SK
SSLAVFDTSKITLQAI.TQRGKGNVVAI.IDTGF.DINHDI.FRLDS.PKDDKHS.FKTKAE.FEE
LKAKHNI.TYKQWVNDKI.VFAHNYANNTETVADIAAAMK.DGYGSEAKNI.SHGTHVAGI.FVG
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDKFGEAYAKA.ITDAVNLGAKTINMSLIGK
TADSLIALNDKVKLALKLAASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKITSEVVETIIEGKLVKLP.IVTSKPF.DKGGKAYD.VVYANYGAKKDFEGKD
FKGKIAL.IERGGGLDFMTKI.THATNAGVVG.IVI.FNDQEKRGNF.LI.PYREL.PVGI.SKVDG
ERIKNTSSQ.LTFNQSF.FEVVDSQGGNRMLEQ.SSWGVT.AEGA.IKPDV.TASGFEI.YSSTYNNQ
YQTM.SGT.SMASPHVAGL.MTML.QSHLAEKY.KGMNLD.SKLLLEL.SKNIL.MSSATAL.YSEEDK
AFYS.PRQQGAGV.VDAEKAI.QAQQY.VT.GNDG.KAKINL.KRVGDK.FDI.TVTI.HKLV.EGVKELY
YQANVATEQ.VNKGK.FALKP.QAL.LD.TNWQKV.I.LRD.KET.QVRFT.IDAS.QFSQ.LKQEMANGY
FLEG.FVR.FKEAKDS.NQELMSI.PFVGFNGD.FANL.QALETP.I.YKTL.SKGS.FYYK.PNDT.THKD
QLEYNESAP.PESNNY.TALLT.QSASWG.VYDVY.VKNGGELE.LAPES.PKRI.I.LGT.FENK.VEDKT
IHLLERDAANNPYFAI.SPNKDG.NRDEIT.PQAT.FLRNVKD.I.SAQVLD.QONGV.I.WQSKV.LPS
YRKN.FHNNP.KQSDGHYRMDA.FQWSGLD.KDKGVVADGF.YTYRL.RYTP.VAEGANS.QESDFKV
QVST.KSPNL.PLLAQ.FDETNRTL.SLAMP.KESSYV.PTYRLQL.VL.SHVVKDE.YGDETSYHYF
HIDQEGKVTL.PKTVKI.GESEVAVDP.KALTL.VVEDKAGNFAT.VKLSDL.LNKAVVSE.KENAI
VISNSFKY.FDNLK.KESMFI.SKEGKV.VNKNLEEBEITLVK.PQTTVTTQ.SLSKEIT.KSGNEKVL
TSTNNNSRVAKI.I.SPKHNGDSVNHT

SEQ ID NO. 4421
STRAIN CJB110

EEQELKNQEQSPVIANVAQQPSPSVTTNI VEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEEYPSKPEPTTNNKESNVVTAASAI.AQKVP.SAYE.VE.VKPE.SK
SSLAVFDTSKITLQAI.TQRGKGNVVAI.IDTGF.DINHDI.FRLDS.PKDDKHS.FKTKAE.FEE
LKAKHNI.TYKQWVNDKI.VFAHNYANNTETVADIAAAMK.DGYGSEAKNI.SHGTHVAGI.FVG
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDKFGEAYAKA.ITDAVNLGAKTINMSLIGK
TADSLIALNDKVKLALKLAASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKITSEVVETIIEGKLVKLP.IVTSKPF.DKGGKAYD.VVYANYGAKKDFEGKD
FKGKIAL.IERGGGLDFMTKI.THATNAGVVG.IVI.FNDQEKRGNF.LI.PYREL.PVGI.SKVDG
ERIKNTSSQ.LTFNQSF.FEVVDSQGGNRMLEQ.SSWGVT.AEGA.IKPDV.TASGFEI.YSSTYNNQ
YQTM.SGT.SMASPHVAGL.MTML.QNHLAEKY.KGMNLD.SKLLLEL.SKNIL.MSSATAL.YSEEDK
AFYS.PRQQGAGV.VDAEKAI.QAQQY.VT.GNDG.KAKINL.KRVGDK.FDI.TVTI.HKLV.EGVKELY
YQANVATEQ.VNKGK.FALKP.QAL.LD.TNWQKV.I.LRD.KET.QVRFT.IDAS.QFSQ.LKQEMANGY
FLEG.FVR.FKEAKDS.NQELMSI.PFVGFNGD.FANL.QALETP.I.YKTL.SKGS.FYYK.PNDT.THKD
QLEYNESAP.PESNNY.TALLT.QSASWG.VYDVY.VKNGGELE.LAPES.PKRI.I.LGT.FENK.VEDKT
IHLLERDAANNPYFAI.SPNKDG.NRDEIT.PQAT.FLRNVKD.I.SAQVLD.QONGV.I.WQSKV.LPS
YRKN.FHNNP.KQSDGHYRMDA.FQWSGLD.KDKGVVADGF.YTYRL.RYTP.VAEGANS.QESDFKV
QVST.KSPNL.PLLAQ.FDETNRTL.SLAMP.KESSYV.PTYRLQL.VL.SHVVKDE.YGDETSYHYF
HIDQEGKVTL.PKTVKI.GESEVAVDP.KALTL.VVEDKAGNFAT.VKLSDL.LNKAVVSE.KENAI
VISNSFKY.FDNLK.KESMFI.SKEGKV.VNKNLEEBEITLVK.PQTTVTTQ.SLSKEIT.KSGNEKVL
TSTNNNSRVAKI.I.SPKHNGDSVNHT

SEQ ID NO. 4422

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

STRAIN 1169NT

EEQELKNQEQSPVIANVAQQPSPSVTTNI VEKTSVTAASANTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNMGADLEEEYPSKPETTNNKESNVVTNASTAI A QKVPSAYEEVKPKSK
SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGF DINHDI FRLDSPKDDKHSFKNKAEFEE
LKAKHNITYGKWNDKIVFAHNYANTTETVADIAAAMKDG YGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAENAVQLMIRIPDKIDSDKFGGEAYAKAITDAVNLGAKTINMSIGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFMGDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVEITIEGKLVKLPVITSKPFDKGA YDVVYANYGAKDFEGKD
FKGKIALIERGGGLDMFTKI THATNAGVVGIVIFNDQEKRGNF LIPYRELPGVVISKVDG
ERIKNTSSQLTFNQRFEVVDSSQGNRMLEQSSWGVTAEGAIKPDV TASGFEIYSSTYNNQ
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK
AFYSPRQGGAGVVDAAEKAIQAQYVVTGNDGKAKINLKR VGDKFDITVTIHKLVEGVKELY
YQANVATEQVNVKGFALKPQALLD TNWQKVI LRDKETQVRPTIDASQFSQKLEQMANGY
FLEGFVRFKKAEDSNQBLMSIPFVGFNGDFASLQALETP IYKTLKSGSFYYPKNDTTHKD
QLEYNESAPPFESNNYATLLTQSASWGYVDVVKNGGELELAPESP KRIILGTFPENKVEDKT
IHLERDAANNPYFAISP NKDGNRDEITPQATFLRNVDI SAQVLDQNGNVIWQSKVLPS
YRKNFHNPNKQSDGHYRMDALQWSSGLDKGKV VADGFPYTRLYRTPVABGANSQESDPKV
QVSTKSPNLP SRAQFDETNRTL SLAMPKGS SYVPIYRLQLVLSHVVKDEEYGETSYFF
HIDQEGKATLPKTVKIGESEVAVDPKALTLVVEDKAGNFATV KLSDLNKA VVSEKENAI
VISNSPKYFDNLKKEPMFISKKEKVVNKNLLEE IILVKPHTT VTTQSLSK EITKSGNEKVL
TSTNNNSRVAKIISP KHNGDSVNHT

PRETTY of: /biotmp/msa209368.2{*} February 10, 2003 02:09 ..

msa209368.2{147_COH1} 1 50
msa209368.2{147_M732}
msa209368.2{147_M781}
msa209368.2{147_18RS21}
msa209368.2{147_2603}
msa209368.2{147_JM9130013}
msa209368.2{147_090}
msa209368.2{147_CJB110}
msa209368.2{147_1169NT}
msa209368.2{147_H36B}
msa209368.2{147_A909}
Consensus *****

msa209368.2{147_COH1} 51 100
msa209368.2{147_M732}
msa209368.2{147_M781}
msa209368.2{147_18RS21}
msa209368.2{147_2603}
msa209368.2{147_JM9130013}
msa209368.2{147_090}
msa209368.2{147_CJB110}
msa209368.2{147_1169NT}
msa209368.2{147_H36B}
msa209368.2{147_A909}
Consensus *****

msa209368.2{147_COH1} 101 150
msa209368.2{147_M732}
msa209368.2{147_M781}
msa209368.2{147_18RS21}
msa209368.2{147_2603}
msa209368.2{147_JM9130013}
msa209368.2{147_090}
msa209368.2{147_CJB110}
msa209368.2{147_1169NT}
msa209368.2{147_H36B}
msa209368.2{147_A909}
Consensus *****

msa209368.2{147_COH1} 151 200
msa209368.2{147_M732}
msa209368.2{147_M781}
msa209368.2{147_18RS21}
msa209368.2{147_2603}
msa209368.2{147_JM9130013}
msa209368.2{147_090}
msa209368.2{147_CJB110}
msa209368.2{147_1169NT}
msa209368.2{147_H36B}
msa209368.2{147_A909}
Consensus *****

msa209368.2{147_COH1} 201 250
SPKtKaEFEE LKAKHNITYG KWNVDKIVFA HNYANNTETV ADIAAAMKDG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_M732}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_M781}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_18RS21}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_2603}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_JM9130013}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_090}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_CJB110}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_1169NT}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_H36B}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_A909}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
Consensus	*****-****	*****	*****	*****	*****
251					
msa209368.2{147_COH1}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInS <i>l</i>	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M732}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInS <i>l</i>	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M781}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInS <i>l</i>	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_18RS21}	YGSEAKNI <i>S</i> H	GTHVAGIFVG	NSKRPAIn <i>g</i> l	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_2603}	YGSEAKNI <i>S</i> H	GTHVAGIFVG	NSKRPAIn <i>g</i> l	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_JM9130013}	YGSEAKNI <i>S</i> H	GTHVAGIFVG	NSKRPAIn <i>g</i> l	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_090}	YGSEAKNI <i>S</i> H	GTHVAGIFVG	NSKRPAIn <i>g</i> l	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_CJB110}	YGSEAKNI <i>S</i> H	GTHVAGIFVG	NSKRPAIn <i>g</i> l	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_1169NT}	YGSEAKNI <i>S</i> H	GTHVAGIFVG	NSKRPAIn <i>g</i> l	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_H36B}	YGSEAKNI <i>S</i> H	GTHVAGIFVG	NSKRPAIn <i>g</i> l	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_A909}	YGSEAKNI <i>S</i> H	GTHVAGIFVG	NSKRPAIn <i>g</i> l	LLEGAAPNAQ	VLLMRIPDKI
Consensus	*****-*	*****	*****-*	*****	*****
301					
msa209368.2{147_COH1}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_M732}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_M781}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_18RS21}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_2603}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_JM9130013}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_090}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_CJB110}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_1169NT}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_H36B}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
msa209368.2{147_A909}	DSDKfGEAYA	KAIiDAVN <i>l</i> g	AKTINMS <i>l</i> GK	TADSLIAlND	KVKLAlKLAS
Consensus	*****	***-*****	*****-*	*****	*****
351					
msa209368.2{147_COH1}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_M732}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_M781}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_18RS21}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_2603}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_JM9130013}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_090}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_CJB110}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_1169NT}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_H36B}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
msa209368.2{147_A909}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNP <i>D</i> Y	GTVNSPAI <i>S</i> E	DTLSVASY <i>S</i> E
Consensus	*****	*****	*****	*****	*****
401					
msa209368.2{147_COH1}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKK <i>l</i> klvrt
msa209368.2{147_M732}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKK <i>l</i> klvrt
msa209368.2{147_M781}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKK <i>l</i> klvrt
msa209368.2{147_18RS21}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKKdfegkd
msa209368.2{147_2603}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKKdfegkd
msa209368.2{147_JM9130013}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKKdfegkd
msa209368.2{147_090}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKKdfegkd
msa209368.2{147_CJB110}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKKdfegkd
msa209368.2{147_1169NT}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKKdfegkd
msa209368.2{147_H36B}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKKdfegkd
msa209368.2{147_A909}	LKTISEVVET	TIEGKL <i>V</i> K <i>L</i> P	IVTSKPF <i>D</i> KG	KAYDVVY <i>Y</i> AN <i>Y</i>	GAKK <i>l</i> .r.g
Consensus	*****	*****	*****	*****	****------
451					
msa209368.2{147_COH1}	lkvrlh.lsv	vvdlil.lks	lmlqmqvllv	slfltikknv	eiF.fltvny
msa209368.2{147_M732}	lkvrlh.lsv	vvdlil.lks	lmlqmqvllv	slfltikknv	eiF.fltvny
msa209368.2{147_M781}	lkvrlh.lsv	vvdlil.lks	lmlqmqvllv	slfltikknv	eiF.fltvny
msa209368.2{147_18RS21}	fkgkialier	gggldf <i>m</i> tki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_2603}	fkgkialier	gggldf <i>m</i> tki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_JM9130013}	fkgkialier	gggldf <i>m</i> tki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_090}	fkgkialier	gggldf <i>m</i> tki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_CJB110}	fkgkialier	gggldf <i>m</i> tki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_1169NT}	fkgkialier	gggldf <i>m</i> tki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_H36B}	fkgkialier	gggldf <i>m</i> tki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_A909}	l.r.dcin.a	wwwt.fyd.n	hscykrcrcw	yryf.rsrkt	wkFsnslp.i
Consensus	-----	-----	-----	-----	-----
501					
550					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_COH1}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M732}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M781}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_18RS21}	pvGiiskvdg	eriKntssql	tfngsfevvd	sgggnrmleq	sswgvtaeaga
msa209368.2{147_2603}	pvGiiskvdg	eriKntssql	tfngsfevvd	sgggnrmleq	sswgvtaeaga
msa209368.2{147_JM9130013}	pvGiiskvdg	eriKntssql	tfngsfevvd	sgggnrmleq	sswgvtaeaga
msa209368.2{147_090}	pvGviskvdg	eriKntssql	tfngsfevvd	sgggnrmleq	sswgvtaeaga
msa209368.2{147_CJB110}	pvGviskvdg	eriKntssql	tfngsfevvd	sgggnrmleq	sswgvtaeaga
msa209368.2{147_1169NT}	pvGviskvdg	eriKntssql	tfngsfevvd	sgggnrmleq	sswgvtaeaga
msa209368.2{147_H36B}	pvGviskvdg	eriKntssql	tfngsfevvd	sgggnrmleq	sswgvtaeaga
msa209368.2{147_A909}	tcGgy..srw	rayKkyfksv	ni.pef.ss.	.prwqsyagt	iklgrds.rs
Consensus	-----*	-----*	-----	-----	-----
					551
msa209368.2{147_COH1}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_M732}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_M781}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_18RS21}	ikpdvtasgf	eysstynnq	yqtsmgtma	sphvaglmtm	lqshlaekyk
msa209368.2{147_2603}	ikpdvtasgf	eysstynnq	yqtsmgtma	sphvaglmtm	lqshlaekyk
msa209368.2{147_JM9130013}	ikpdvtasgf	eysstynnq	yqtsmgtma	sphvaglmtm	lqshlaekyk
msa209368.2{147_090}	ikpdvtasgf	eysstynnq	yqtsmgtma	sphvaglmtm	lqshlaekyk
msa209368.2{147_CJB110}	ikpdvtasgf	eysstynnq	yqtsmgtma	sphvaglmtm	lqshlaekyk
msa209368.2{147_1169NT}	ikpdvtasgf	eysstynnq	yqtsmgtma	sphvaglmtm	lqshlaekyk
msa209368.2{147_H36B}	ikpdvtasgf	eysstynnq	yqtsmgtma	sphvaglmtm	lqshlaekyk
msa209368.2{147_A909}	nqa.cnsfwl	.nlffnl..s	ipnnvwykyg	fttccrindn	asksfg.ei.
Consensus	-----	-----	-----	-----	-----
					601
msa209368.2{147_COH1}	g.i.ilknk.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M732}	g.i.ilknk.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M781}	g.i.ilknk.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_18RS21}	gmnlidskkl1	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_2603}	gmnlidskkl1	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_JM9130013}	gmnlidskkl1	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_090}	gmnlidskkl1	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_CJB110}	gmnlidskkl1	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_1169NT}	gmnlidskkl1	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_H36B}	gmnlidskkl1	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_A909}	rdefrf.kia	riv.khphel	nsii...rg.	gvlfittsarc	rsc.c.Ksyp
Consensus	-----	-----	-----	-----	-----*
					651
msa209368.2{147_COH1}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.gqnk.
msa209368.2{147_M732}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.gqnk.
msa209368.2{147_M781}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.gqnk.
msa209368.2{147_18RS21}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_2603}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_JM9130013}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_090}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_CJB110}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_1169NT}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_H36B}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_A909}	ssilicywkrw	qs.n.sqtsg	r.i.yhsyns	.tccrcqriv	lss.csnrts
Consensus	-----	-----	-----	-----	-----
					701
msa209368.2{147_COH1}	ikvnlplnhk	pc.iligrk.	ffvikkkhkd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_M732}	ikvnlplnhk	pc.iligrk.	ffvikkkhkd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_M781}	ikvnlplnhk	pc.iligrk.	ffvikkkhkd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_18RS21}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKeqmangy
msa209368.2{147_2603}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKeqmangy
msa209368.2{147_JM9130013}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKeqmangy
msa209368.2{147_090}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKeqmangy
msa209368.2{147_CJB110}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKeqmangy
msa209368.2{147_1169NT}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKeqmangy
msa209368.2{147_H36B}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKeqmangy
msa209368.2{147_A909}	k.r.icp.tt	slary.laes	nss..rntss	iyf.f.s.i.s	eiKrtgdgkwl
Consensus	-----	-----	-----	-----	-----*
					751
msa209368.2{147_COH1}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhrf	irrfkvvst
msa209368.2{147_M732}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhrf	irrfkvvst
msa209368.2{147_M781}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhrf	irrfkvvst
msa209368.2{147_18RS21}	flegfvrffe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgksfy
msa209368.2{147_2603}	flegfvrffe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgksfy
msa209368.2{147_JM9130013}	flegfvrffe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgksfy
msa209368.2{147_090}	flegfvrffe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgksfy
msa209368.2{147_CJB110}	flegfvrffe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgksfy
msa209368.2{147_1169NT}	flegfvrffe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgksfy
msa209368.2{147_H36B}	flegfvrffe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgksfy
msa209368.2{147_A909}	flrrfctf.r	sgg..sgvne	ysfcri.w.f	celtat.ntd	l.daf.r.fl
Consensus	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	801			850	
msa209368.2{147_COH1}	inqmiqlikt	nwstmnqlll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M732}	inqmiqlikt	nwstmnqlll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M781}	inqmiqlikt	nwstmnqlll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_18RS21}	ypkndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_2603}	ypkndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_JM9130013}	ypkndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_090}	ypkndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_CJB110}	ypkndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_1169NT}	ypkndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_H36B}	ypkndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_A909}	l.tk.yns.r	pigvq.issf	.kqglyclvn	tisvlglc.l	cqkwwgvriss
	Consensus	-----	-----	-----	-----
	851			900	
msa209368.2{147_COH1}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M732}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M781}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_18RS21}	pespKriiilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_2603}	pespKriiilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_JM9130013}	pespKriiilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_090}	pespKriiilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_CJB110}	pespKriiilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_1169NT}	pespKriiilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_H36B}	pespKriiilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_A909}	tgesKknyfr	nf.e.g.g.n	nssfgrkrcse	.sifchfsk.	rwk.g.nhsp
	Consensus	-----	-----	-----	-----
	901			950	
msa209368.2{147_COH1}	qls.emlrif	llkf.ikmem	lfgkvrifyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_M732}	qls.emlrif	llkf.ikmem	lfgkvrifyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_M781}	qls.emlrif	llkf.ikmem	lfgkvrifyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_18RS21}	atflrnvkdi	saqvl dqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_2603}	atflrnvkdi	saqvl dqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_JM9130013}	atflrnvkdi	saqvl dqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_090}	atflrnvkdi	saqvl dqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_CJB110}	atflrnvkdi	saqvl dqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_1169NT}	atflrnvkdi	saqvl dqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_H36B}	atflrnvkdi	saqvl dqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_A909}	gnflkkc.gy	fcssrskwwk	cylak.gfti	ls.kfp..sk	ak.wslsygc
	Consensus	-----	-----	-----	-----
	951			1000	
msa209368.2{147_COH1}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M732}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M781}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_18RS21}	lqwsgldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstkspnlp
msa209368.2{147_2603}	lqwsgldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstkspnlp
msa209368.2{147_JM9130013}	lqwsgldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstkspnlp
msa209368.2{147_090}	lqwsgldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstkspnlp
msa209368.2{147_CJB110}	lqwsgldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstkspnlp
msa209368.2{147_1169NT}	lqwsgldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstkspnlp
msa209368.2{147_H36B}	lqwsgldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstkspnlp
msa209368.2{147_A909}	psvewfr.gw	qscsrwFlYl	sftlhtsarr	sk.sgvr.l.s	ssky.vtkss
	Consensus	-----	-----	-----	-----
	1001			1050	
msa209368.2{147_COH1}	helslmklie	h.a.pclrkv	vmflhivyn.	fyml.Kmkn	mgmrl1tiis
msa209368.2{147_M732}	helslmklie	h.a.pclrkv	vmflhivyn.	fyml.Kmkn	mgmrl1tiis
msa209368.2{147_M781}	helslmklie	h.a.pclrkv	vmflhivyn.	fyml.Kmkn	mgmrl1tiis
msa209368.2{147_18RS21}	sraqfdetnr	t1slampkes	syvptyrlql	v1shvvKdee	ygdet1syhyf
msa209368.2{147_2603}	sraqfdetnr	t1slampkes	syvptyrlql	v1shvvKdee	ygdet1syhyf
msa209368.2{147_JM9130013}	sraqfdetnr	t1slampkes	syvptyrlql	v1shvvKdee	ygdet1syhyf
msa209368.2{147_090}	sraqfdetnr	t1slampkes	syvptyrlql	v1shvvKdee	ygdet1syhyf
msa209368.2{147_CJB110}	sraqfdetnr	t1slampkes	syvptyrlql	v1shvvKdee	ygdet1syhyf
msa209368.2{147_1169NT}	sraqfdetnr	t1slampkes	syvptyrlql	v1shvvKdee	ygdet1syhyf
msa209368.2{147_H36B}	sraqfdetnr	t1slampkes	syvptyrlql	v1shvvKdee	ygdet1syhyf
msa209368.2{147_A909}	ftssv..n.s	niklsha.gk	.lcsyissti	sfisccKr.r	iwr.dflplf
	Consensus	-----	-----	-----	-----
	1051			1100	
msa209368.2{147_COH1}	i.ikkvk.hf	lkrlr.ervr	lr.tlrr.hl	lwkiklvilq	r.nclts.ir
msa209368.2{147_M732}	i.ikkvk.hf	lkrlr.ervr	lr.tlrr.hl	lwkiklvilq	r.nclts.ir
msa209368.2{147_M781}	i.ikkvk.hf	lkrlr.ervr	lr.tlrr.hl	lwkiklvilq	r.nclts.ir
msa209368.2{147_18RS21}	hidqegkvtl	pktvkigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_2603}	hidqegkvtl	pktvkigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_JM9130013}	hidqegkvtl	pktvkigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_090}	hidqegkvtl	pktvkigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_CJB110}	hidqegkvtl	pktvkigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_1169NT}	hidqegkvtl	pktvkigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_H36B}	hidqegkvtl	pktvkigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_A909}	pyrsrr.sdt	s.ns.drre.	gcsrp.dldt	ccgr.sw.fr	ngkiv.ple.
	Consensus	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

		1101			1150
msa209368.2	{147_COH1}	q.yqrkctl.	.fltvsnili	t.rKnlclfl	kkeK..tri. kk.h.lslkl
msa209368.2	{147_M732}	q.yqrkctl.	.fltvsnili	t.rKnlclfl	kkeK..tri. kk.h.lslkl
msa209368.2	{147_M781}	q.yqrkctl.	.fltvsnili	t.rKnlclfl	kkeK..tri. kk.h.lslkl
msa209368.2	{147_18RS21}	avvsekenai	visnsfkyfd	nlkKepmfis	kkeKvvnknl eeiiilvqpqt
msa209368.2	{147_2603}	avvsekenai	visnsfkyfd	nlkKepmfis	kkeKvvnknl eeiiilvqpqt
msa209368.2	{147_JM9130013}	avvsekenai	visnsfkyfd	nlkKepmfis	kkeKvvnknl eeiiilvqpqt
msa209368.2	{147_090}	avvsekenai	visnsfkyfd	nlkKesmfis	kegKvvnknl eeitlvkpqt
msa209368.2	{147_CJB110}	avvsekenai	visnsfkyfd	nlkKesmfis	kegKvvnknl eeitlvkpqt
msa209368.2	{147_1169NT}	avvsekenai	visnsfkyfd	nlkKepmfis	kkeKvvnknl eeiiilvqpqt
msa209368.2	{147_H36B}	avvsekenai	visnnfkyfd	nlkKepmfis	kegKvvnknl eeialvqpqt
msa209368.2	{147_A909}	gsisirekry	snf.qfqif.	.leKrtvyvf	.rrKsskqes rrnsis.aan
	Consensus	-----	-----	---*-----	---*-----
		1151			1200
msa209368.2	{147_COH1}	qlllnhclkk	.lngemrkss	llqtiivae.	lrsyhlnitg illti-----
msa209368.2	{147_M732}	qlllnhclkk	.lngemrkss	llqtiivae.	lrsyhlnitg illti-----
msa209368.2	{147_M781}	qlllnhclkk	.lngemrkss	llqtiivae.	lrsyhlnitg illti-----
msa209368.2	{147_18RS21}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT----
msa209368.2	{147_2603}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhTlpst
msa209368.2	{147_JM9130013}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT----
msa209368.2	{147_090}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT----
msa209368.2	{147_CJB110}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT----
msa209368.2	{147_1169NT}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT----
msa209368.2	{147_H36B}	tvttqslske	itqsgnekvl	tstnnssrv	akiispkhng dsvnhT----
msa209368.2	{147_A909}	ysyysiiv.r	nnsirk.esp	hfykq...qs	s.dhit.t.r gfc.py-----
	Consensus	-----	-----	-----	-----*****
		1201			1233
msa209368.2	{147_COH1}	-----	-----	-----	---
msa209368.2	{147_M732}	-----	-----	-----	---
msa209368.2	{147_M781}	-----	-----	-----	---
msa209368.2	{147_18RS21}	-----	-----	-----	---
msa209368.2	{147_2603}	sdratnglfv	gtlallsl1	lylkkpktkn	nsk
msa209368.2	{147_JM9130013}	-----	-----	-----	---
msa209368.2	{147_090}	-----	-----	-----	---
msa209368.2	{147_CJB110}	-----	-----	-----	---
msa209368.2	{147_1169NT}	-----	-----	-----	---
msa209368.2	{147_H36B}	-----	-----	-----	---
msa209368.2	{147_A909}	-----	-----	-----	---
	Consensus	*****	*****	*****	***

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

SEQ ID NO. 4501
STRAIN 2603
 ATGAAAAAGATTAGAAAAAGTTTAGGACTTCTACTATGTTGCTTTTATAGGATTGGTACAA
 TTAGCGTTTTTTCCGGTAGCCAGTGTAAATGCTGATACCCCTAATCAACTAACAATCACAC
 CAGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGGACTGTG
 ACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATAGCGAATGAAACCAGAAG
 TATAAGAGTATCTTGACTTCTCCTACTGATACTAATGGTCAGACAAAGATAGCACTCCCA
 AATGGTTTCTGACTTTGGTTCGTGCTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCT
 TTTTATATTGAATTACCAGATGATAAGTTTATCAAATCAATTACAGATAAATCCTAAGCGA
 AAAGTTGAAACAGGCCGATTAATACTTATAAATATACAAAAGAAGGAAAGATAAAGAAA
 AGGCTATCCGGAGTAAATTTGTTTATACGATAACCAGAATCAGCCAGTTTCGCTTTAAA
 AATGGACGATTACGACCGATCAAGATGGGATTACTTCATTAGTAACTGATGATAAGGGA
 GAAATGAGGTTGAAGGTTTATACCTGGTAAGTATATTTTTCGAGAAGCAAAAGCACTA
 ACGGTTTACCGTATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAAACACAG
 GAAGTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCATCACAA
 CCGCTTTTCCACAATCATTTCTTCTTAAACAGGAAATGATTATTGGTGGAGGATGACA
 ATTCTTGGTTGTATTATTTGGGAATTTGTTTATCTTTTAAAGAAAACATAAAATAGC
 AAATCTGAAAGAAACGATACAGTA

SEQ ID NO. 4502
STRAIN 090
 GATACCCCTAATCAACTAACAATCACAC
 AGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTAT
 TGGACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATA
 TAGCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATA
 CTAATGGTCAGACAAAGATAGCACTCCCAATGGTTCGTACTTTGGTTCGT
 CTTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGA
 ATTACAGATGATAAGTTTATCAAATCAATTACAGATAAATCCTAAGCGGAA
 AAGTTGAAACAGGCCGATTAATACTTATAAATATACAAAAGAAGGAAAG
 ATAAAGAAAAGGCTATCAGGAGTAAATTTGTATTTATACGATAACAGAA
 TCAGCCAGTTTCGCTTTAAAATGGACGATTTCAGACCGATCAAGATGGGA
 TTACTTCATTAGTAACTGATGATAAGGGAGAAATGAGGTTGAAGGTTTAA
 TTACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTACCG
 TATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAAACACAGG
 AAGTAgAGGTTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAA
 CCATCACAAACCG

SEQ ID NO. 4503
STRAIN H36B
 GATACCCCTAATCAACTAACAATCACACAGA
 TAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGG
 ACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATAG
 CGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATACTA
 ATGGTCAGACAAAGATAGCACTCCCAATGGTTCGTACTTTGGTTCGTGCT
 TATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAAT
 ACCAGATGATAAGTTTATCAAATCAATTACAGATAAATCCTAAGCGAAAAG
 TTGAAAACAGGCCGATTAATACTTATAAATATACAAAAGAAGGAAAGATA
 AAGAAAAGGCTTCCGGAGTAAATTTGTATTTATACGATAACAGAAATCA
 GCCAGTTTCGCTTTAAAATGGACGATTTCAGACCGATCAAGATGGGATTA
 CTTTATTAGTAACTGATGATAAGGGAGAAATGAGGTTGAAGGTTTATTA
 CCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTACCGTAT
 ATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAAACACAGGAAG
 TAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCA
 TCACAACCGC

SEQ ID NO. 4504
STRAIN 18RS21
 GATACCCCTAATCAACTAACAATCACACAG
 ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG
 GACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATA
 GCCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATACT
 AATGGTCAGACAAAGATAGCACTCCCAATGGTTCGTACTTTGGTTCGTGCT
 TTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAAT
 TACCAGATGATAAGTTTATCAAATCAATTACAGATAAATCCTAAGCGAAAAG
 GTTGAACAGGCCGATTAATACTTATAAATATACAAAAGAAGGAAAGATA
 AAAGAAAAGGCTTCCGGAGTAAATTTGTATTTATACGATAACAGAAATC
 AGCCAGTTTCGCTTTAAAATGGACGATTTCAGACCGATCAAGATGGGATT
 ACTTCATTAGTAACTGATGATAAGGGAGAAATGAGGTTGAAGGTTTATTT
 ACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTACCGTAT
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAAACACAGGAAG
 GTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCA
 ATCACAACCC

SEQ ID NO. 4505
STRAIN CJB110
 GATACCCCTAATCAACTAACAATCACACA
 GATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTAT
 GGACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGAT
 AGCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCCTACTGATACT
 TAAATGGTCAGACAAAGATAGCACTCCCAATGGTTCGTACTTTGGTTCGTG
 CTTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAA
 TTACCAGATGATAAGTTTATCAAATCAATTACAGATAAATCCTAAGCGAAA
 AGTTGAAAACAGGCCGATTAATACTTATAAATATACAAAAGAAGGAAAGATA

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

TAAAGAAAAGGCTaTCAGGAGTAATATTTGTATTATACGATAACCCAGAAT
CAGCCAGTTTCGCTTTAAAAATGGACGATTACGACCCGATCAAGATGGGAT
TACTTCATTAGTAAGTATGATAAGGGAGAAATTTAGGTTGAAGGTTTAT
TACCTGGTAAGTATATTTTCGAGAAGCAAAGCACTAAGCTGGTTaCCGT
ATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAACACAGGA
AGTAGAGGTAGAAAACGAAAAAGAACTCCTCCACCAACAAATCCTAAAC
CATCAACACC

SEQ ID NO. 4506

STRAIN 1169NT

GATACCCCTAATCAACTAACATCACACAG
ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG
GACTGTGACTGACCAACTTAAAGTTGATTTATTGAGCCAAATGACAGATA
GCCAATTGAACCAAGATATAAGAGTATCTTGACTTCTCCTACTGATACT
AATGGtCagaCAAAGATAGCACTCCCAAATGGTTTCGACTTTGGTTCGTGC
TTATAAAGCTGATCAAGCGTTTCAACAATAGTACCTTTTATATGAAAT
TACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAAA
GTTGAAAACAGGCCGATTAAAACCTTATAAATATACAAAAGAAAGGAAAGAT
AAAGAAAAGGCTATCAGGAGTAATATTTGTATTATACGATAACCCAGAATC
AGCCAGTTTCGCTTTAAAAATGGACGATTACGACCCGATCAAGATGGGAT
ACTTCATTAGTAAGTATGATAAGGGAGAAATTTAGGTTGAAGGTTTAT
ACCTGGTAAAGTATATTTTCGAGAAGCAAAGCACTAAGCTGGTTACCGTA
TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAACACAGGAA
GTAGAGGTAGAAAACGAAAAAGAACTCCTCCACCAACAAATCCTAAACC
ATCAACACC

PRETTY of: /biotmp/msa184750.2{*} May 13, 2003 06:23 ..

msa184750.2{150_090} 1 50
msa184750.2{150_1169NT}
msa184750.2{150_CJB110}
msa184750.2{150_18RS21}
msa184750.2{150_2603} atgaaaaaga ttagaaaaag ttaggactt ctactatggt gcttttagg
msa184750.2{150_H36B}
Consensus *****

msa184750.2{150_090} 51 100
msa184750.2{150_1169NT} ---GATACCC
msa184750.2{150_CJB110} ---GATACCC
msa184750.2{150_18RS21} ---GATACCC
msa184750.2{150_2603} attggtacaa ttagcgtttt ttcggtagc cagtgtaaat gctGATACCC
msa184750.2{150_H36B} ---GATACCC
Consensus *****

msa184750.2{150_090} 101 150
msa184750.2{150_1169NT} CTAATCAACT AACAAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_CJB110} CTAATCAACT AACAAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_18RS21} CTAATCAACT AACAAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_2603} CTAATCAACT AACAAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_H36B} CTAATCAACT AACAAATCACA CAGATAGGAC TTCAGCCAAA TACTACAGAG
Consensus *****

msa184750.2{150_090} 151 200
msa184750.2{150_1169NT} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAAC TAAAAGTTGA
msa184750.2{150_CJB110} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAAC TAAAAGTTGA
msa184750.2{150_18RS21} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAAC TAAAAGTTGA
msa184750.2{150_2603} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAAC TAAAAGTTGA
msa184750.2{150_H36B} GAGGGGATTT CTTATCGTTT ATGGACTGTG ACTGACAAC TAAAAGTTGA
Consensus *****

msa184750.2{150_090} 201 250
msa184750.2{150_1169NT} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_CJB110} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_18RS21} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_2603} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_H36B} TTTATTGAGC CAAATGACAG ATAGCGAATT GAACCAGAAG TATAAGAGTA
Consensus *****

msa184750.2{150_090} 251 300
msa184750.2{150_1169NT} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_CJB110} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_18RS21} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_2603} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_H36B} TCTTGACTTC TCCTACTGAT ACTAATGGTC AGACAAAGAT AGCACTCCCA
Consensus *****

301 350

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

msa184750.2{150_090}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_1169NT}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_CJB110}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_18RS21}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_2603}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_H36B}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_1169NT}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_CJB110}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_18RS21}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_2603}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_H36B}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_1169NT}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_CJB110}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_18RS21}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_2603}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_H36B}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTcAg	GAGTAATATT
msa184750.2{150_1169NT}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTcAg	GAGTAATATT
msa184750.2{150_CJB110}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTcAg	GAGTAATATT
msa184750.2{150_18RS21}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTcAg	GAGTAATATT
msa184750.2{150_2603}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTcAg	GAGTAATATT
msa184750.2{150_H36B}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTwTcAg	GAGTAATATT
Consensus	*****	*****	*****	*****_**_*	*****
msa184750.2{150_090}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_1169NT}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_CJB110}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_18RS21}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_2603}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_H36B}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_1169NT}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_CJB110}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_18RS21}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_2603}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_H36B}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_1169NT}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_CJB110}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_18RS21}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_2603}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_H36B}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_1169NT}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_CJB110}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_18RS21}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_2603}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_H36B}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_1169NT}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_CJB110}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_18RS21}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_2603}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_H36B}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CCg-----	-----800
msa184750.2{150_1169NT}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CC-----	-----

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

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msa184750.2{150_CJB110} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_18RS21} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_2603} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgCtttttc cacaatcatt
msa184750.2{150_H36B} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgC-----
Consensus *****
*****

msa184750.2{150_090} ----- 801 ----- 850
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} tcttcctaaa acaggaatga ttatgtgtgg aggactgaca attcctgtgt
msa184750.2{150_H36B} -----
Consensus *****
*****

msa184750.2{150_090} ----- 851 ----- 900
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} gtattatattt ggggaattttg tttatccttt taagaaaaac taaaaatagc
msa184750.2{150_H36B} -----
Consensus *****
*****

msa184750.2{150_090} ----- 901 ----- 924
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} aaatctgaaa gaaacgatac agta
msa184750.2{150_H36B} -----
Consensus *****
*****

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SEQ ID NO. 4507

STRAIN 2603

```

MKKIRKSLGGLLCCFLGLVQLAFFSVASVNADTPNQLTITQIGLQPNTTEEGISYRLWTV
TDNLKVDLLSQMTDSELNPKYKSIILTSPTDTNGQTKIALPNGSYFGRAYKADQSVSTIVP
FYIELPDDKLSNQLQINPKRKVETGRLKLIKYTKEGKIKKRLSGVIFVLYDNQNPVRFK
NGRFTTDDGITSVLTDDKGEIEVEGLLPGKYIFREAKALTYRISMKDVAVVAVVANKTQ
EVEVENEKETPPPTNPKPSQPLFPQSFLPKTGMIGGGTLILGCIILGILFIFLRKTRKNS
KSERNDTV

```

SEQ ID NO. 4508

STRAIN 090

```

DTPNQLTITQIGLQPNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNPKYKSIILTSPTDT
NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
YTKEGKIKKRLSGVIFVLYDNQNPVRFKNGRFTTDDGITSVLTDDKGEIEVEGLLPGK
YIFREAKALTYRISMKDVAVVAVVANKTQEVENEKETPPPTNPKPSQ

```

SEQ ID NO. 4509

STRAIN H36B

```

DTPNQLTITQIGLQPNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNPKYKSIILTSPTDT
NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
YTKEGKIKKRLSGVIFVLYDNQNPVRFKNGRFTTDDGITSVLTDDKGEIEVEGLLPGK
YIFREAKALTYRISMKDVAVVAVVANKTQEVENEKETPPPTNPKPSQ

```

SEQ ID NO. 4510

STRAIN 18RS21

```

DTPNQLTITQIGLQPNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNPKYKSIILTSPTDT
NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
YTKEGKIKKRLSGVIFVLYDNQNPVRFKNGRFTTDDGITSVLTDDKGEIEVEGLLPGK
YIFREAKALTYRISMKDVAVVAVVANKTQEVENEKETPPPTNPKPSQ

```

SEQ ID NO. 4511

STRAIN 1169NT

```

DTPNQLTITQIGLQPNTTEEGISYRLWTVTDNLKVDLLSQMTDSELNPKYKSIILTSPTDT
NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
YTKEGKIKKRLSGVIFVLYDNQNPVRFKNGRFTTDDGITSVLTDDKGEIEVEGLLPGK
YIFREAKALTYRISMKDVAVVAVVANKTQEVENEKETPPPTNPKPSQ

```

PRETTY of: /biotmp/msa184868.2{*} May 13, 2003 06:25 ..

```

msa184868.2{150_090} 1 ----- 50
msa184868.2{150_2603} mkkirkslgl llccflglvq laffsvasvn -DTPNQLTIT QIGLQPNTTE
msa184868.2{150_H36B} ----- -DTPNQLTIT QIGLQPNTTE
msa184868.2{150_1169NT} ----- -DTPNQLTIT QIGLQPNTTE
msa184868.2{150_18RS21} ----- -DTPNQLTIT QIGLQPNTTE
Consensus *****
*****

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```

msa184868.2{150_090} 51 ----- 100
EGISYRLWTV TDNLKVDLLS QMTDSELNPK YKSIILTSPTD TNGQTKIALP

```

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

msa184868.2{150_2603}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNOK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_H36B}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNOK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_1169NT}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNOK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_18RS21}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNOK	YKSILTSPTD	TNGQTKIALP
Consensus	*****	*****	*****	*****	*****
msa184868.2{150_090}	NGSYFGRAYK	ADQSVSTIVP	FYIELEPDDKL	SNQLQINPKR	KVETGRCLKLI
msa184868.2{150_2603}	NGSYFGRAYK	ADQSVSTIVP	FYIELEPDDKL	SNQLQINPKR	KVETGRCLKLI
msa184868.2{150_H36B}	NGSYFGRAYK	ADQSVSTIVP	FYIELEPDDKL	SNQLQINPKR	KVETGRCLKLI
msa184868.2{150_1169NT}	NGSYFGRAYK	ADQSVSTIVP	FYIELEPDDKL	SNQLQINPKR	KVETGRCLKLI
msa184868.2{150_18RS21}	NGSYFGRAYK	ADQSVSTIVP	FYIELEPDDKL	SNQLQINPKR	KVETGRCLKLI
Consensus	*****	*****	*****	*****	*****
msa184868.2{150_090}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_2603}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_H36B}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_1169NT}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_18RS21}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
Consensus	*****	*****	*****	*****	*****
msa184868.2{150_090}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_2603}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_H36B}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_1169NT}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_18RS21}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
Consensus	*****	*****	*****	*****	*****
msa184868.2{150_090}	PPPTNPKPSQ	p-----	-----	-----	-----
msa184868.2{150_2603}	PPPTNPKPSQ	plfpqsflpk	tgmiigggl	ilgciilgil	fiflrktkns
msa184868.2{150_H36B}	PPPTNPKPSQ	p-----	-----	-----	-----
msa184868.2{150_1169NT}	PPPTNPKPSQ	p-----	-----	-----	-----
msa184868.2{150_18RS21}	PPPTNPKPSQ	p-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
msa184868.2{150_090}	-----	-----	-----	-----	-----
msa184868.2{150_2603}	ksaerndtv	-----	-----	-----	-----
msa184868.2{150_H36B}	-----	-----	-----	-----	-----
msa184868.2{150_1169NT}	-----	-----	-----	-----	-----
msa184868.2{150_18RS21}	-----	-----	-----	-----	-----
Consensus	*****	-----	-----	-----	-----

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

SEQ ID NO. 4601
STRAIN A909
 TGACAAATATATTTTACCCAACGGTGGTTTAGAGCAAGCAGGTGTAACCTATATTACCTTT
 CTCACCGAATAATATCAGTGAGGATTTAGAGATTTATGTCAGGAAATGCTTTTCGTCCAGA
 TAACAAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTAAACGATATCATGA
 ATTTCTCGGAGATTTATGCGTCAGTTCACCTAGTCTAGGTGTAGCTGGGGCACATGGAAA
 AACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATTACAGACACTTCTTTCT
 AATTGGAGATGGTACAGGACGGTGGTCTGCTAATGCTAAATTAACCTTTGTTGTTGAAAGCTGA
 TGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTAATACCAATATGA
 TTTTGACCACTCCGTGATTTTACAGGCCCTAGAGGACGTATTCATGCTTTAATGACTA
 TGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATGCCAAAACCTCATGAAAT
 CACTTCTGAGGCACCAATATATTTATGGTTTGAAGATCAAATGATTTTATAGCAAA
 AGACATCACTCGAATCTGTTAATGGTTCGACTTTAAGGTTTCTATAACCAAGAAAGAAAT
 TGGTCAGTTTCATGTACCGATACGGTAAACATAATATCTTAAATGCAACTGCTGTTAT
 TGCTAACCTTTACATAATGGGAATGATATGGCATTAGTAGCTGAGCATTGGAAGACATT
 TTCAGGGTAAAGCGTCGTTTACTGAGAAGATTTATGACGATACTGTCATTATTGATGA
 CTTTGGCTCACCATCTCACTGAGATTTATGCGACATTAGATGCTGCTCGACAAAAATACCC
 GTCAAAAGAAATTTAGCTATTTTCCAAACCGCATACGTTCACTCGTACGATAGCTCTTTT
 AGACGAATTTGCCCTGCTTGGAGTCAAGCGGATAGCGTTTATCTCGCTCAAATATATGG
 TCTGCTAGAGAAGTAGATAATGGTGAAGGTGAGGTAGAAGATTAGCTGCTAAGATTGT
 CAAACACTCAGATTTAGTGACAGTCGAAAATGCTCTCGCTTTACTCAATCATGATATGCT
 TGCTATGCTTTATGGGTGCTGGAGACATTCAAATGTATGAGCGCTCTTTTGAAGAATT
 ATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4602
STRAIN 1169NT
 AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGGTGGTTTAGAGCAAGC
 AGGTGTAACCTATATTTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTTATGTC
 AGGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTA
 TCATTTTAAACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACCTAGTCTAGG
 TGTAGCTGGGGCACATGAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAA
 TATTACAGACACTTCTTTCCCTAATTGGAGATGGTACAGGACGTTGGTTCTGCTAATGCTAA
 TACTTTGTTGTTGAAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
 CTCAAATATTACCAATATTGATTTTGAACCTCCTGATTTATTACAGGCTAGAGGACGT
 ATTCATGCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGA
 AGATCCAAAACCTCATGAAATCACTTCTGAGGCACCAATATATTATATGGTTTGAAGA
 TTCAAATGATTTTATAGCAAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT
 TTTCTATAACCAAGAAAGAAATGGTCAAGTTTCATGTACCGATACGGTAAACATAATAT
 CTTAAATGCAACTGCTGTTATGCTAACCTTTACATAATGGGAATTTGATATGGCATTAGT
 AGCTGAGCATTGGAAGACATTTTCAGGGTAAAGCGTCGTTTACTGAGAAGATTATTGA
 CGATACTGTCATTATTTGATGACTTTGCTCACCATCTACTGAGATTTATGGGACATTAGA
 TGCTGCTCGACAAAAATACCCGTCAAAAGAAATTTAGCTATTTTCCAAACCGCATACGTT
 CACTCGTACGATAGCTCTTTTACAGCAATTTGCCATGCTTTGAGTCAAGCGGATAGCGT
 TTATCTCGCTCAAATATATGTTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAAGGTAGA
 AGATTAGCTGCTAAGATTGTCAAAACACTCAGATTTAGTGACAGTCGAAAATGCTCTCGCC
 TTACTCAATCATGATAATGCTGCTATGCTTTATGGGTGCTGGAGACATTCAAATGTA
 TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4603
STRAIN 090
 AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGGTGGTTTAGAGCAAGCA
 GGTGTAACCTATATTTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTTATGTC
 GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
 CATTTTAAACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACCTAGTCTAGGT
 GTAGCTGGGGCACATGAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAAT
 ATTACAGACACTTCTTTCCCTAATTGGAGATGGTACAGGACGTTGGTCTGCTAATGCTAAT
 TACTTTGTTGTTGAAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
 TCAATTTATACCAATATTGATTTTGAACCTCCTGATTTATTACAGGCTAGAGGACGTA
 TTCATGCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAA
 GATTCAAAACCTCATGAAATCACTTCTAAGGCACCAATATATTATATGGTTTGAAGAT
 TCAATGATTTTATAGCAAAAAGACATCACTCGAATGTTAATGGTTCTGACTTTAAGGTT
 TTCTATAACCAAGAAAGAAATGGTCAAGTTTCATGTACCGATACGGTAAACATAATATC
 TFAAATGCAACTGCTGTTATGCTAACCTTTACATAATGGGAATTTGATATGGCATTAGTA
 GCTGAGCATTGGAAGACATTTTCAGGGTAAACCGTCGTTTACTGAGAAGATTATTGAC
 GATACTGTCATTATTTGATGACTTTGCTCACCATCTACTGAGATTTATGCGACATTAGAT
 GCTGCTCGACAAAAATACCCGTCAAAAGAAATTTAGCTATTTTCCAAACCGCATACGTT
 ACTCGTACGATAGCTCTTTTACAGCAATTTGCCATGCTTTGAGTCAAGCGGATAGCGTT
 TATCTGCTCAAATATATGTTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAAGGTAGA
 GATTAGCTGCTAAGATTGTCAAAACACTCAGATTTAGTGACAGTCGAAAATGCTCTCGCT
 TTACTCAATCATGATAATGCTGCTATGCTTTATGGGTGCTGGAGACATTCAAATGTA
 GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4604
STRAIN H36B
 AAAAGCAGGCTCTAGTgACGTTgACAAATATt:ATTTTACTCAACGTTGGTTAGAGCAAGCAGGT
 ATAACCTATATTTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTTATGTCAGGA
 AATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCAT
 TTTAAACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACCTAGTCTAGGTGTA
 GCTGGGGCACATGAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATT
 ACAGACACTTCTTTCCCTAATTGGAGATGGTACAGGACGTTGGTCTGCTAATGCTAATAC
 TTTGTTGTTGAAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCA
 ATTATTACCAATATTGATTTTGAACCTCCTGATTTATTACAGGCTAGAGGACGTTATTC
 AATGCTTTTAAAGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAAGAT

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

CCAAACTTCATGAAATCACTTCTGAGGCCACCAATATATTATTATGGTTTTGAAGATTCA
AATGATTTTATAGCAAAGATATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTTC
TATAACCAAGAAGAAATGGTTCAGTTTCCAGTACCAGCATACGGTAAACATAATATCTTA
AATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCT
GAGCATTGGAAGACATTTTCAGGGGTAAAACGTCGTTTACTGAGAAAATTATTGACGAT
ACTGTCAATTTATGATGACTTTGCTCACCATCCTACTGAGATTATTGGCAGATTAGATGCT
GCTCGACAAAATACCCCGTCAAAGAAAATGTAGCTATTTTCCAACCCGATACGTTCACT
CGTACGATAGCTCTTTTAGACGAAATTTGCCATGCCTTGAGTCAAGCGGATAGCGTTTAT
CTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAAGGTAGAAGAT
TTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTA
CTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTC AATTGTATGAG
CGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4605
STRAIN 18RS21

AAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCCAACGTGGTTTAGAGCAAGCA
GGTGTAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTTATTGCA
GGAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
CATTTTAAACGATATCAATGAAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT
ATTACAGACACTTCTTTCTAATTTGGAGATGGTACAGGACGTTGGTCTGCTAATGCTAAT
TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATAC
TCAATTTATACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGTA
TTCAATGCCTTTAATGACTATGCTAAGCAAGTTCAAAAGGTTTATTTCATTTATGGAGAA
GATCCAAAACCTTCATGAAATCACTTCTGAGGCCAATATATTTATGTTTGAAGAT
TCAAATGATTTTATAGCAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT
TTCTATAACCAAGAAGAAATTTGGTTCAGTTTTCATGTACCAGCATACGGTAAACATAATATC
TTAAATGCAACTGCTGTTTATGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
GCTGAGCATTGGAAGACGTTTTCAGGGGTAAAAGCGTCGTTTACTGAGAAGATTATTGAC
GATACGTCTATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGGCAGATTAGAT
GCTGCTCGACAAAATACCCCGTCAAAGAAAATGTAGCTATTTTCCAACCCGATACGTTT
ACTCGTACGATAGCTCTTTTAGACGAAATTTGCCATGCCTTGAGTCAAGCGGATAGCGTT
TATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAAGGTAGA
AATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
TTACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTC AATTGTAT
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4606
STRAIN M732

AAAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCCAACGTGGTTTAGAGCAAGCAG
GTGTAACCTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTTATTGCG
GAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC
ATTTTAAACGATATCAATGAAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
TAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATA
TTACAGACACTTCTTTCTAATTTGGAGATGGTACAGGACGTTGGTCTGCTAATGCTAAT
ACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACT
CAATTTATACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGTTAT
TCAATGCCTTTAATGACTATGCTAAGCAAGTTCAAAAGGTTTATTTCATTTATGGAGAA
ATCCAAAACCTTCATGAAATCACTTCTGAGGCCAATATATTTATGTTTGAAGATT
CAAATGATTTTATAGCAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTT
TCTATAACCAAGAAGAAATTTGGTTCAGTTTTCATGTACCAGCATACGGTAAACATAATATC
TAAATGCAACTGCTGTTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAG
CTGAGCATTGGAAGACATTTTCAGGGGTAAAAGCGTCGTTTACTGAGAAGATTATTGACG
ATACTGTCAATTTGATGACTTTGCTCACCATCCTACTGAGATTATTGGCAGATTAGATG
CTGCTCGACAAAATACCCCGTCAAAGAAAATGTAGCTATTTTCCAACCCGATACGTTT
CTCGTACGATAGCTCTTTTAGACGAAATTTGCCATGCCTTGAGTCAAGCGGATAGCGTTT
ATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAAGGTAGA
AATTTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
TACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTC AATTGTATG
AGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4607
STRAIN M781

AAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCCAACGTGGTTTAGAGCAAGCAG
GTGTAACCTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTTATTGCG
GAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC
ATTTTAAACGATATCAATGAAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT
TATTACAGACACTTCTTTCTAATTTGGAGATGGTACAGGACGTTGGTCTGCTAATGCTAA
TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
CTCAATTTATACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGTT
ATTC AATGCTTTAATGACTATGCTAAGCAAGTTCAAAAGGTTTATTTCATTTATGGAGAA
AGATCCAAAACCTTCATGAAATCACTTCTGAGGCCAATATATTTATGTTTGAAGAT
TTCAAATGATTTTATAGCAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT
TTTCTATAACCAAGAAGAAATTTGGTTCAGTTTTCATGTACCAGCATACGGTAAACATAATAT
CTTAAATGCAACTGCTGTTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGT
AGCTGAGCATTGGAAGACATTTTCAGGGGTAAAAGCGTCGTTTACTGAGAAGATTATTGA
CGATACTGTCAATTTGATGACTTTGCTCACCATCCTACTGAGATTATTGGCAGATTAGTA
TGCTGCTCGACAAAATACCCCGTCAAAGAAAATTTAGCTATTTTCCAACCCGATACGTT
CACTCGTACGATAGCTCTTTTAGACGAAATTTGCCATGCCTTGAGTCAAGCGGATAGCGT
TTATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAAGGTAGA
AGATTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT
TTACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTC AATTGTATG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4608

STRAIN CJB110

AAAAAGCAGGCTCTAGTGACGTTGACAAATATATTTTACCACCGTGGTTAGAGCAAGCA
GGTGTAACTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCA
GGAAATGCTTTTCCTCCGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
CAATTTAAACGATATCATGAATTTCTCGGAGATTTATGCGCTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAAT
ATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTTGTTCTGCTAATGCTAAT
TACTTTGTGTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATAC
TCAATTTATTACCAATATTGATTGTTGACCATCCTGATTATTTTACAGGCCTAGAGGACGTA
TTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAA
GATTCAAAACCTTCATGAATCACTTCTAAGGCACCAATATATTTATTATGGTTTTGAAGAT
TCAAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGTT
TTCTATAACCAAGAAAGAAATTTGGTCAAGTTTCATGTACAGCATACGGTAAACATAATATC
TTAAATGCAACTGCTGTTTATGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
GCTGAGGATTTGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAGATTATTGAC
GATACTGTCAATTAATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT
GCTGCTCGACAAAAATACCCGTCAAAGAAATTTAGCTAATTTTCCAACCGCATACGTTT
ACTCGTACGATAGCTCTTTTAGACGATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT
TATCTTGTCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAAGTAGAA
GATTTAGCTGCTAAGATTGTTCAAACTCAGATTAGTGACAGTCCGAAAATGCTTCGCTT
TTACTCAATCATGATAATGCTGCTATGTTTATGGTGGTGGAGACATTCAATTTGAT
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4609

STRAIN JM9130013 (reverse complement)

GTTCAAAAAGCAGGCTCTAGTGACGTTGACAAATATATTTTACTCAACGTTGGTTTGA
GCAAGCAGGTATAACTATATACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGAT
TATGTCAGGAAATGCTTTTCCTCCGATAACAATGAAGAGTTGGCTTATGTTATTGAAA
GGCTATCATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAAGTTCACTAG
TCTAGGTGCTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTT
AAAAAATATTACAGACACTTCTTTCCTAATTGGAGATGGTACAGGACGTTGTTCTGCTAA
TGCTAATTACTTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCC
AGAATACTCAATATATTACCAATATTGATTTTGCACCATCCTGATTATTTTACAGGCCTAGA
GGACTATTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTA
TGGAGAAGATCCAAAACITTCATGAATCACTTCTGAGGCACCAATATATTTATTATGGTTT
TGAAGATTCAATGATTTTATAGCAAAAGATATCACTCGAAGCTTAAATGGTTCTGACTT
TAAGGTTTTCTATAACCAAGAAAGAAATTTGGTCAAGTTTACGTCACGATACGGTAAACA
TAATATCTTAAATGCAACTGCTGTTATGCTAACCTTTACATAATGGGAATTGATATGGC
ATTAGTAGCTGAGCATTGGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAAAT
TATTGACGATACTGTCAATATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGAC
ATTAGATGCTGCTCGACAAAAATACCCGTCAAAGAAATTTAGCTAATTTTCCAACCGCA
TACCTTCACTCGTACGATAGCTCTTTTAGACGAAATTTGCCATGCTTGGTCAAGCGGA
TAGCGTTTATCTCGCTCAAATAATGTTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAA
GGTAGAAGATTAGCTGCTAAGATTGTTCAAACTCAGATTAGTGACAGTCCGAAAATGCT
CTCGCTTTACTCAATCATGATAATGCTGCTATGTTTATGGTGGTGGAGACATTCA
ATTGATGAGCGCTCTTTGAGAATATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4610

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTTGACAAATATLATTTTACCCACCGTGGTTAGAGCAAGCAGGTTGAA
CTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGTCAGGAAATG
CTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTCATTTTAA
AACGATATCATGAATTTCTCGGAGATTTTATGCGTCAAGTTCACTAGTCTAGGTTAGCTG
GGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTTAAAAAATATTACAG
ACACTTCTTTCCTAATTGGAGATGGTACAGGACGTTGTTCTGCTAATGCTAATTACTTTG
TGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTA
TTACCAATATTGATTTTGCACCATCCTGATTATTTTACAGGCCTAGAGGACGTAATCAATG
CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATCCAA
AACTTCATGAATCACTTCTGAGGCACCAATATATTTATTATGTTTTTGAAGATTCAATG
ATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGTTTTCTATA
ACCAAGAAGAAATTTGTCAGTTTTCATGTACAGCATACGGTAAACATAATATCTTAAATG
CAACTGCTGTTTATGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC
ATTTGAAGACATTTTCAAGGGTAAAGCGTCTGTTTACTGAGAAGATTATTGACGATACTG
TCATTTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTC
GACAAAAATACCCGTCAAAGAAATTTAGCTAATTTTCCAACCGCATACGTTCACTCGTA
CGATAGCTCTTTTAGACGAAATTTGCCCATGCTTGGTCAAGCGGATAGCGTTTATCTGCT
CTCAAATATTGTTTCTGCTAGAGAAGTAGATAATGGTGAAGGTGAAGGTGAAGATTGAG
CTGCTAAGATTGTTCAAACTCAGATTAGTGACAGTCCGAAAATGCTTCGCTTTACTCA
ATCATGATAATGCTGCTATGTTTATGGTGGTGGAGACATTCAATTTGATGAGCGCT
CTTTGAGAATATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4611

STRAIN 2603

atgtcaaaaacttatcattttatttggtattaaaggatccggaatgagtgccctagcactg
atgcttcatacaaatgggacataaacgtccaaggaagtgaacttgacaaatattttacc
caacgtgggttagagcaagcaggtgtaactatattaccttctcaccgaataatcag
gagatttagagattattgcaggaatgctttctgctccagataacaatgaagagtggct
tatgctattgaaagggtatcaattttaaagcatatcatgaatttctcggagatttatg
cgtcagttcaactagttaggtgtagctggggcacatggaaaaacctcaacgacaggttta
tagctcatggttttaaaaaatattacagacactctcttccataattggagatggtacagga

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

cgtgggtctgctaattactttgtggttgaagctgatgaatacgaacgtcatttt
atgccgtaccatccagaataactcaattattaccaatattgatatttgaccatcctgattat
tttacaggcttagagacgtatccaatgcctttaatgactatgctaagcaagttcaaaaa
ggtttattcatttatggagaagatccaaaactcatgaaatcacttctgaggcaccata
tattattatggttttgagatttcaaatgattttatagcaaaagacatcactcgaactggt
aatggtctgactttaaggttttctataaccaagaagaatctggcagtttcatgtacca
gcatacggtaaacataatcttaaatgcaactgctggttatgctaaccctttacataatg
ggatttgatagcatttagtagctgagcatttgaagacgttttcaggggtaagcgtcgt
tttactgagaagattatgacgatactgctcattatgatgactttgctcaccatcctact
gagatatttgcgacattagatgctgctcgacaaaaataccgctcaaaagaatctgtagct
attttccaaccgcatagcttactcgtacgtagctcttttagacgaatttgcccatgcc
ttgagtcaaggcagtagcgtttatctcgctcaaatataggttctgctagagaagtagat
aatggtgaggtgaggtagaagatttagctgctaaagatttgctcaaacctcagatttagtg
acagtgcgaaatgtctcgcttactcaatcatgataatgctgctatgctcttatgggt
gctggagacattcaattgatgagcgtcttttgaagaattattagtaacctaaactaaa
aatacacia

SEQ ID NO. 4612

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTTGACAAATATATTTTTACCCAACCTGGTATTAGAGCAAGCAGGTGTA
CTATATTACCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTTAGCAGGAAATG
CITTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCAITTTA
AACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACCTAGTCTAGGTGACTG
GGGCACATGGAAAAACCTCAACGACAGGTTTATAGCTCATGTTTAAAAAATAATACAG
ACACTTCITTTCTAATTGGAGATGGTACAGGACGCTGGTTCGCTAATGCTAATTACTTTG
TGTTTGAAGCTGATGAATACGACGCTCATTTTATGCGGTACCATCCAGAATACTCAATTA
TTACAATATTGATTTTGGACCATCCTGATTTATTTACAGGCCTAGAGGACGTTATCAATG
CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATCCAA
AACTTCATGAAATCACITTCGAGGCACCAATATATTTATGTTTGAAGATTCAAATG
ATTTTATAGCAAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTCTATA
ACCAAGAAGAAATGGTCAGTTTATGATACCAGCATAACGTTAAACATAATATCTTAAATG
CAACTGCTGTTTATGCTAACCTTTACATAANTGGGAANTGATNTGGCATTTAGTAGCTGAGC
ATTTGAAGACATTTTCAGGGTAAAGCGTCTGTTTACTGAGAAGATTATTGACGATACTG
TCATTTATGATGACTTTGCTCACCATCCTACTGAGATTTATGCGACATTAGATGCTGCTC
GACAAAAATACCCGTCAAAAGAAATTTAGCTATTTTCCAACCGCATACGTTCACTTCGTA
CGATAGCTCTTTAGACGAATTTGCCCATGCTTGAAGTCAAGCGGATAGCGTTTATCTCG
CTCAAATATATGTTCTGCTAGAGAAGTAGATAATCGTGAGGTGAAGTGAAGATTTACTCA
CTGCTAAGATTGCAAACTCAGATTTAGTGACAGTCGAAAATGCTCTCGCCTTACTCA
ATCATGATAATGCTGCTATGCTCTTTATGGTGTCTGGAGACATTCAAATTTATGAGCGCT
CITTTGAAGAATTTATAGCTAACCTAACCTAAAATACACAA

PRETTY of: /biotmp/msa56524.2{*} November 26, 2002 08:06 ..
PRETTY of: /biotmp/msa253045.2{*} January 31, 2003 03:51 ..

1 50
msa253045.2{157_090} -----
msa253045.2{157_CJB110} -----
msa253045.2{157_H36B} -----
msa253045.2{157_JM9130013} -----
msa253045.2{157_1169NT} -----
msa253045.2{157_A909} -----
msa253045.2{157_COH1} -----
msa253045.2{157_M732} -----
msa253045.2{157_M781} -----
msa253045.2{157_18RS21} -----
msa253045.2{157_2603} atgtcaaaaa cttatcattt tattggattt aaaggatccg gaatgagtc
Consensus *****

51 100
msa253045.2{157_090} ----- -aaagcaggc tctagtgcag
msa253045.2{157_CJB110} -----A Aaaagcaggc tctagtgcag
msa253045.2{157_H36B} ----- Aaaagcaggc tctagtgcag
msa253045.2{157_JM9130013} -----GttcaA Aaaagcaggc tctagtgcag
msa253045.2{157_1169NT} ----- Aaaagcaggc tctagtgcag
msa253045.2{157_A909} ----- -caggc tctagtgcag
msa253045.2{157_COH1} ----- Aaaagcaggc tctagtgcag
msa253045.2{157_M732} ----- -aaagcaggc tctagtgcag
msa253045.2{157_M781} ----- -aaagcaggc tctagtgcag
msa253045.2{157_18RS21} ----- -aaagcaggc tctagtgcag
msa253045.2{157_2603} cctagcactg atgcttcac aaatgggacA taacgtccaa ggaagtgcag
Consensus *****

101 150
msa253045.2{157_090} tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
msa253045.2{157_CJB110} tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
msa253045.2{157_H36B} tTGACAAATA TTATTTTACT CAACGTGGTT TAGAGCAAGC AGGTaTAACT
msa253045.2{157_JM9130013} tTGACAAATA TTATTTTACT CAACGTGGTT TAGAGCAAGC AGGTaTAACT
msa253045.2{157_1169NT} tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
msa253045.2{157_A909} -TGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
msa253045.2{157_COH1} tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
msa253045.2{157_M732} tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
msa253045.2{157_M781} tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT
msa253045.2{157_18RS21} tTGACAAATA TTATTTTACc CAACGTGGTT TAGAGCAAGC AGGTgTAACT

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_2603}	tTGACAAATA	TTATTTTAcc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
Consensus	-*****	*****-	*****	*****	****-*****
	151				200
msa253045.2{157_090}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_CJB110}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_H36B}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_JM9130013}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_1169NT}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_A909}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_COH1}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M732}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M781}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_18RS21}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_2603}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
Consensus	*****	*****	*****	*****	*****
	201				250
msa253045.2{157_090}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_CJB110}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_H36B}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_JM9130013}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_1169NT}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_A909}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_COH1}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M732}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M781}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_18RS21}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_2603}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
Consensus	*****	*****	*****	*****	*****
	251				300
msa253045.2{157_090}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_CJB110}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_H36B}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_JM9130013}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_1169NT}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_A909}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_COH1}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M732}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M781}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_18RS21}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_2603}	AAAAGGGCTA	TCALTTTAA	CGATATCATG	AATTTCTCGG	AGATTTTATG
Consensus	*****	*****	*****	*****	*****
	301				350
msa253045.2{157_090}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_CJB110}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_H36B}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_JM9130013}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_1169NT}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_A909}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_COH1}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M732}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M781}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_18RS21}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_2603}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa253045.2{157_090}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_CJB110}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_H36B}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_JM9130013}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_1169NT}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_A909}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_COH1}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_M732}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_M781}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_18RS21}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_2603}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
Consensus	*****	*****	*****	*****	*****
	401				450
msa253045.2{157_090}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_CJB110}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_H36B}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_JM9130013}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_1169NT}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_A909}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_COH1}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M732}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M781}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_18RS21}	TAATTGGAGA	TGGTACAGGA	CGTGGTCTCG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_2603}	TAATTGGAGA	TGGTACAGGA	CGTGGTCTCG	CTAATGCTAA	TTACTTTGTG
Consensus	*****	*****	*****	*****	*****
	451				500
msa253045.2{157_090}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_CJB110}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_H36B}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_JM9130013}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_1169NT}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_A909}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_COH1}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M732}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M781}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_18RS21}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_2603}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
Consensus	*****	*****	*****	*****	*****
	501				550
msa253045.2{157_090}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_CJB110}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_H36B}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_JM9130013}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_1169NT}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_A909}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_COH1}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M732}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M781}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_18RS21}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_2603}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
Consensus	*****	*****	*****	*****	*****
	551				600
msa253045.2{157_090}	TAGAGGACGT	ATTCAATGct	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_CJB110}	TAGAGGACGT	ATTCAATGct	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_H36B}	TAGAGGACGT	ATTCAATGct	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_JM9130013}	TAGAGGACGT	ATTCAATGct	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_1169NT}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_A909}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_COH1}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_M732}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_M781}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_18RS21}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
msa253045.2{157_2603}	TAGAGGACGT	ATTCAATGcc	TTTAATGACT	ATGCTAAGCA	AGTTCAAAA
Consensus	*****	*****	*****	*****	*****
	601				650
msa253045.2{157_090}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_CJB110}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_H36B}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_JM9130013}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_1169NT}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_A909}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_COH1}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_M732}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_M781}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_18RS21}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_2603}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
Consensus	*****	*****	****-*****	*****	*****
	651				700
msa253045.2{157_090}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_CJB110}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_H36B}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_JM9130013}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_1169NT}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_A909}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_COH1}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M732}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M781}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_18RS21}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_2603}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
Consensus	*****	*****	*****	*****	*****
	701				750
msa253045.2{157_090}	AAGAcATCAC	TCGAACGTGT	AATGGTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_CJB110}	AAGAcATCAC	TCGAACGTGT	AATGGTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_H36B}	AAGAcATCAC	TCGAACGTGT	AATGGTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_JM9130013}	AAGAcATCAC	TCGAACGTGT	AATGGTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_1169NT}	AAGAcATCAC	TCGAACGTGT	AATGGTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_A909}	AAGAcATCAC	TCGAACGTGT	AATGGTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_COH1}	AAGAcATCAC	TCGAACGTGT	AATGGTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_M732}	AAGAcATCAC	TCGAACGTGT	AATGGTCTG	ACTTTAAGGT	TTTCTATAAC

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M781}	AAGAcATCAC	TCGAActGTT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_18RS21}	AAGAcATCAC	TCGAActGTT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_2603}	AAGAcATCAC	TCGAActGTT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_CJB110}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_H36B}	CAAGAAGAAA	TTGGTCAGTT	TCAcGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_JM9130013}	CAAGAAGAAA	TTGGTCAGTT	TCAcGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_1169NT}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_A909}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_COH1}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_M732}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_M781}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_18RS21}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
msa253045.2{157_2603}	CAAGAAGAAA	TTGGTCAGTT	TCAtGTACCA	GCATACGGTA	AACATAATAT
Consensus	*****	*****	***-*****	*****	*****
msa253045.2{157_090}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_CJB110}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_H36B}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_JM9130013}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_1169NT}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_A909}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_COH1}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_M732}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_M781}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_18RS21}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
msa253045.2{157_2603}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAAATGATA
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_CJB110}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_H36B}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_JM9130013}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_1169NT}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_A909}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_COH1}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_M732}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_M781}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_18RS21}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGTCGT
msa253045.2{157_2603}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGTCGT
Consensus	*****	*****	*****-*	*****	***-*****
msa253045.2{157_090}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_CJB110}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_H36B}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_JM9130013}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_1169NT}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_A909}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_COH1}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_M732}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_M781}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_18RS21}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
msa253045.2{157_2603}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA
Consensus	*****	*-*****	*****	*****	*****
msa253045.2{157_090}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_CJB110}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_H36B}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_JM9130013}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_1169NT}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_A909}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_COH1}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_M732}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_M781}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_18RS21}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
msa253045.2{157_2603}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACTGTT	CACCTCGTACG
msa253045.2{157_CJB110}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACTGTT	CACCTCGTACG
msa253045.2{157_H36B}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACTGTT	CACCTCGTACG
msa253045.2{157_JM9130013}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACTGTT	CACCTCGTACG
msa253045.2{157_1169NT}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACTGTT	CACCTCGTACG
msa253045.2{157_A909}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACTGTT	CACCTCGTACG
msa253045.2{157_COH1}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACTGTT	CACCTCGTACG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M732}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATAAGTT	CCTCTGTACG
msa253045.2{157_M781}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATAAGTT	CCTCTGTACG
msa253045.2{157_18RS21}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATAAGTT	CCTCTGTACG
msa253045.2{157_2603}	CGTCAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATAAGTT	CCTCTGTACG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1051	ATAGCTCTTT	TAGACGATTT	TGCCCATGCT	1100
msa253045.2{157_CJB110}	ATAGCTCTTT	TAGACGATTT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_H36B}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_JM9130013}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_1169NT}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_A909}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_COH1}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_M732}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_M781}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_18RS21}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
msa253045.2{157_2603}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1101	TTATCTGCT	CAAATATATG	GTTCTGCTAG	1150
msa253045.2{157_CJB110}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_H36B}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_JM9130013}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_1169NT}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_A909}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_COH1}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_M732}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_M781}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_18RS21}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
msa253045.2{157_2603}	TTATCTGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1151	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	1200
msa253045.2{157_CJB110}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_H36B}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_JM9130013}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_1169NT}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_A909}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_COH1}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_M732}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_M781}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_18RS21}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
msa253045.2{157_2603}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1201	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	1250
msa253045.2{157_CJB110}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_H36B}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_JM9130013}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_1169NT}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_A909}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_COH1}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_M732}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_M781}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_18RS21}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
msa253045.2{157_2603}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1251	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	1300
msa253045.2{157_CJB110}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_H36B}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_JM9130013}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_1169NT}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_A909}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_COH1}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_M732}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_M781}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_18RS21}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
msa253045.2{157_2603}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT
Consensus	*****	*****	*****	*****	*****
msa253045.2{157_090}	1301	TATTAGCTAA	CCTAACTAAA	AATACACAA	1329
msa253045.2{157_CJB110}	TATTAGCTAA	CCTAACTAAA	AATACACAA	AATACACAA	
msa253045.2{157_H36B}	TATTAGCTAA	CCTAACTAAA	AATACACAA	AATACACAA	
msa253045.2{157_JM9130013}	TATTAGCTAA	CCTAACTAAA	AATACACAA	AATACACAA	
msa253045.2{157_1169NT}	TATTAGCTAA	CCTAACTAAA	AATACACAA	AATACACAA	
msa253045.2{157_A909}	TATTAGCTAA	CCTAACTAAA	AATACACAA	AATACACAA	

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_COH1}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_M732}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_M781}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_18RS21}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_2603}	TATTAGCTAA	CCTAACTAAA	AATACACAA
Consensus	*****	*****	*****

SEQ ID NO. 4613
STRAIN A909 frame: 2
 DKYYFTQRGLEQAGVTILPFPSPNNI SEDLEI IAGNAFRPDNNEELAYVIEKGYHFKRYHE
 FLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANANYFVFEAD
 EYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVNAFNQYAKQVQKGLFIYGEDPKLHEI
 TSEAPIYYGFEDSNDPIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNILNATAVI
 ANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLDAARQKYP
 SKEI VAI FQPHTFTRTIALLDEFahalSQADSVYLAQI YGSAREVDNGEVKVEDLAAKI V
 KHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4614
STRAIN 1169NT frame: 2
 KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNI SEDLEI IAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVNAFNQYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYGFEDSNDPIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD
 AARQKYP SKEI VAI FQPHTFTRTIALLDEFahalSQADSVYLAQI YGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4615
STRAIN 090 FRAME:1
 KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNI SEDLEI IAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVNAFNQYAKQVQKGLFIYGE
 DSKLHEITSKAPIYYGFEDSNDPIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD
 AARQKYP SKEI VAI FQPHTFTRTIALLDEFahalSQADSVYLAQI YGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4616
STRAIN H36B frame: 2
 KAGSSDVKYYFTQRGLEQAGITILPFPSPNNI SEDLEI IAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVNAFNQYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYGFEDSNDPIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD
 AARQKYP SKEI VAI FQPHTFTRTIALLDEFahalSQADSVYLAQI YGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4617
STRAIN 18RS21 frame: 1
 KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNI SEDLEI IAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVNAFNQYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYGFEDSNDPIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD
 AARQKYP SKEI VAI FQPHTFTRTIALLDEFahalSQADSVYLAQI YGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4618
STRAIN M732 frame: 2
 KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNI SEDLEI IAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVNAFNQYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYGFEDSNDPIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD
 AARQKYP SKEI VAI FQPHTFTRTIALLDEFahalSQADSVYLAQI YGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4619
STRAIN JM9130013 frame: 2
 FKKAGSSDVKYYFTQRGLEQAGITILPFPSPNNI SEDLEI IAGNAFRPDNNEELAYVIEK
 GYHFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 ANYFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVNAFNQYAKQVQKGLFIY
 GEDPKLHEITSEAPIYYGFEDSNDPIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD
 AARQKYP SKEI VAI FQPHTFTRTIALLDEFahalSQADSVYLAQI YGSAREVDNGEVKVE
 VEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4620
STRAIN M781 frame: 1
 KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNI SEDLEI IAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVFNANFYAKQVQKGLFIYGE
DPKLHEITSEAPIYYGFEDSNDFAKDIITRTVNGSDFKVFYNQEEIGQFHVPAVGKHN
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLD
AARQKYPKSEIVAIFQPHTFTRTIALLDEFALHSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4621

STRAIN CJB110 frame: 3

KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEI IAGNAFRPDNNEELAYVIEKGY
HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNKNTDTSFLIGDGTGRGSANAN
YFVFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVFNANFYAKQVQKGLFIYGE
DSKLHEITSKAPIYYGFEDSNDFAKDIITRTVNGSDFKVFYNQEEIGQFHVPAVGKHN
LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLD
AARQKYPKSEIVAIFQPHTFTRTIALLDEFALHSQADSVYLAQIYGSAREVDNGEVKVE
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4622

STRAIN 2603 frame: 1

MSKTYHFIGIKGSGMSALMLHQMGNVQGSVDVKYYFTQRGLEQAGVTILPFPSPNNIS
EDLEI IAGNAFRPDNNEELAYVIEKGYQFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGL
LAHVLNKNTDTSFLIGDGTGRGSANANYFVFEADEYERHFMPYHPEYSIITNIDFDHPDY
FTGLEDFVFNANFYAKQVQKGLFIYGEDPKLHEITSEAPIYYGFEDSNDFAKDIITRTV
NGSDFKVFYNQEEIGQFHVPAVGKHNILNATAVIANLYIMGIDMALVAEHLKTFSGVKRR
FTEKIIDDTVIIDDFAHHPTEIATLDAAARQKYPKSEIVAIFQPHTFTRTIALLDEFALH
LSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMG
AGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4623

STRAIN COH1 frame: 3

GSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEI IAGNAFRPDNNEELAYVIEKGYHF
KRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNKNTDTSFLIGDGTGRGSANANYF
VFEADEYERHFMPYHPEYSIITNIDFDHPDYFTGLEDFVFNANFYAKQVQKGLFIYGEDP
KLHEITSEAPIYYGFEDSNDFAKDIITRTVNGSDFKVFYNQEEIGQFHVPAVGKHNILN
ATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLDAA
RQKYPKSEIVAIFQPHTFTRTIALLDEFALHSQADSVYLAQIYGSAREVDNGEVKVEDL
AAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

PRETTY of: /biotmp/msa56635.2{*} November 26, 2002 08:08 ..

msa253220.2{157_090} 1 50
msa253220.2{157_CJB110}
msa253220.2{157_1169NT}
msa253220.2{157_18RS21}
msa253220.2{157_M732}
msa253220.2{157_M781}
msa253220.2{157_COH1}
msa253220.2{157_H36B}
msa253220.2{157_JM9130013}
msa253220.2{157_2603}
msa253220.2{157_A909}
Consensus

msa253220.2{157_090} 51 100
msa253220.2{157_CJB110}
msa253220.2{157_1169NT}
msa253220.2{157_18RS21}
msa253220.2{157_M732}
msa253220.2{157_M781}
msa253220.2{157_COH1}
msa253220.2{157_H36B}
msa253220.2{157_JM9130013}
msa253220.2{157_2603}
msa253220.2{157_A909}
Consensus

msa253220.2{157_090} 101 150
msa253220.2{157_CJB110}
msa253220.2{157_1169NT}
msa253220.2{157_18RS21}
msa253220.2{157_M732}
msa253220.2{157_M781}
msa253220.2{157_COH1}
msa253220.2{157_H36B}
msa253220.2{157_JM9130013}
msa253220.2{157_2603}
msa253220.2{157_A909}
Consensus

msa253220.2{157_090} 151 200
FEADEYERHF MPYHPEYSII TNIDFDHPDY FTGLEDFVNA FNDYAKQVQK

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253220.2{157_CJB110}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_1169NT}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_18RS21}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M732}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M781}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_COH1}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_H36B}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_JM9130013}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_2603}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_A909}	FEADYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
Consensus	*****	*****	*****	*****	*****
	201				250
msa253220.2{157_090}	GLFIYGEDsK	LHEITSkAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_CJB110}	GLFIYGEDsK	LHEITSkAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_1169NT}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_18RS21}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_M732}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_M781}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_COH1}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_H36B}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_JM9130013}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_2603}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
msa253220.2{157_A909}	GLFIYGEDpK	LHEITSeAPI	YYYGFEDSND	FIAKDITRTV	NGSDFKVFYN
Consensus	*****	*****	*****	*****	*****
	251				300
msa253220.2{157_090}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_CJB110}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_1169NT}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_18RS21}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M732}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M781}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_COH1}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_H36B}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_JM9130013}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_2603}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_A909}	QEEIGQFHPV	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
Consensus	*****	*****	*****	*****	*****
	301				350
msa253220.2{157_090}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_CJB110}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_1169NT}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_18RS21}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_M732}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_M781}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_COH1}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_H36B}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_JM9130013}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_2603}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
msa253220.2{157_A909}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYPskeIVA	IFQPHTFTRT
Consensus	*****	*****	*****	*****	*****
	351				400
msa253220.2{157_090}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_CJB110}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_1169NT}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_18RS21}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_M732}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_M781}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_COH1}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_H36B}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_JM9130013}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_2603}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
msa253220.2{157_A909}	IALLDeFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSDLV
Consensus	*****	*****	*****	*****	*****
	401				443
msa253220.2{157_090}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_CJB110}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_1169NT}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_18RS21}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M732}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M781}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_COH1}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_H36B}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_JM9130013}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_2603}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_A909}	TVENVSPLLN	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
Consensus	*****	*****	*****	*****	***

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

SEQ ID NO. 4701

STRAIN A909

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAA

SEQ ID NO. 4702

STRAIN H36B

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAA

SEQ ID NO. 4703

STRAIN 18RS21

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAA

SEQ ID NO. 4704

STRAIN M732

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAA

SEQ ID NO. 4705

STRAIN COH1

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAAGAAAA

SEQ ID NO. 4706

STRAIN M781

TATTTTTTAAACAACAAAAAAGGAAAAGAGC
 TAAGGAAAAATGCAGAAAAATTCTATGGAGAATATAAAGAAAATCCAGAA
 GAATATCATCAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGC
 TGTGATACTTTAAAGATATAAAGGTAATTTGAATCAGGTGAATTGA
 CAACAGAGGATATCGTCTCAGCCGTTAAGGAAAAAAGCGGAGAAGTAGTT
 GACTTTGCTAATGATTTGTCATCAAGCTAAATCAAATTTCTCAGACGA
 GGATACTGCTAAAAAAGAGATAAGGCTCCTGAAACAAAAGTAGAAGATA
 TTGTCATTGATTATAAAGAAAACACAGAAGATAAAGAAAA

SEQ ID NO. 4707

STRAIN 2603

tattttttaacaacaaaaaaggaaaagagctaaggaaaaatgcagaaaa
 attctatggagaatataaagaaaatccagaagaatcatcaaataagct
 aagataaagcaagtgaatattcaaatttagctgttgatacttttaagat
 tataaaggtaatttgaatcaggtgaattgacaacagaggatatacgtctc
 agccgttaaggaaaaaagcggagaagtagttgactttgctaatgattttg
 tcaatcaagctaaatcaaattctcagacagggatactgctaaaaaagaa
 gataaggctcctgaaacaaaagtagaagatattgtcatttgattataaaga
 aaacacagaagataaagaaaa

SEQ ID NO. 4708

STRAIN 090

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACTTTAAAGAT

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

TATAAAGGTTAAATTTGAATCAGGTGAATTGACCAACAGAGGATATCGTCTC
AGCCGTTAAGGAAAAAGCGGAGAGTAGTTGACTTTGCTAATGATTTTG
TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATATGCTAAAAAAGAA
GATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTGATTATAAAGA
AAACACAGAAGATAAGAAAA

SEQ ID NO. 4709

STRAIN CJB110

TATTTTAAACAACAAAAAAGGAAAAAGGCTAAGGAAAA
ATGCAGAAAAATTTCTATGGAGAATATAAAGAAAAATCCAGAAGAAATATCAT
CAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATA
TTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACCAACAGAGG
ATATCGTCTCAGCCGTAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT
AATGATTTTGTCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACTGC
TAAAAAAGAAGATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTG
ATTATAAAGAAAAACAGAAGATAAAGAAAA

SEQ ID NO. 4710

STRAIN 1169NT

TATTTTAAACAACAAAAAAGGAAAAAGGCTAAGGAAAA
AATGCAGAAAAATTTCTATGGAGAATATAAAGAAAAATCCAGAAGAAATATCA
TCAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATA
CTTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACCAACAGAG
GATATCGTCTCAGCCGTTAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT
TAATGATTTTGTCAATCAAGCTAAATCAAATTTCTCAGATGAGGATACTG
CTAAAAAAGAAAAAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATT
GATTATAAAGAAAAACAGAAGATAAAGAAAA

SEQ ID NO. 4711

STRAIN JM9130013

TATTTTAAACAACAAAAAAGGAAAAAGGCTAAGGAAAA
ATGCAGAAAAATTTCTATGGAGAATATAAAGAAAAATCCAGAAGAAATATCAT
CAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATA
TTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACCAACAGAGG
ATATCGTCTCAGCCGTTAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT
AATGATTTTGTCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACTGC
TAAAAAAGAAGATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTG
ATTATAAAGAAAAACAGAAGATAAAGAAAA

PRETTY of: /biotmp/msa68511.2{*} January 22, 2003 05:47 ..

msa68511.2{164_090} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA 1
msa68511.2{164_18RS21} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA 50
msa68511.2{164_2603} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
msa68511.2{164_A909} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
msa68511.2{164_CJB110} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
msa68511.2{164_COH1} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
msa68511.2{164_H36B} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
msa68511.2{164_JM9130013} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
msa68511.2{164_M732} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
msa68511.2{164_M781} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
msa68511.2{164_1169NT} TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA
Consensus *****

msa68511.2{164_090} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA 51
msa68511.2{164_18RS21} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA 100
msa68511.2{164_2603} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_A909} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_CJB110} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_COH1} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_H36B} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_JM9130013} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_M732} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_M781} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_1169NT} ATTCTATGGA GAATATAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
Consensus *****

msa68511.2{164_090} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT 101
msa68511.2{164_18RS21} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT 150
msa68511.2{164_2603} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_A909} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_CJB110} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_COH1} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_H36B} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_JM9130013} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_M732} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_M781} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_1169NT} AAGATAAAGC AAGTGAATAT TCAAATTTAG CTGTTGATAC TTTTAAAGAT
Consensus *****

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

	151			200
msa68511.2{164_090}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_18RS21}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_2603}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_A909}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_CJB110}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_COH1}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_H36B}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_JM9130013}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_M732}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_M781}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
msa68511.2{164_1169NT}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG	ACAACAGAGG ATATCGTCTC
Consensus	*****	*****	*****	*****
	201			250
msa68511.2{164_090}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_18RS21}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_2603}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_A909}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_CJB110}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_COH1}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_H36B}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_JM9130013}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_M732}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_M781}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
msa68511.2{164_1169NT}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT	TGACTTTGCT AATGATTTTG
Consensus	*****	*****	*****	*****
	251			300
msa68511.2{164_090}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_18RS21}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_2603}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_A909}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_CJB110}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_COH1}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_H36B}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_JM9130013}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_M732}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_M781}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
msa68511.2{164_1169NT}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG	AGGATACTGC TAAAAAAGAA
Consensus	*****	*****	*****	*****
	301			350
msa68511.2{164_090}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_18RS21}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_2603}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_A909}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_CJB110}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_COH1}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_H36B}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_JM9130013}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_M732}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_M781}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
msa68511.2{164_1169NT}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT	ATTGTCATTG ATTATAAAGA
Consensus	-*****	*****	*****	*****
	351		372	
msa68511.2{164_090}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_18RS21}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_2603}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_A909}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_CJB110}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_COH1}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_H36B}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_JM9130013}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_M732}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_M781}	AAACACAGAA	GATAAAGAAA	AA	
msa68511.2{164_1169NT}	AAACACAGAA	GATAAAGAAA	AA	
Consensus	*****	*****	**	

SEQ ID NO. 4712
STRAIN 2603
YFLITTKGKELRKNKAEKFKYGEYKENPEEYHQIAKDKASEYSLNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4713
STRAIN A909 frame: 1
YFLITTKGKELRKNKAEKFKYGEYKENPEEYHQIAKDKASEYSLNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVDFANDFVNQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4714

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

STRAIN H36B frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4715
STRAIN 18RS21 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4716
STRAIN M732 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4717
STRAIN COH1 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4718
STRAIN M781 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4719
STRAIN 090 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4720
STRAIN CJB110 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4721
STRAIN 1169NT frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKENKAPETKVEDIVIDYKENTE
DKEK

SEQ ID NO. 4722
STRAIN JM9130013 frame: 1
YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGFESGEL
TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDSDTAKKEDKAPETKVEDIVIDYKENTE
DKEK

PRETTY of: /biotmp/msa68746.2(*) January 22, 2003 05:54 ..

1 50
msa68746.2{164_090} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_1169NT} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_18RS21} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_2603} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_A909} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_CJB110} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_COH1} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_H36B} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_JM9130013} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_M732} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
msa68746.2{164_M781} YFLTTKKGKE LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD
Consensus *****

51 100
msa68746.2{164_090} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_1169NT} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_18RS21} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_2603} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_A909} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_CJB110} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_COH1} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_H36B} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_JM9130013} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_M732} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE
msa68746.2{164_M781} YKGFESGEL TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

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Consensus *****
msa68746.2{164_090} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_1159NT} nKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_18RS21} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_2603} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_A909} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_CJB110} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_COH1} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_H36B} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_JM9130013} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_M732} dkAPETKVED IVIDYKENTE DKEK
msa68746.2{164_M781} dkAPETKVED IVIDYKENTE DKEK
Consensus -*****

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Table 48: Comparative Sequences relating to SAG1474

SEQ ID NO: 4801

STRAIN 2603

aatagtagtactgagacaagtgccttcagtagttcctactacaaatactatcgt
tcaaaactaatgacagtaaatcctaccgcaaaaatttgatcagaatcaggac
aatctgtaaataggtcaagtaaaaccagataattctgcgggcgcttacaaca
gttgacacgcctcatcatatttcagctccagatgctttaaaacaactca
atcaagtcctgtcgttgagagtacttctaactaagttactgaagagactt
acaacaacaaaagatgggtcaagatttagccaacatgggtgagaagtggtcaa
gttactagttaggaaactcgttaaatatggcatacagataattatgtctaaaga
aaaccatctttaaatgtagtattactactagacgccaagaagctattg
aagaggctagaaaacttaagataccaatcagccgttttaggtgttccc
ttgtagtcaaggggttagggcacagatataaaggtgggtgaaaccaataa
tggttgatctatgtagatggaaaaatagcacattgacagtagctatg
tcaaaaaatataaagatttaggatttattatcttaggacaacgaacttt
ccagagtagtgggtggcgttaataaacagattctaaattatacgggtctaac
gcataatccttgggatcttgctcataatgctgggtgctcttctgggtgaa
gtgacagcagccattgctagcgggaatgacgccaatgcttagcggtagtgat
gctgggtggttctatccgtattccatctcttggacgggcttggtagggtt
aaaaccaacaagaggatgggtgagtaataaagcagcagattcgtatagta
cagcagttcattttccatataactaagtcctagagacgcagaaaacatt
ttaacttatctaaagaaaagcagcaaacgctagtagtcaatgattt
aaaactcttccaatgcttatactttgaaatcaccaatgggaacagaaag
ttagcaagatgctaaaaacgctatttaggacaacgctcacattcttaaga
aaacaaggttcaagtaaacagagatagactaccaattgtaggttagagc
atatacgcgtgatttcaacctgggtattggcagggaggagcttttt
caacaatgaaaaagacttaaaaaacatgggtttactaaagaagacggtt
gatccttacttgggcagttcatgttatttatcaaaatcagataaagc
tgaacttaagaaaatctattatggaagcccaaaaacataggtatgattatc
gtaaggcaatggagaagcttcacaagcaatttccctatttcttatcgcca
acgacggcaagtttagccctctaataacagatccatagtaaacagagga
agataaaaagagcgtttataataggaacttgagccaagaagaagaa
ttgctctctttaatgcagcagggagcctatgtagctagaacacctttt
acacaatgctaatatgacagggactcccagctatcagtagtcccagctta
cttatctgagtaggtttaccatagggacagtagtaagcaggtgcaa
actatgtagtggatataataaattgcaacttcttgaaaaaacatcat
gggtttaatgtaataagcagaataatagataaagaagtgaaacctc
tactggcctaatcacgctactaacctccctctttaaagctcattcatcat
tagtaaaattagaagaaaattcacagttactcaagtagtctctctaaa
aatggatgaaatcgtctgttaaaaataaacatccgtaatggcatatca
aaaagca

SEQ ID NO: 4802

STRAIN 090

AATAGTACTGAGACAAGTGCCTTCAGTAGTTCCTACTACAA
ATACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAATTTGTATCA
GAATCAGGACAATCTGTAATAGGTCAAGTAAAACCAGATAATCTCGCGGC
GCTTACAACAGTTGACACGCCTCATCATATTTAGCTCCAGATGCTTTAA
AAACAACCTCAATCAAGTCTCTGTTGAGAGTACTTCTACTAAGTTAAGT
GAAGAGACTTACAACAAAAGATGGTAAAGATTTAGCCAACATGGTGAG
AAGTGGTCAAGTTACTAGTGAGGAACCTCGTTAATATGGCATAACGATATTA
TTGCTAAAGAAAACCCATCTTTAAATGACAGTCAATTACTACTAGACGCCAA
GAAGCTTATGAAGAGGCTAGAAAACCTTAAAGATACCAATCAGCCGTTTTT
AGGTGTTCCCTTTGTTAGTCAAGGGGTTAGGGCACAGTATTAAGGTGGTG
AAACCAATAATGGCTTGATCTATGCAGATGGAAAATTAGCACATTTGAC
AGTAGCTATGTCAAAAATATAAAGATTTAGGATTTATTATTTTAGGACA
AACGAACTTTCCAGAGTATGGTGGCGTAATAAACAAGATTTCAAAATTA
ACGGTCTAACGCATAATCCTTGGGATCTTGTCTATAATGCTGGTGGCTCT
CTGGTGGAAAGTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAG
CGGTAGTGATGCTGGTGGTTCTATCCGTATTCATCTTCTGGACGGGCT
TGGTAGGTTTTAAAACCAACAAGAGGATGGTGGTAAATGAAAAGCCAGAT
TCGTATAGTACAGCAGTTCAITTTCCATTAACCTAAGTCATCTAGAGACGC
AGAAAATTATTAACCTTATCTAAAGAAAAGCGATCAACCGCTAGTATCAG
TTAATGATTTAAAATCTTTACCAATTGCTTATACTTTGAAATCACCAATG
GGAACAGAAGTTAGTCAAGATGCTAAAACGCTATTATGGACAACGTCAC
ATTCTTAAGAAAACAAGGATTCAAAGTAAACAGAGATAGACTTACCAATG
ATGGTAGAGCATTAAATGCGTGATTATTCAACCTGGCTATTGGCATGGGA
GGAGCTTTTTCAACAATTGAAAAGACTTAAAACCATGGTTTTACTAA
AGAAGACGTTGATCCTATTACTTGGGCAGTTCAAGTTATTATCAAAAT
CAGATAAGGCTGAACCTTAAAGAAATCTATTATGGAAGCCAAAACATATG
GATGATTTATCGTAAGGCAATGGAGAGCTTCAACAAGCAATTTCCATTTT
CTTATCGCCAACGACCGCAAGTTTAGCCCTCTAAATACAGATCCATATG
TAAACAGAGGAAGATAAAGAGCGGATTTAATAATGGAAAACCTTAGGCCAA
GAAGAAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAG
AACACCTTTTTACACAAAATGCTAATATGACAGGACTCCAGCTATCAGTA
TCCCAGCTTACTTATCTGAGTCTGGTTTACCCTTAGGGACGATGTTAATG
GCAGGTGCAAACTATGATATGGTATTAATTAATTTGCAACTTTCTTTGA
AAAACATCATGGTTTTAATGTTAATGGCAAAGAATAATAGATAAAGAG
TGAAACCATCTACTGGCCTAATACAGCCTACTAACCCTCTTTAAGCT
CATTATCATTTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATC
TATCTCTAAAATAATGGATGAAATCGTCTGTTAAAATAAACCATCCGTAA
TGGCATATCAAAAAGCA

SEQ ID NO: 4803

Table 48: Comparative Sequences relating to SAG1474

STRAIN A909

TACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAAT
TTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGTAAAACAGATAAT
TCTGGCGCGCTTACAACAGTTGACACGCGCTCATCATATTTTCAGCTCCAGA
TGCTTTAAAAACAACCTCAATCAAGTCTGTGCTGTTGAGAGTACTTCTACTA
AGTTAACTGAAGAGACTTACAACAAAAAGATGGTCAAGATTTAGCCAAC
ATGGTGAGAAAGTGGTCAAGTTACTAGTGAGGAACTCGTTAAATATGGCATA
CGATATATTGCTAAAGAAAACCCATCTTTAAATGCAGTCATTACTACTA
GACGCCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGATACCAATCAG
CCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGTTAGGGCACAGTATTAA
AGGTGGTGAACCAATAATGGCTTGATCTATGCGATGGAAAAATTAGCA
CATTTGACAGTAGCTATGTCAAAAAATATAAGATTTAGGATTTATATT
TTAGGACAAACGAACTTCCAGAGTATGGTGGCGTAAATATAACAGATTC
TAAATATACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTG
TTGGCTCTTCTGGTGAAGTGCAGCAGCCATTGCTAGCGGAATGACGCCA
ATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCATCTTCTTG
GACGGGCTTGGTAGGTTTAAAAACCAACAGAGGATTTGGTGAGTAATGAAA
AGCCAGATTCGTATAGTACAGCAGTTTCTTTCCATTAACTAAGTCTACT
AGAGACCGCAGAAACATTATTAACCTTACTAAAGAAAAGCGATCAAACGCT
AGTATCAGTTAATGATTTAAAACTTTTCCAAATGCTTATACTTTGAAAT
CACCAAATGGGAAACAGAAAGTTAGTCAAGATGCTAAAAACGCTATTATGGAC
AACGTCACaTTCTTAAAGAAAACAAGGATTCAAAGTAAACAGAGATAGACTT
ACCAATTTGATGGTAGAGCATTAAATGCGTGATTTCAACCTTGGCTATTG
GCAATGGGAGGAGCTTTTTCAACAATTGAAAAGACTTAAAAAACATGGT
TTTACTAAAGAAGACGTTGATCCTATTTACTTGGGCAGTTTCATGTTATTTA
TCAAATTCAGATAAGGCTGAACCTAAGAAATCTATTATGGAAGCCCAAA
AACATATGGATGATTTATCGTAAGGCAATGGAGAAGCTTCAACAAGCAATTT
CCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCTAATAACAGA
TCCATATGTaACAGAGGAAGATAAAAAGCGGATTTATAATATGAAAACCT
TGAGCCAAAGAAGAAAAGAAATGCTCTCTTTAATCGCCAGTGGGAGCCATG
TTGCGTAGAACACCTTTTACACAAATTTGCTAATATGACAGGACTCCCAGC
TATCAGTATCCGACTTACTTACTGAGTCTGGTTTACCCATAGGGACGA
TGTTAATGGCAGGTGCAACTATGATATGGTATTAAATTAATTTGCAACT
TTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAAGATAATAGA
TAAAGAGTGAAACCATCTACTGGCCTAATACAGCCTACTAACTCCCTCT
TTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACT
CAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACC
ATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4804

STRAIN COH1

AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAAT
ACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAATTTGCATCAGA
ATCAGGCAAACTCTGTAATAGGTCAAGTAAAACAGCTAATCTCTGGCGCGC
TTACAACAGTTGACACGCGCTCATATTTTCAGCTCCAGATGCTTTAAAAACA
ACTCAATCAAGTCTGTGCTGGAGAGTCCCTTCTACTAAGTTAACTGAAGA
GACATACAAACAAAAAGATGGTCAAGATTTAGCCAACATGGTGAAGTG
GTCAGTTACTAGTGAAGAACTCGTCAATATGGCATAACGATATTATCGCT
AAAGAAAACCCATCTTTAAATGCAAGTCACTACTAGACGCCAAGAAAGC
CAITGAAGAGGCTAGAAAACCTTAAAGATACTAATCAGCCGTTTTTAGGTG
TTCCCTTGTAGTCAAGGGTTAGGGCACAGTATTAAAGGTGGTGAACCC
AATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAG
CTATGTCAAAAAATATAAGATTTAGGATTTATTATTTTAGGACAAACGA
ATTTTCCAGATATGGTGGCGTAAATATAACAGACTCTAAATATATACGGT
CCAAACGATAATCCTTGGAACTTTGCTCATAACGCTGGTGGCTCTTCTGG
TGGAAATGCAGCAGCTATTGCTAGCGGAATGACGCCAATTTGCTAGCGGCA
GTGATGCTGGTGGTCTATCCGTATTCATCTTTGGACGGGCTTAGTA
GGTTTTAAACCAACAGAGGATTTGGTGAGTAAATGAAAAGCCAGATTCGTA
TAGTACAGCAGTTTCAATTTCCATTAACCTAAGTCACTAGAGACGCAGAAA
CATTGTTAACTTACCTAAAAGAAAAGCGATCAAACGCTAGTATCAGTTAAT
GATTTAAATCTTTACCAATTTGCTTATACTTTGAAATCACCATGGGAAC
AGAAGTTAGTCAAGATGCTAAAAATGCTATTATGACAAACGTCACATTTCT
TAAGAAAACAAGGATTCAAAGTGCAGAGATAGATTTACCAATTTGATGGT
AGAGCAITAAATGCGTGATTAATCAACCTTGGCTATTGGCATGGGAGGAGC
TTTTTCAACAATTTGAAAAGACTTAAAAAACATGGTTTTACTTAAAGAAG
ACGTTGATCCCATTTACTTGGGCAGTTTATGTTATTTATCAAATTCAGAT
AAGGCTGAACTTAAAGAACTATTGTTGGAAGCCCAAAAACATATGGATGA
TTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTTCTTATTTCTTAT
CGCCAACGACCGCAAGTTTAGCCCTCTAATAACAGATCCATATGTAACA
GAGAAAGATAAAAGAGCGATTTATAATATGGAAAAACCTGAGCCAAAGAAGA
AAGAATTTGCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACAC
CTTTTACACCAATTTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCG
ACTTACTTATCTGAGTCTGGTTTACCCTATAGGACGATGTTAATGGCAGG
TGCAAACTATGATATGGTATTAATTAATTTGCAACTTTCTTTGAAAAAC
ATCATGGTTTTAATGTTAATGGCAAAGAATAATAGATAAAGAAGTGAAA
CCATCTGCTGACCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATT
ATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCT
CTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCA
TATCAAAAAGCA

SEQ ID NO: 4805

STRAIN M732

TCAGTAGCTCCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCC

Table 48: Comparative Sequences relating to SAG1474

TACCGCAAAATTGTCATCAGAATCAGGACAACTCTGTAATAGGTCAAGTAA
 ACCCAGCTAATCTGCGGCGCTTACAACAGTTGACACGCCTCATATTTCA
 GCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCGTGCGTTGAGAGTCC
 TTCTACTAAGTTAACTGAAGAGACATACAAACAAAAGATGGTCAAGATT
 TAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGTCAAT
 ATGGCATACGATATTATCGCTAAAGAAAACCCATCTTTAAATGCAGTCAT
 TACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACCTAAAGATA
 CTAATCAGCCCGTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCAC
 AGTATTAAGAGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAA
 AATTAGCACATTGACAGTAGCTATGTCAAAAAATATAAAGATTTAGGT
 TTATTATTTTAGGACAAACGAATTTCCAGAGTATGGGTGGCGTAATATA
 ACAGACTCTAAATTATACGGTCAACGCATATCTTTGGGATCTTGCTCA
 TAACGCTGGTGGCTCTTCTGGTGGAAAGTGACAGCCTATGCTAGCGGAA
 TGACGCCAATGCTAGCGGAGTATGCTGGTGGTCTATCCGTTATCCA
 TCTTCTGGACGGGCTTAGTAGGTTTAAACCAACAAGAGGATTTGGTGAG
 TAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTCATTTCCATTAACCTA
 AGTCATCTAGAGACGCAGAAAACATTTGTTAACTTACCTAAAGAAAAGCGAT
 TAAACGCTAGTATCAGTTAATGATTTAAAACTTTTACCAATTGCTTATAC
 TTTGAAATCACCATGGGAACAGAAGTTAGTCAAGATGCTAAAAATGCTA
 TTATGGACAACGTCACATCTTAAAGAAAACAAGGATTCAAAGTGACAGAG
 ATAGATTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACCTT
 GGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAGACTTAAAAA
 AACATGGTTTTACTAAAGAAGACGTTGATCCATTACTTGGGCGAGTTCAT
 GTTATTTATCAAAATCAGATAAGGCTGAACTTAAAGAAATCTATTGGGA
 AGCCAAAACATATGGATGATTATCGTAAGCAATGGAGAAGCTTCCACA
 AGCAATTTCTATTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCTA
 AATACAGATCCATATGTTACAGAGAAAGATAAAAGAGCGGATTTATAATAT
 GAAAACCTTGAGCCAAAGAAGAAAGAAATGCTCTCTTAAATCGCCAGTGGG
 AGCCTATGTTGGTGAAGAACCTTTTACACCAATGCTAATATGACAGGA
 TCCCCAGCTATCAGTATCCGACTTACTTATCTGAGTCTGGTTTTAGGTT
 AGGGACGATGTTAATGGCAGGTGCAACTATGATATGGTATTAAATTAAT
 TTGCAACTTTCTTTGAAAACATCATGGTTTTAATGTTAAATGGCAAAGA
 ATAATAGATAAAGAAGTGAACCCATCTGCTGACCTAATACAGCCTACTAA
 CTCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCAC
 AAGTTACTCAAGTATCTATCTTAAAAAATGGATGAAATCGTCTGTTAAA
 AATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4806

STRAIN 18RS21

AATAGTACTGAGACAAGTGTCTCAGTAGTTCCTACTACAAATACTATCGT
 TCAAACTAATGACAGTAATCCTACCGCAAAATTTGTATCAGAATCAGGAC
 AATCTGTAATAGGTCAAGTAAAACAGATAAATCTGCGGCGCTTACAACA
 GTTGACAGCCCTCATCATATTTAGCTCCAGATGCTTTAAAAACAACCTCA
 ATCAAGTCTGTGAGAGTACTTCTACTAAGTTAACTGAAGAGACTT
 ACAACAAAAGATGGTCAAGATTTAGCCAAACATGGTGAGAAGTGGTCAA
 GTTACTAGTGAGGAACCTCGTTAATATGGCATACGATATTATTGCTAAAGA
 AAACCCATCTTTAAATGCAGTCAATACTACTAGACGCCAAGAAGCTATTG
 AAGAGGCTAGAAAACCTTAAAGATACCAATCAGCCGTTTTTAGGTGTTCC
 TTGTTAGTCAAGGGGTTAGGGCACAGTATTTAAAGTGGTGAACCAATAA
 TGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAGCTATG
 TCAAAAAATAAAGATTTAGGATTTATTTAATTTTAGGACAACGAACTTT
 CCAGAGTATGGTGGCGTAAATATAACAGATTTCTAAATTATACGGTCTAAC
 GCATAATCCTTGGGATCTTGTCTATAATGCTGGTGGCTCTCTGGTGGAA
 GTGCAGCAGCCATTGCTAGCGGAATGACGCCAATGCTAGCGGTAGTGAT
 GCTGGTGGTCTATCCGTTATCCATCTTCTTGGACGGGCTTGGTAGGTTT
 AAAACCAACAAGAGGATTTGGTGAATGATAAAGCCAGATTCGTATAGTA
 CAGCAGTTCATTTCCATTAACCTAAGTCACTAGAGACGCAGAAAATTA
 TTAACCTATCTAAAGAAAAGCGATCAACCGCTAGTATCAGTTAATGATTT
 AAAATCTTTACCAATGCTTATACTTTGAAATCACCATGGGAACAGAAG
 TTAGTCAAGATGCTAAAAAGCTATTATGGACAACGTCACATTTTAAAGA
 AAACAAGGATTCAAAGTAAACAGAGATAGACTTACCAATGATGGTAGAGC
 ATTAATGCGTGATTTTCAACCTTGGCTATTGGCATGGGAGGAGCTTTT
 CAACAATTGAAAAGACTTAAAAAATCATGGTTTTACTAAAGAAGAGCTT
 GATCCTATTACTTGGGCGTTCATGTTATTTATCAAAATTCAGATAAGGC
 TGAACCTTAAAGAAATCTATTATGGAAGCCAAAAACATATGGATGATFATC
 GTAAGGCAATGGAGAAGCTTCAACAAGCAATTTCTATTTCTTATCGCCA
 ACGACCGCAAGTTAGCCCTCTAAATACAGATCCATATGTAACAGAGGA
 AGATAAAAGAGCGATTTATAATATGGAACCTTGGCCAAAGAAGAAAGAA
 TTGCTCTCTTAAATCGCCAGTGGGAGCCTATGTTGGGTAGAACACCTTTT
 ACACAAATTTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCGACTTA
 CTTATCTGAGTCTGGTTTACCCTATAGGAGCAGATGTTAATGGCAGGTGCAA
 ACTATGATATGGTATTAATTAATTTGCAACTTTCTTTGAAAACATCAT
 GTTTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAGTGAACCATC
 TACTGGCCATAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTCATCAT
 TAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCTTAAA
 AATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCA
 AAAAGCA

SEQ ID NO: 4807

STRAIN M781

TGCTTCAGTAGTCTCTACTACAAATACTATCGTCAAACCTAATGACAGTA
 ATCCTACCGCAAAATTTGTCATCAGAATCAGGACAATCTGTAATAGGTCAA
 GTAAAACAGCTAATCTGCGGCGCTTACAACAGTTGACACGCCTCATAT

Table 48: Comparative Sequences relating to SAG1474

TTCAGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTGTTGAGA
 GTCCTTCTACTAAGTTAACTGAAGAGACATACAAAACAAAAGATGGTCAA
 GATTTAGCCAACATGGTGAGAAAGTGGTCAAGTTACTAGTGGAGAACTCGT
 CAATATGGCATAACGATATTTATCGCTAAAGAAAACCCATCTTTAAATGCAG
 TCATTTACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACTTAAA
 GATACATTAACAGCCGTTTATAGGTGTTCCCTTGTAGTCAAGGGGTTAGG
 GCACAGTATLAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGATG
 GAAAATTAGCACATTTGACAGTAGCTATGTCAAAAATATAAAGATTTA
 GGATTTATTATTTAGGACAAAAGaATTTTCCAGAGTATGGGTGGCGTAA
 TATAACAGACTCTAAATTTATACGGTCCAACGCATAATCCTTGGaATCTTG
 CTCATAACGCTGGTGGCTCTTCTGGTGGAAAGTGCAGCAGCTATTTGCTAGC
 GGAATGACGCCAATTGCTAGCGGCAGTGTATGCTGGTGGTTCTATCCGTAT
 TCCATCTTCTTGGACGGGCTTAGTAGGTTTAAAACCAACAGAGGATTGG
 TGAGTAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTCATTTTCCATTA
 ACTAAGTCATCTAGAGACGCAGAAAACATTTGTTAACTTACCTAAAGAAAAG
 CGATCAACGCTAGTATCAGTTAATGATTTAAAATCTTTACCAATTTGCTT
 ATACTTTGAAATCACCATTGGGAACAGAAGTTAGTCAAGATGCTAAAAAT
 GCTATTATGGACAACGCTCACATTTCTAAGAGAACAAGGATTCAAAGTGAC
 AGAGATAGATTTACCAATTTGATGGTAGAGCATTAATGCTGATTTATTCAA
 CCTTGGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTA
 AAAAACAATGGTTTTACTAAAGAAAGCGTTGATCCCATTTACTTGGGCGAT
 TCAATGTTATTTTACAAAATTCAGATAAGGCTGAACTTAAGAAATCTATTG
 TGGAAAGCCAAAACATATGGATGATTTATCGTAAGGCAATGGAGAAGCTT
 CACAAGCAATTTCCATTTCTTATCGCCAACGACCGCAAGTTTAGCCCC
 TCTAAATACAGATCCATATGTAAACAGaGAAAGATAAAAGAGCGATTTATA
 ATATGGAAAACCTGAGCCAAAGAAAGAAATTTGCTCTCTTAAATCGCCAG
 TGGGAGCCTATGTTGGGTAGAACACCTTTTACACCAATTTGCTAATAAGAC
 AGGACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTAC
 CCATAGGGACGATGTTAAATGGCAGGTGCAAACTATGATATGGTATTAAT
 AAATTTGCAACTTTCTTTGAAAACATCATGGTTTAAATGTTAAATGGCA
 AAGAATAATAGATAAAGAAGTGAACCATCTGCTGACCTAATACAGCCTA
 CTAACCTCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAAT
 TCACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGT
 TAAAAATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4810
STRAIN CJB110

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 GCAAAAATTTGTATCAGAAATCAGGACAATCTGTAAATAGGTCAGTAAAACC
 AGATAAATCTCGCGCGCTTACAACAGTTGACACGCTCATCATATTTAG
 CTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGCTGTTGAGAGTACT
 TCTACTAAGTTAACTGAAGAGACTTACAAAACAAAAGATGGTAAAGATTT
 AGCCAACATGGTGAAGAAGTGGTCAAGTTACTAGTGGAGAACTCGTTAATA
 TGGCATACGATATTTATGCTAAAGAAAACCCATCTTTAAATGAGTCAAT
 ACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGATA
 CAATCAGCCGTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCACA
 GTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAAA
 ATTAGCACATTTGACAGTAGCTATGTCAAAAATATAAAGATTTAGGATT
 TAITATTTTAGGACAAAACGAATTTCCAGATATGGGTGGCGTAAATATA
 CAGATTTCAAATTTATACGGTCTAACGCATAATCCTTGGGATCTTGTCTAT
 AATGCTGGTGGCTCTTCTGGTGAAGTGCAGCAGCCATTGCTAGCGGAAT
 GAGCCCAATTTGCTAGCGGTAGTGTGCTGGTGGTTCTATCCGTATTTCCAT
 CTTCTTGGACGGGCTTGGTAGGTTTAAAACCAACAGAGGATTTGGTGAGT
 CATGAAAAGCCAGATTCGTATATGACAGCAGTTCAATTTTCCATTAACTAA
 GTCATCTAGAGACGCAGAAAACATTTAATTAATTTATCTAAGAAAAGCGATC
 AAACGCTAGTATCAGTTAATGATTTAAAATCTTTACCAATTTGCTTAACT
 TTGAAATCACCATGGGAACAGAAGTTAGTCAAGATGCTAAAACGCTAT
 TATGGACAACCGTCAATTTCTAAGAAAACAGGATTCAAAGTAAACAGAGA
 TAGACTTACCAATTTGATGGTAGAGCATTAATGCGTGATTTATCAACCTTG
 GCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTAAAAAA
 AcATGGTTTTACTAAAGAAGACGTTGATCTTACTTGGGCGATTCATG
 TTATTTATCAAAATTCAGATAAGGCTGAACCTAAGAAAATCTATTATGGAA
 GCCAAAACATATGGATGATTTATCGTAAGGCAATGGAGAAGCTTCAACA
 GCAATTTCTATTTCTTATCGCCAACGACCGCAAGTTTAGCCCCCTAA
 ATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTTATAATATG
 GAAAACCTGAGCCAAGAAGAAGAAATGGCTCTCTTTAATCGCCAGTGGGA
 GCCTATGTTGGGTAGAACACCTTTTACAAAATTTGCTAATAAGACAGGAC
 TCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCATA
 GGGACgATGTTAATGGCAGGTGCAAACTATGATATGGTATTAATTAATTT
 TGCAACTTTCTTTGAAAACATCATGGTTTTAATGTTAAATGGCAAGAA
 TAATAGATAAAGAAGTGAACCATCTACTGGCCTAATACAGCCTACTAAC
 TCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCACA
 AGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAA
 ATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4811
STRAIN 1169NT

AATAGTACTGAGACAAGTGTCTCAGTAGCTCCTACTACAAATACTATCGT
 TCAAACCTAATGACAGTAATCCTACCGCAAAATTTGCATCAGAACTCAGGAC
 AATCTGTAATATGTCAAGTAAAACAGATAAATCTGCGGCGCTTACACACA
 GTTGACACGCGCTCATATTTAGCTCCAGATGATTTAAAACAACCTCAATC
 AAGTCTGTGTTGAGAGTACTTCTACTAAGTTAACTGAAGAGACATACA
 AACAAAAGATGGTCAAGATTTAGCCACATGGTGAAGAGTGGTCAAGTT

Table 48: Comparative Sequences relating to SAG1474

ACTAGTGAGGAACTCGTCAATATGGCATACGATATTATTGCTAAAGAAAA
 CCCCTCTTTAAATGCAAGTCATTACTACTAGACGCCAAGAAGCCATTGAAG
 AGGCTAGAAAACCTAAAGATACTAATCAGCCATTTTGGTGTTCCTCGT
 TTAGTCAAGGGGTAGGGCAAGTATTAAAGGTGGTGAACCAATAATGG
 CTTGATCTATGCAGATGGAAAAATAGCACATTTGACAGTAGCTATGTCA
 AAAAATATAAAGATTAGGATTTATTTATTTAGGACAAACGAACTTTCCA
 GAGTATGGGTGGCGTAATATAACAGATTCTAATTATACGGTCCAACGCA
 TAACCCTCGGAATCTTGGCTCATAATGCTGGTGGCTCTTCTGGTGGAGTG
 CAGCAGCCATTGCTAGCGGATGACGCCAATTTGCTAGCGGTAGTGTGCT
 GGTGGTTCATCCGATTTCCATCTTCTGGACGGGCTTGGTAGGTTTAAA
 ACCAACAGAGGATTGGTGAATGAAAGCCAGATTTCGTATAGTACAG
 CAGTTCATTTTCCATTAACTAAGTCACTAGAGACGCAGAAACATTATTA
 ACTTATCTAAAGAAAGCGATCAAAACGCTAGTATCAGTTAATGATTTAAA
 ATCTTTACCAATTGCTTATACTTTGAAATCACCAATGGGAACAGAAGTTA
 GTCAGATGCTAAAAACGCTATTATGGCAACCGTCACTTCTTAAGAAAA
 CAAGGATCAAAGTAAACAGAGATAGACTTACCAATTTGATGGTAGAGCATT
 AATGCGTATTATTCAACCTTGGCTATTGGCATGGGAGGAGCTTTTTCAA
 CAATTGAAAAGACTTAAAAAACATGGTTTTACTAAGAAGACGTTGAT
 CCTATTACTTGGCAGTTCATGTTATTTATCAAAATTCAGATAAGGCTGA
 ACTTAAGAAAATCTATTATGGAAAGCCAAAAACATATGGATGATTTATCGTA
 AGGCAATGGAGAGCTTCACAAGCAATTTCCATTTTCTATCGCCAACG
 ACCGCAAGTTTGGCCCTCTAAATACAGATCCATAATGTAACAGAGGAAGA
 TAAAAGAGCGATTTAATAATATGAAAACCTTGGCCAAAGAAAGAAAGATTG
 CTCCTTTAATCGCCAGTGGGAGCCTATGTTGGGTAGAACACCTTTTACA
 CAAATTTGCTAATATGACAGGACTCCAGCTATCAGTATCCGACTTACTT
 ATCTGAGTCTGGTTTACCATAGGAGCAGATGTTAATGGCAGGTGCAAACT
 ATGATATGGTATTAATTAATTTGCAACTTTCTTGA AAAACATCATGGT
 TTTAATGTTAAATGGCAAGAAATAATAGATAAAGAAGTGAACCATCTAC
 TGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTTCATCATTAG
 TAAATTTAGAAGAAAATTCACAGTTACTCAAGTATCTATCTCTAAAAAA
 TGGATGAAATCGTCTTTAAAAATAAACCATCCGTAATGGCATATCAAAA
 AGCA

SEQ ID NO: 4812
 STRAIN JM9130013

TTCCAGTAGTCTCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATC
 CTACCGCAAAAATTTTCATCAGAATCAGGACAATCTGTAATAGGTCAAGTA
 AAACCAGCTAATTTCTGTGGCGCTTACAACAGTTGACACGCTCATATTTCA
 AGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTCTGGTGGAGAGT
 CTTCTACTAAGTTAACTGAAGAGACATACAAAACAAAAGATGGTCAAGAG
 TTAGCCAAACATGGTGAAGTGGTCAAGTACTAGTGGAGAACTCGTCAA
 TATGGCATACGATTTATTGCTAAGAAAACCCATCTTTAAATGCAAGTCA
 TTTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGAT
 ACCAATCAGCCGTTTTAGTGTTCCTTGTAGTCAAGGGGTTAGGGCA
 CAGTATTAAAGGTGGTGAACCAATAATGGCTTGTATGATGACAGGTGGAA
 AAATTAGCACATTTGACAGTAGCTATGTCAAAAATATAAAGATTTAGGA
 TTTATTATTTTAGGCAAAACGAACTTTCCAGAGTATGGATGGCGCAATAT
 AACAGATTCTAAATTTATACGGTCCAACGCATAACCCCTTGAATCTTGGCT
 ATAATGCTGGTGGCTCTTCTGGTGGAGTGCAGCAGTTATTGCTAGCGGG
 ATGACGCCAAATGCTAGCGGTAGTGTATGCTGGTGGTTCTATCCGATTTCC
 ATCTTCTGGACGGGCTTGGTAGGTTTAAAACCAACAAGAGGATTGGTGA
 GTAATGAAAAGCCAGATTCGTATAGTACAGCAGTTCAATTTCCATTAACCT
 AAGTCATCTAGAGACGCAGAAAACATTATTAACCTTATCTAAAGAAAAGCGA
 TCAAACGCTAGTATCAGTTAATGATTTAAAATCTTTACCAATTTGCTTATA
 CTTTGAATACCAATGGGAACAGAAAGTATGTCAGATGCTAAAAATGCT
 ATTTAGGACAAAGCTCATATTTCTTAAAGAAAACAAAGGATTCAAAGTGACAGA
 GATAGACTTACCAATTTGATGGTAGAGCAATTAATGCGTGAATTTCAACCT
 TGGCTATTGGTATGGGAGGAGCTTTTCAACAATTGAAAAGAACTTAAAA
 AAACATGGTTTTACTTAAAGAAAGCGTTGATCCCATTACTTGGGGAGTTCA
 TGTATTATTCAAAAATTCAGATAAGGCTGAACTTAAAGAAATCTATTATGG
 AAGCCAAAACATATGGATGATATCGTAAGGCAATGGAGAAGCTTAC
 AAGCAATTTCTATTTCTTATCGCCAAACGACCGCAAGTTAGCCCTCT
 AAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATAATA
 TGGAAAACCTTGAAGCAAGAAAGAAATTTGCTCTTTAATCGCCAGTGG
 GAGCCTATGTTGCGTAGAACACCTTTTACACAAATGCTAATATGACAGG
 ACTCCAGCTATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCA
 TAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATAAA
 TTTGCAACTTTCTTTGAAAATATCATGGTTTAAATGTTAAATGGCAAAG
 AATAATAGATAAAGAAAGTGAACCACTACTGGCCATAACAGCCTACTA
 ACTCCCTCTTTAAAGCTCATTTCATCATTAGTAAATTTAGAAGAAAATTC
 CAAGTTACTCAAGTATCTATCTCTAAAAATGGATGAAATCGTCTGTTAA
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SEQ ID NO: 4813
 STRAIN H36B

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 AAAACAGCTAATTTCTGTGGCGCTTACAACAGTTGACACGCTCATATTT
 CAGTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTCTGGTGGAGT
 CCTTCTACTAAGTTAACTGAAGAGACATACAAAACAAAAGATGGTCAAGA
 TTTAGCCAAACATGGTGAAGTGGTCAAGTTACTAGTGGAGAACTCGTCA
 ATATGGCATACGATAATTTGCTAAGAAAACCCATCTTTAATGCAAGT
 ATTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGA

Table 48: Comparative Sequences relating to SAG1474

TACCAATCAGCCGTTTTAGGTGTTCCCTTGTAGTCAAGGGGTAGGGC
ACAGTATTAAAGTGGTGAACCAATAATGGCTTGATCTATGCAGGTGGA
AAAATTAGCACATTTGACAGTAGCTATGTCAAATAATATAAGATTTAGG
ATTTATTATTTTAGGACAAACGAACTTCCAGAGTATGGATGGCGCAATA
TAACAGATTCTAAATATAACGGTCCACGCAATAACCTTGGAACTTTGCT
CATAATGCTGGTGGCTCTTCTGGTGGAAAGTGCAGCAGTTATGCTAGCGG
GATGACGCCAATGCTAGCGGTAGTGTCTGGTGGTTCTATCCGTATTC
CATCTTCTGGACGGGCTTGGTAGGTTTAAAACCAACAAGAGGATTGGTG
AGTAATGAAAAGCCAGATTTCGTATAGTACAGCAGTTTCATTTCCATTAA
TAAGTCACTAGAGACGCGAAGAACATTATTAACCTTCTAAAGAAAAGCG
ATCAAACGCTAGTATCAGTTAATGATTTAAAATCTTTACCAATGCTTAT
ACTTTGAATCAACCAATGGGAACAGAACTTAGTCAAGATGCTAAAATGC
TATTTATGGACAACGTCATATCTTAAGAAAACAAGGATTCAAAAGTGACAG
AGATAGACTTACCAATTTGATGGTAGAGCATTAAATGCGTGATTTCAACC
TTGGCTATGGGTATGGGAGGAGCTTTTTCAACAATGAAAAGAGCTTAAA
AAAACATGGTTTTACTAAAGAAGACGTTGATCCCATTTACTTGGGCGATT
ATGTTATTTATCAAATTCAGATAAGGCTGAACTTAAGAAATCTATTATG
GAAGCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCA
CAAGCAATTTCCATTTCTTATCGCCAACGACCGCAAGTTTAGCCCTC
TAAATACAGATCCATATGTAACAGAGGAAGATAAAAAGAGCGATTATAAT
ATGAAAACCTGAGCCAAGAAAGAAATGCTCTCTTAAATCGCCAGTG
GGAGCCTATGTTGGGTAGAACACCTTTTACACAAATGCTAATATGACAG
GACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCC
ATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGTTAATATAA
ATTTGCAACTTTCTTTGAAAATAATCAATGGTTTTAATGTTAAATGGCAAA
GAATAATAGATAAAGAAGTAAACCATCTACTGGCCTAATACAGCCACT
AACTCCCTTTTAAAGCTCATTTCATCATAGTAAATTTAGAAGAAAATTC
ACAAGTTACTCAAGTATCTATCTCTAAAATAATGGATGAAATCGTCTGTTA
AAAATAAA

PRETTY of: /biotcmp/msa71927.2{*} January 22, 2003 07:23 ..

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msa71927.2{173_M781} -----tgc ttcagtagct ccTACTACAA ATACTATCGT
msa71927.2{173_M732} -----tcagtagct ccTACTACAA ATACTATCGT
msa71927.2{173_H36B} -----c ttcagtagtt ccTACTACAA ATACTATCGT
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Consensus ----- *****

51 100
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msa71927.2{173_2603} TCAAAC TAAT GACAGTAATC CTACCGCAA AATTTgtATCA GAATCAGGAC
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msa71927.2{173_CJB110} TCAAAC TAAT GACAGTAATC CTACCGCAA AATTTgtATCA GAATCAGGAC
msa71927.2{173_COH1} TCAAAC TAAT GACAGTAATC CTACCGCAA AATTTgcATCA GAATCAGGAC
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msa71927.2{173_H36B} TCAAAC TAAT GACAGTAATC CTACCGCAA AATTTtcATCA GAATCAGGAC
msa71927.2{173_JM9130013} TCAAAC TAAT GACAGTAATC CTACCGCAA AATTTtcATCA GAATCAGGAC
msa71927.2{173_1169NT} TCAAAC TAAT GACAGTAATC CTACCGCAA AATTTgcATCA GAATCAGGAC
Consensus *****

101 150
msa71927.2{173_18RS21} AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
msa71927.2{173_2603} AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
msa71927.2{173_A909} AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
msa71927.2{173_090} AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
msa71927.2{173_CJB110} AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
msa71927.2{173_COH1} AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA
msa71927.2{173_M781} AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA
msa71927.2{173_M732} AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA
msa71927.2{173_H36B} AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA
msa71927.2{173_JM9130013} AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA
msa71927.2{173_1169NT} AATCTGTAAT AtGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA
Consensus ***** *_***** *****_* *****_**** *****

151 200
msa71927.2{173_18RS21} GTTGACACGC CtcaTCATAT TTCAGTCCA GATGcTTTAA AAACAAC TCA
msa71927.2{173_2603} GTTGACACGC CtcaTCATAT TTCAGTCCA GATGcTTTAA AAACAAC TCA
msa71927.2{173_A909} GTTGACACGC CtcaTCATAT TTCAGTCCA GATGcTTTAA AAACAAC TCA
msa71927.2{173_090} GTTGACACGC CtcaTCATAT TTCAGTCCA GATGcTTTAA AAACAAC TCA
msa71927.2{173_CJB110} GTTGACACGC C . . .TCATAT TTCAGTCCA GATGcTTTAA AAACAAC TCA
msa71927.2{173_COH1} GTTGACACGC C . . .TCATAT TTCAGTCCA GATGcTTTAA AAACAAC TCA
msa71927.2{173_M781} GTTGACACGC C . . .TCATAT TTCAGTCCA GATGcTTTAA AAACAAC TCA
msa71927.2{173_M732} GTTGACACGC C . . .TCATAT TTCAGTCCA GATGcTTTAA AAACAAC TCA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_H36B}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_JM9130013}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
msa71927.2{173_1169NT}	GTTGACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACTCA
Consensus	*****	*-*****	*****	***-*****	*****
201					
msa71927.2{173_18RS21}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_2603}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_A909}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_090}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_CJB110}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_COH1}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_M781}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_M732}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_H36B}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_JM9130013}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_1169NT}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
Consensus	*****	*****	*-*****	*****	*****
251					
msa71927.2{173_18RS21}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_2603}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_A909}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_090}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_CJB110}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_COH1}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M781}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M732}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_H36B}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_JM9130013}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_1169NT}	ACAAACAAAA	AGATGGTcAA	GATTTAGCCA	ACATGGTGAG	AAGTGGTCAA
Consensus	*****	*****	**-*****	*****	*****
301					
msa71927.2{173_18RS21}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_2603}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_A909}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_090}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_CJB110}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_COH1}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_M781}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_M732}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_H36B}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_JM9130013}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_1169NT}	GTTACTAGTG	AGGAACTCGT	LAATATGGCA	TACGATATTA	TtGCTAAAGA
Consensus	*****	*****	-*****	*****	*-*****
351					
msa71927.2{173_18RS21}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_2603}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_A909}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_090}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_CJB110}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_COH1}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_M781}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_M732}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_H36B}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_JM9130013}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_1169NT}	AAACCCaTCT	TTAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
Consensus	*****	*****	*****	*****	*****
401					
msa71927.2{173_18RS21}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_2603}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_A909}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_090}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_CJB110}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_COH1}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M781}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M732}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_H36B}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_JM9130013}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_1169NT}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
Consensus	*****	*****	*****	*****	*****
451					
msa71927.2{173_18RS21}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_2603}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_A909}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_090}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_CJB110}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_COH1}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_M781}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M732}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_H36B}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_JM9130013}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_1169NT}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_2603}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_A909}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_090}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_CJB110}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_COH1}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M781}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M732}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_H36B}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_JM9130013}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_1169NT}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_2603}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_A909}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_090}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_CJB110}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_COH1}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_M781}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_M732}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_H36B}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_JM9130013}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
msa71927.2{173_1169NT}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAAcTTT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTcLAAC
msa71927.2{173_2603}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTcLAAC
msa71927.2{173_A909}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTcLAAC
msa71927.2{173_090}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTcLAAC
msa71927.2{173_CJB110}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTcLAAC
msa71927.2{173_COH1}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAc	TCTAAATTAT	ACGGTcCAAC
msa71927.2{173_M781}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAc	TCTAAATTAT	ACGGTcCAAC
msa71927.2{173_M732}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAc	TCTAAATTAT	ACGGTcCAAC
msa71927.2{173_H36B}	CCAGAGTATG	GgTGGCGcAA	TATAACAGAT	TCTAAATTAT	ACGGTcCAAC
msa71927.2{173_JM9130013}	CCAGAGTATG	GgTGGCGcAA	TATAACAGAT	TCTAAATTAT	ACGGTcCAAC
msa71927.2{173_1169NT}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTcCAAC
Consensus	*****	*-*****	*****-	*****	*****-***
msa71927.2{173_18RS21}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_2603}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_A909}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_090}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_CJB110}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_COH1}	GCATAAaCCT	tGGaATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_M781}	GCATAAaCCT	tGGaATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_M732}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_H36B}	GCATAAaCCT	tGGaATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_JM9130013}	GCATAAaCCT	tGGaATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
msa71927.2{173_1169NT}	GCATAAaCCT	tGGaATCtTG	CTCATAAaGC	TGGTGGCTCT	TCtGGTGGAA
Consensus	*****	***-*****	*****-*	*****	*****
msa71927.2{173_18RS21}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_2603}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_A909}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_090}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_CJB110}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_COH1}	GTGCAGCAGc	tATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGcAGTGAT
msa71927.2{173_M781}	GTGCAGCAGc	tATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGcAGTGAT
msa71927.2{173_M732}	GTGCAGCAGc	tATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGcAGTGAT
msa71927.2{173_H36B}	GTGCAGCAGt	tATTGCTAGC	GGgATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_JM9130013}	GTGCAGCAGt	tATTGCTAGC	GGgATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_1169NT}	GTGCAGCAGc	cATTGCTAGC	GGrATGACGC	CAATTGCTAG	CGGtAGTGAT
Consensus	*****	-*****	*-*****	*****	***-*****
msa71927.2{173_18RS21}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_2603}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_A909}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_090}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_CJB110}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_COH1}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M781}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_M732}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_H36B}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_JM9130013}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_1169NT}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
Consensus	*****	*****	*****	*****	*_*****
801					
msa71927.2{173_18RS21}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_2603}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_A909}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_090}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_CJB110}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_COH1}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M781}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M732}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_H36B}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_JM9130013}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_1169NT}	AAAACCAACA	AGAGGATTGG	TGAGTaatGA	AAAGCCAGAT	TCGTATAGTA
Consensus	*****	*****	*****	*****	*****
851					
msa71927.2{173_18RS21}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_2603}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_A909}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_090}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_CJB110}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_COH1}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M781}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M732}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_H36B}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_JM9130013}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_1169NT}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
Consensus	*****	*****	*****	*****	*****-
901					
msa71927.2{173_18RS21}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_2603}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_A909}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_090}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_CJB110}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_COH1}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_M781}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_M732}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_H36B}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_JM9130013}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_1169NT}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
Consensus	*****	*****	*****	*****	*****
951					
msa71927.2{173_18RS21}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_2603}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_A909}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_090}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_CJB110}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_COH1}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_M781}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_M732}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_H36B}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_JM9130013}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
msa71927.2{173_1169NT}	AAAATCITTA	CCAATTGCTT	ATACITTTGAA	ATCACCAAATG	GGAAACAGAAG
Consensus	*****	*****	*****	*****	*****
1001					
msa71927.2{173_18RS21}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_2603}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_A909}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_090}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_CJB110}	TTAGTCAAGA	TGCTAAAAAc	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_COH1}	TTAGTCAAGA	TGCTAAAAAAt	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_M781}	TTAGTCAAGA	TGCTAAAAAAt	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_M732}	TTAGTCAAGA	TGCTAAAAAAt	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_H36B}	TTAGTCAAGA	TGCTAAAAAAt	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_JM9130013}	TTAGTCAAGA	TGCTAAAAAAt	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_1169NT}	TTAGTCAAGA	TGCTAAAAAAt	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
Consensus	*****	*****	*****	*****	*****
1051					
msa71927.2{173_18RS21}	aaACAAGGAT	TCAAAGTaaC	AGAGATAGAc	TTACCAaATTG	ATGGTAgAGC
msa71927.2{173_2603}	aaACAAGGAT	TCAAAGTaaC	AGAGATAGAc	TTACCAaATTG	ATGGTAgAGC
msa71927.2{173_A909}	aaACAAGGAT	TCAAAGTaaC	AGAGATAGAc	TTACCAaATTG	ATGGTAgAGC
msa71927.2{173_090}	aaACAAGGAT	TCAAAGTaaC	AGAGATAGAc	TTACCAaATTG	ATGGTAgAGC
msa71927.2{173_CJB110}	aaACAAGGAT	TCAAAGTaaC	AGAGATAGAc	TTACCAaATTG	ATGGTAgAGC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_COH1}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_M781}	gAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_M732}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_H36B}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_JM9130013}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_1169NT}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC
Consensus	*****	*****	*****	*****	*****
1101					
msa71927.2{173_18RS21}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_2603}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_A909}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_090}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_CJB110}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_COH1}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M781}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M732}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_H36B}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_JM9130013}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_1169NT}	ATTAAATGCGT	GATTATTCAA	CCTTGGCTAT	TGGcATGGGA	GGAGCTTTTT
Consensus	*****	*****	*****	*****	*****
1151					
msa71927.2{173_18RS21}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_2603}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_A909}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_090}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_CJB110}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_COH1}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M781}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M732}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_H36B}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_JM9130013}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_1169NT}	CAACAATTGA	AAAAGACTTA	AAAAAACATG	GTTTTACTAA	AGAAGACGTT
Consensus	*****	*****	*****	*****	*****
1201					
msa71927.2{173_18RS21}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_2603}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_A909}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_090}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_CJB110}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_COH1}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_M781}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_M732}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_H36B}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_JM9130013}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
msa71927.2{173_1169NT}	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	TATCAAAT	CAGATAAGGC
Consensus	*****	*****	*****	*****	*****
1251					
msa71927.2{173_18RS21}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_2603}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_A909}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_090}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_CJB110}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_COH1}	TGAACCTAAG	AAATCTATTg	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_M781}	TGAACCTAAG	AAATCTATTg	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_M732}	TGAACCTAAG	AAATCTATTg	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_H36B}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_JM9130013}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
msa71927.2{173_1169NT}	TGAACCTAAG	AAATCTATTa	TGGAAGCCCA	AAAACATATG	GATGATTATC
Consensus	*****	*****	*****	*****	*****
1301					
msa71927.2{173_18RS21}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_2603}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_A909}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_090}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_CJB110}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_COH1}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_M781}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_M732}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_H36B}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_JM9130013}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_1169NT}	GTAAGGCCAAT	GGAGAAGCCT	CACAAGCAAT	TTCCCTATTTT	CTTATCGCCA
Consensus	*****	*****	*****	*****	*****
1351					
msa71927.2{173_18RS21}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_2603}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_A909}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_090}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_CJB110}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_COH1}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGaA
msa71927.2{173_M781}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGaA
msa71927.2{173_M732}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TtACAGAGaA
msa71927.2{173_H36B}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_JM9130013}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
msa71927.2{173_1169NT}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCATATG	TaACAGAGgA
Consensus	*****	*****	*****	*****	*-*****-
1401					
msa71927.2{173_18RS21}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_2603}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_A909}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_090}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_CJB110}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_COH1}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M781}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M732}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_H36B}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_JM9130013}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_1169NT}	AGATAAAAGA	GCGATTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
Consensus	*****	*****	*****	*****	*****
1451					
msa71927.2{173_18RS21}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_2603}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_A909}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_090}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_CJB110}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_COH1}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M781}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M732}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_H36B}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_JM9130013}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_1169NT}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
Consensus	*****	*****	*****	*****	*****
1501					
msa71927.2{173_18RS21}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_2603}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_A909}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_090}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_CJB110}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_COH1}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M781}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M732}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_H36B}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_JM9130013}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_1169NT}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
Consensus	****-*****	*****	*****	*****	*****
1551					
msa71927.2{173_18RS21}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_2603}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_A909}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_090}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_CJB110}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_COH1}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M781}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M732}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_H36B}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_JM9130013}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_1169NT}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
Consensus	*****	*****	*****	*****	*****
1601					
msa71927.2{173_18RS21}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_2603}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_A909}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_090}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_CJB110}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_COH1}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_M781}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_M732}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_H36B}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_JM9130013}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_1169NT}	ACTATGATAT	GGTATTAATT	AAATTTGCAA	CTTTCCTTGA	AAAACATCAT
Consensus	*****	*****	*****	*****	*****
1651					
msa71927.2{173_18RS21}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_2603}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_A909}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_090}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_CJB110}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_COH1}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_M781}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_M732}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_H36B}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_JM9130013}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_1169NT}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
Consensus	*****	*****	*****	*****	*****

	1701			1750	
msa71927.2{173_18RS21}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_2603}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_A909}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_090}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_CJB110}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_COH1}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_M781}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_M732}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_H36B}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_JM9130013}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
msa71927.2{173_1169NT}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT
Consensus	*.***.***	*****	*****	*****	*****

	1751			1800	
msa71927.2{173_18RS21}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_2603}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_A909}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_090}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_CJB110}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_COH1}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_M781}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_M732}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_H36B}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_JM9130013}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
msa71927.2{173_1169NT}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA
Consensus	*****	*****	*****	*****	*****

	1801			1850	
msa71927.2{173_18RS21}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_2603}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_A909}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_090}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_CJB110}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_COH1}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_M781}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_M732}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
msa71927.2{173_H36B}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	-----	-----
msa71927.2{173_JM9130013}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatat--
msa71927.2{173_1169NT}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca
Consensus	*****	*****	*****	-----	-----

	1851
msa71927.2{173_18RS21}	aaaagca
msa71927.2{173_2603}	aaaagca
msa71927.2{173_A909}	aaaagca
msa71927.2{173_090}	aaaagca
msa71927.2{173_CJB110}	aaaagca
msa71927.2{173_COH1}	aaaagca
msa71927.2{173_M781}	aaaagca
msa71927.2{173_M732}	aaaagca
msa71927.2{173_H36B}	-----
msa71927.2{173_JM9130013}	-----
msa71927.2{173_1169NT}	aaaagca
Consensus	-----

SEQ ID NO: 4814
 STRAIN 2603 frame: 1
 NSTETSASVVPITNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALITVDPHHISAP
 DALKTTQSSPVVESTSTKLTEETYKQKQDLANMVRSGQVTSEELVNMAYDI IAKENPS
 LNAVITTRRQSAIEBEARKLKDNTQPPFLGVPLLVKGLGHSI KGGETNNGLIYADGKI STFD
 SSVVKKYKDLGFI ILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSCGSAAAIAS
 GMTPIASGSDAGSIRI PSSWTGLVGLKPTRGLVSNKSPDYSYTAHVHPLTKSSRDAETL
 LTYLKKSDQTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTPFLRKQGFVKVTEID
 LPIDGRALMRDYSFLAIGMGGAFFSTIEKDLKKGHGFTEKEDVDPITWAVHVIYQNSDKAELK
 KSIMEAQKHMDDYRKAMEKHLKQFPI FLSPTASLAPLNTDPYVTEEDKRAI YMENLSQ
 EERIALFNROWEPLMRLRTPFTQIANMTGLPAISIPTYLSEGLPIGTMLMAGANYDMVLI
 KPATFFKHHGFNVKQWR I IDKEVKPSTGLIQPTNSLFAHSSLVNLENSQVTQVSIK
 KWKSSVKNKPSVMAYQKA

SEQ ID NO: 4815
 STRAIN_090 frame: 1
 NSTETSASVVPITNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALITVDPHHISAP

Table 48: Comparative Sequences relating to SAG1474

DALKTTQSSPVVESTSTKLTTEETYKQKDGKDLANMVRSGQVTSEELVNMAFYDI IAKENPS
LNAVITTRRQEAIEBARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFD
SSYVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIAS
GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETL
LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSDAKNAIMDNVTFLRKQGFVTEIDL
LPIDGRALMRDYSTLAI GMGGAFSTIEKDLKKGHGFTEKEDVDPITWAVHVIYQNSDKAELK
KSIMEAQKHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
EERIALFNRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
KFATTFEKHHGFNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSI SK
KMKSSVKNKPSVMAYQKA

SEQ ID NO: 4816

STRAIN A909 frame: 2

TTNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAPDALKTTQSSPV
VESTSTKLTTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDI IAKENPSLNAVITTRRQ
AIEBARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDSSYVKYKDLG
FIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIASGMTPIASGSDA
GGSIIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSDQTL
VSVNDLKSLPIAYTLKSPMGTEVSDAKNAIMDNVTFLRKQGFVTEIDLPI DGRALMRD
YSTLAI GMGGAFSTIEKDLKKGHGFTEKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKHM
DYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ EERIALFNRQW
EPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI KFATTFEKHHG
FNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSI SKKMKSSVKNKPS
VMAYQKA

SEQ ID NO: 4817

STRAIN COH1 frame: 1

NSTETSASVAFTTNTIVQINDSNPTAKFVSESGQSVIGQVKPANSAAALTTVDTPHHISAPD
ALKTQSSPVVESTSTKLTTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDI IAKENPSL
NAVITTRRQEAIEBARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDSSYVKYK
DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASG
MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLL
TYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSDAKNAIMDNVTFLRKQGFVTEIDL
PIDGRALMRDYSTLAI GMGGAFSTIEKDLKKGHGFTEKEDVDPITWAVHVIYQNSDKAELK
KSIVEAQKHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
EERIALFNRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
KFATTFEKHHGFNVKQRIIDKEVKPSADLIQPTNSLFAHSSLVNLEENSQVTQVSI SKK
WMKSSVKNKPSVMAYQKA

SEQ ID NO: 4818

STRAIN M732 frame: 1

SVAPTNTNTIVQINDSNPTAKFVSESGQSVIGQVKPANSAAALTTVDTPHHISAPDALKTTQ
SPVVESTSTKLTTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDI IAKENPSLNAVITTR
RQEAIEBARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDSSYVKYK
DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASG
MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYL
KKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSDAKNAIMDNVTFLRKQGFVTEIDLPI DGRAL
MRDYSTLAI GMGGAFSTIEKDLKKGHGFTEKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ
KHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ EERIALF
NRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI KFATTFEK
HHGFNVKQRIIDKEVKPSADLIQPTNSLFAHSSLVNLEENSQVTQVSI SKKMKSSVKN
KPSVMAYQKA

SEQ ID NO: 4819

STRAIN 18RS21 frame: 1

NSTETSASVVPNTNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAP
DALKTTQSSPVVESTSTKLTTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDI IAKENPS
LNAVITTRRQEAIEBARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFD
SSYVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIAS
GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETL
LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSDAKNAIMDNVTFLRKQGFVTEIDL
LPIDGRALMRDYSTLAI GMGGAFSTIEKDLKKGHGFTEKEDVDPITWAVHVIYQNSDKAELK
KSIMEAQKHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
EERIALFNRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
KFATTFEKHHGFNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSI SK
KMKSSVKNKPSVMAYQKA

SEQ ID NO: 4820

STRAIN M781 frame: 2

ASVAPTNTNTIVQINDSNPTAKFVSESGQSVIGQVKPANSAAALTTVDTPHHISAPDALKTTQ
SSPVVESTSTKLTTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDI IAKENPSLNAVITTR
RQEAIEBARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDSSYVKYK
KDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASG
MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYL
KKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSDAKNAIMDNVTFLRKQGFVTEIDLPI DGRAL
MRDYSTLAI GMGGAFSTIEKDLKKGHGFTEKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ
KHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ EERIALF
NRQWEPMLRRTPFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI KFATTFE
KHHGFNVKQRIIDKEVKPSADLIQPTNSLFAHSSLVNLEENSQVTQVSI SKKMKSSV
KNKPSVMAYQKA

SEQ ID NO: 4821

STRAIN CJB110 frame: 3

Table 48: Comparative Sequences relating to SAG1474

VPTTNTIVQTNSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAPDALKTTQSS
PVVESTSTKLTEETIKYKQKDGKDLANMVRSGQVTSEELVNMAFYDI IAKENPSLNAVITTRR
QEAIEEARLKDNTNQPFLGVPPLLVKGLGHSIKGGETNNGLIYADGKISTFDSYVVKYKQD
LGFIILGQTNFPPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGGSSAAA IASGMTPIASG
DAGGSIRIPSSWTGLVGLKPTRGLVSHKPKDSYSTAVHFPPLTKSSRDAETLLTYLKKSDQ
TLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFLLRQKQFKVTEIDLPI DGRALM
RDYSTLAIGMGGAFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKH
MDDYRKAMEKHLKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFNR
QWEPMLRRTPTFTQIANMTGLPAISIPTYLSESGLPITGMLMAGANYDMVLIKFATPFEEKH
HGFNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSI SKKWMKSSVKK
KPSVMAYQKA

SEQ ID NO: 4822

STRAIN 1169NT frame: 1

NSTETSASVAPTNTIIVQTNSNPTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAPD
DLKTTQSSPVVESTSTKLTEETIKYKQKDGKDLANMVRSGQVTSEELVNMAFYDI IAKENPSL
NAVITTRRQEAIEEARLKDNTNQPFLGVPPLLVKGLGHSIKGGETNNGLIYADGKISTFDS
SYVVKYKQD LGFIILGQTNFPPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGGSSAAA IASG
MTPIASGDAGGSIRIPSSWTGLVGLKPTRGLVSHKPKDSYSTAVHFPPLTKSSRDAETLL
TYLKKSDQTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFLLRQKQFKVTEIDL
PIDGRALMRDYSTLAIGMGGAFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKS
IMEAQKH MDDYRKAMEKHLKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFNR
QWEPMLRRTPTFTQIANMTGLPAISIPTYLSESGLPITGMLMAGANYDMVLIKFATPFEEKH
HGFNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSI SKKWMKSSVKK
KPSVMAYQKA

SEQ ID NO: 4823

STRAIN JM9130013 frame: 2

SVAPTNTIIVQTNSNPTAKFVSESGQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS
SPVVESTSTKLTEETIKYKQKDGQELANMVRSGQVTSEELVNMAFYDI IAKENPSLNAVITTR
RQEAIEEARLKDNTNQPFLGVPPLLVKGLGHSIKGGETNNGLIYAGGKISTFDSYVVKYK
DLGFIILGQTNFPPEYGWRNITDSKLYGPTHNPWDLAHNAGGSSGGSSAAV IASGMTPIASG
SDAGGSIRIPSSWTGLVGLKPTRGLVSHKPKDSYSTAVHFPPLTKSSRDAETLLTYLKKSD
QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVIFLLRQKQFKVTEIDLPI DGRAL
MRDYSTLAIGMGGAFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKH
MDDYRKAMEKHLKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFN
RQWEPMLRRTPTFTQIANMTGLPAISIPTYLSESGLPITGMLMAGANYDMVLIKFATPFEEK
YHGFNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSI SKKWMKSSVK
NKPSVMAY

SEQ ID NO: 4824

STRAIN H36B frame: 3

SVVPTTNTIIVQTNSNPTAKFVSESGQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS
SPVVESTSTKLTEETIKYKQKDGQELANMVRSGQVTSEELVNMAFYDI IAKENPSLNAVITTR
RQEAIEEARLKDNTNQPFLGVPPLLVKGLGHSIKGGETNNGLIYAGGKISTFDSYVVKYK
DLGFIILGQTNFPPEYGWRNITDSKLYGPTHNPWDLAHNAGGSSGGSSAAV IASGMTPIASG
SDAGGSIRIPSSWTGLVGLKPTRGLVSHKPKDSYSTAVHFPPLTKSSRDAETLLTYLKKSD
QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVIFLLRQKQFKVTEIDLPI DGRAL
MRDYSTLAIGMGGAFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKH
MDDYRKAMEKHLKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFN
RQWEPMLRRTPTFTQIANMTGLPAISIPTYLSESGLPITGMLMAGANYDMVLIKFATPFEEK
YHGFNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSI SKKWMKSSVK
NK

PRETTY of: /biotmp/msa72034.2{*} January 22, 2003 07:25 ..

Table with 4 columns: Accession/ID, Position, Sequence, and Consensus. It lists multiple sequence alignments for SAG1474, including entries for msa72034.2 and consensus sequences at positions 1, 50, 51, and 100.

Table 48: Comparative Sequences relating to SAG1474

Consensus	***--*****	*-*****	****-*****	*****--	*****--	*****
	101					150
msa72034.2{173_090}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_18RS21}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_2603}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_A909}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_CJB110}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_COH1}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_M732}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_M781}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_1169NT}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_H36B}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_JM9130013}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
Consensus	*****	*****	*****	*****	*****	*****
	151					200
msa72034.2{173_090}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_18RS21}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_2603}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_A909}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_CJB110}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_COH1}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_M732}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_M781}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_1169NT}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_H36B}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_JM9130013}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
Consensus	*****	*****	***-*****	*****	*****	*****
	201					250
msa72034.2{173_090}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_18RS21}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_2603}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_A909}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_CJB110}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_COH1}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_M732}	PEYGWRNITD	SKLYGxTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_M781}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_1169NT}	PEYGWRNITD	SKLYGpTHNP	rnLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_H36B}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
msa72034.2{173_JM9130013}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAaIAS	GMPPIASGSD	
Consensus	*****	*****	***-*****	*****	*****	*****
	251					300
msa72034.2{173_090}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_18RS21}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_2603}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_A909}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_CJB110}	AGGSIRIPSS	WTGLVGLKPT	RGLVShEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_COH1}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_M732}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_M781}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_1169NT}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_H36B}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_JM9130013}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPD	SYSTAVHFPL	TKSSRDAETL	
Consensus	*****	*****	*****	*****	*****	*****
	301					350
msa72034.2{173_090}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_18RS21}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_2603}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_A909}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_CJB110}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_COH1}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_M732}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_M781}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_1169NT}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_H36B}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
msa72034.2{173_JM9130013}	LTYLKKSDDQT	LVSVDLKSL	PIAYTLKSPM	GTEVSDAKN	AIMDNVtFLR	
Consensus	*****	*****	*****	*****	*****	*****
	351					400
msa72034.2{173_090}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_18RS21}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_2603}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_A909}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_CJB110}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_COH1}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_M732}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_M781}	eQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_1169NT}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_H36B}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	
msa72034.2{173_JM9130013}	KQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV	

Table 48: Comparative Sequences relating to SAG1474

msa72034.2{173_JM9130013}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
Consensus	-*****	*****	*****	*****	*****
	401				450
msa72034.2{173_090}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_18RS21}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_2603}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_A909}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_CJB110}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_COH1}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_M732}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_M781}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_1169NT}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_H36B}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
msa72034.2{173_JM9130013}	DPITWgVHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFFIFLSP
Consensus	****-****	*****	***-*****	*****	*****
	451				500
msa72034.2{173_090}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_18RS21}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_2603}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_A909}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_CJB110}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_COH1}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_M732}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_M781}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_1169NT}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_H36B}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_JM9130013}	TTASLAPLNT	DPYVTEdDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
Consensus	*****	*****-***	*****	*****	*****
	501				550
msa72034.2{173_090}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_18RS21}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_2603}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_A909}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_CJB110}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_COH1}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_M732}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_M781}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_1169NT}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_H36B}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKyh
msa72034.2{173_JM9130013}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKyh
Consensus	*-*****	*****	*****	*****	*****-*
	551				600
msa72034.2{173_090}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_18RS21}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_2603}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_A909}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_CJB110}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_COH1}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_M732}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_M781}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_1169NT}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_H36B}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
msa72034.2{173_JM9130013}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SOVTQVSISK
Consensus	*****	*****-*	*****	*****	*****
	601		619		
msa72034.2{173_090}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_18RS21}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_2603}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_A909}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_CJB110}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_COH1}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M732}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M781}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_1169NT}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_H36B}	KWMKSSVKNK	-----			
msa72034.2{173_JM9130013}	KWMKSSVKNK	psvmay---			
Consensus	*****	-----			

Table 49: Comparative Sequences related to SAG1502

SEQ ID NO: 4901

STRAIN 2603

aaacatccgataccttaaatgatcaaaaatccttagcaattggtgaacagat
agaatatgatttttgataaattcgataaattcagaagccttctttttatgcaa
cat tagctagawttcgcggtatggatagagaaatcaaaaatttataga
gaaaatccaaatagtc aaatcctttcaattgggtgtggacttgatacaag
gtttgaaagagtcgataatgggcaaaatagggtggtataaccttgatttgc
cagaggttatggagataagaaaatattttttgaagagcatgaaagagtt
actaatatagcaaaaatcagccctagatgaaacttggcacgggaggtaaa
tccccaaaatgccccctttctaactcgtgtcagaaggtgttttaattgttc
taaaagaagatgacgtagagacttttcttcatatcctgacaaaattcattt
agccaatttatggcacaatttgatttgggtcataaggaattgatataaa
aggaaagcaacatgatcacgtaaaagtataggatcacagaatttcagtttg
gtatcacagatgggtcatgagatttgggttttagaccctaaattaaagcaa
ataaatctgatttaactttacagatgagatgagcaaatttgagttaggcac
acttcgctcttacttccaacaattcgtaaatttaataattggttaggtg
tgtacgaaatataaagcatc

SEQ ID NO: 4902

STRAIN 090

TAATGATCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTG
ATAAATTCGATAAATT CAGAAGCTTCTTTTATGCAACATTAGCTAGAATT
CGCGTTATGGATAGAGAAATCAAAAATTTATAGAGAAAATCCAAATAG
TCAAATCCTTCAATGGTTGTGGACTTGATACAAGGTTTGAAGAGTCCG
ATAATGGACA AAAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAG
ATAAGAAAATTTATTTTGAAGAGCATGAAGAGTTACTAATATAGCAAA
ATCAGCCATAGATGAAACTTGGACACGGGAGGTAATCCCCAAAATGCC
CTTTCTAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGAC
GTAGAGACTTTTCTCATATCCTGACAAAATTCATTTAGCCAATTTATGGC
ACAAATTTGATTTGTGTATAAGGAAATGATTAATAAAGGAAAAGCAACATG
ATACAGTAAAGTATATGGATACAGAATTTCAAGTTTGGTATCACAGATGGT
CATGAGATTGTGGATTAGACCCTAAATTAAGCAAAATAAATCTGATTA
CTTACAGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTTTAC
TTCCAACAATTCGTAATTTAATAAATTTAGTGTGTACGAATATAAA
GCATC

SEQ ID NO: 4903

STRAIN A909

AAACATCCGATACTTAATGA
TCAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTGATAAAAT
TCGATAAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGAATTCGCGTT
ATGGATAGAGAAATCAAAAATTTATAGAGAAAATCCAAATAGTCAAAAT
CCTTTCaAATTGGTTGTGGACTTGATACAAGGTTTGAAGAGTCGATAATG
GACAAAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAGATAAGA
AAATTaTTTTTGAAGAGCATGAAAAGAGTTACTAATATAGCAAAAATCAGC
CCTAGATGAAACTTGGACACGGGAGGTAATCCCCAAAATGCCCTTTTTC
TAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGACGTAGAG
ACTTTTCTCATATCCTGACAAAATTCATTTAGCCAATTTATGGCACAAT
TGATTTGTGTATAAGGAAATGATTAATAAAGGAAAAGCAACATGATACAG
TAAAGTATATGGATACAGAATTTCAAGTTTGGTATCACAGATGGTCATGAG
ATTTGGATTAGACCCTAAATTAAGCAAAATAAATCTGATTAACCTTAC
AGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCA
CAATTCGTAATTTAATAAATTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4904

STRAIN H36B

AAACATCCGATACTTAATGATCAAAAATCCTTAGCA
ATTGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAAATTCAGAAGC
TTCTTTTATGCAaCaATTAGCTAGAATTCGCGTTATGGATAGAGAAAATCA
AAAAATTTATAGAGAAAATCCAAATAGTCATATCCTTTCaAATTGGCTGT
GgACTTGATACAAGGTTTGAAGAGTCGATAATGGCAAAATTAGGTGGTATA
TAACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTAATTTTTGAAG
AGCATGAAAAGAGTTACTAATATAGCAAAAATCAGCCcTAGATGAAAATTTGG
ACACGGGAGGTAATCCCAAAAATGCCCTTTTCTAATCGTGTGAGAAGG
TGTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCC
TGACAAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTCAgAAG
GAAATGATTAATAAAGGAAAAGCAACATGATACAGTAAAGTATATGGATAC
AGAATTCAGTGGGTATCACAGATGGTCATGAAATTTGGATTTAGACC
CTAAATTAAGCAAAATAAATCTGATTAACCTTACAGATGAGATGAGCAAA
TTTTAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAA
TAATTTAGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4905

STRAIN 18RS21

AACATCCGATACTTAATGATCAAAAATCCTTAGCAAT
TGTGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAAATTCAGAAGCTT
CTTTTATGCAaCaATTAGCTAGAATTCGCGTTATGGATAGAGAAAATCAAA
AAATTTATAGAGAAAATCCAAATAGTCaAATCCTTTCAATTTGGTTGTGG
ACTTGATACAAGGTTTGAAGAGTCGATAATGGCAAAATTAGGTGGTATA
ACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTAATTTTTGAAGAG
CATGAAAAGAGTTACTAATATAGCAAAAATCAGCCCTAGATGAAAATTTGGAC
ACGGGAGGTAATCCCAAAAATGCCCTTTTCTAATCGTGTCAgAAGGTTG
TTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCCTG

Table 49: Comparative Sequences related to SAG1502

ACAAATTCATTTAGCCAATTTATGGCACaATTTGATTGTGTGCATAaGGA
AATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG
AATTTCAAGTTGGTATCACAGATGGTCATGAGATTTGGATTAGACCCT
AAATTAAGCAAATAAATCTGATTAACCTTACAGATGAGATGAGCAAAT
TGAGTTAGGCACACTTCGCTCTTACTTCCAACAATTCGTAATTTAATA
ATGTTTAGGTGTGTACGAATATAaGCAATC

SEQ ID NO: 4906

STRAIN M732

AAACATCCGATACTTAATGATCAAAAATCCTTAGCAATTTGTAACA
GATAGAATATGATTTGGATAAATTCGATAATTCAGAAGCTTCTTTTATG
CAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAAAAATTTAT
AGAGAAAATCCAAATAGTCAAATCCTTTCAATTTGGTTGGACTTGATAC
AAGGTTTGAAGAGTTCGATAAAGGACAAATTAGGTGGTATAACCTTGATT
TGCCAGAGTTTATGGAGATAAGAAAATTTATTTTGAAGAGCATGAAAGA
GTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGACACGGGAGGT
AAATCCCAAAAATGCCCTTTTCTAATCGTGTGAGAAGGTGTTTTAATGT
TTCTAAAAGAAAGATGACGTAGAGACTTTTCTTCAATCTGACAAATTC
TTTAGCCAAATTTATGGGCAAAATTTGATTTGTGTGCATAAGGAAATGATTA
TAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAGAATTTCAAT
TTGGTATCACAGATGGTCATGAGATTTGGATTTAGACCCTAAATTAAG
CAAATAAATCTGATTAACCTTACAGATGAGATGAGCAAATTTGAGTTAgG
CACACTTCGCTCTTACTTCCAACAATTCGTAATTTAATAATTTGTTAG
GtGTGTACGAATATAAAGCATC

SEQ ID NO: 4907

STRAIN COH1

AAACATCCGATACTTAATGATCAAAAATCCTTAGCAA
TTGTTGAACAGATAGAATATGATTTGGATAAATTCGATAATTCAGAAGCT
TCITTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA
AAAATTTATTAGAGAAAATCCAAATAGTCAAATCCTTTCAATTTGGTTGTG
GACTTGATACAAGGTTTGAAGAGTTCGATAAAGGACAAATTAGGTGGTAT
AACCTTGATTTCGCCAGAGTTTATGGAGATAAGAAAATTTATTTTGAAGA
GCATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGGA
CACGGGAGGTTAAATCCCAAAAATGCCCTTTTCTAATCGTGTGAGAAGGT
GTTTTAATGTTTTCTAAAAGAAAGATGACGTAGAGACTTTTCTTCAATCT
GACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTGCATAAGG
AAATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA
GAATTTCAAGTTGGTATCACAGATGGTCATGAGATTTGGATTTAGACC
TAAATTAAGCAAATAAATCTGATTAACCTTACAGATGAGATGAGCAAAT
TTGAGTTAGGCACACTTCGCTCTTACTTCCAACAATTCGTAATTTAATA
AATGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4908

STRAIN M781

AAACATCCGATACTTAATGATCA
AAAATCCTTAGCAATTTGTAACAGATAGAATATGATTTGGATAAATTCG
ATAATTCAGAAGCTTCTTTTATGCAACATFAGCTAGAATTCGCGTTATG
GATAGAGAAATCAAAAATTTATTTAGAGAAAATCCAAATAGTCAAATCCT
TTCAATTTGGTTGTGGACTTGATACAAGGTTTGAAGAGTTCGATAAAGGAC
AAATTAGGTGGTATAACCTTGATTTGCCAGAGTTTATGGAGATAAGAAAA
TTATTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAATCAGCCCT
AGATGAAACTTGGACACGGGAGGTTAAATCCCAAAAATGCCCTTTTCTAA
TCGTGTGAGAAGGTGTTTTAATGTTTTCTAAAAGAAAGATGACGTAGAGACT
TTTCTTCAATCTGACAAATTCATTTAGCCAATTTATGGCACAATTTGA
TTTGTGTGCATAAAGGAAATGATTAATAAAGGAAAGCAACATGATACAGTAA
AGTATATGGATACAGAATTTCAAGTTGGTATCACAGATGGTCATGAGATT
TGAGTTAGACCCTTAAATTAAGCAAATAAATCTGATTAACCTTACAGA
TGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTACTTCCAACAA
TTCGTAATTTAATAATTCGTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4909

STRAIN CJB110

AAACATCCGATACTTAATGATCAAAAATCCTTAGCAA
TTGTTGAACAGATAGAATATGATTTTGATAAATTCGATAATTCAGAAGCT
TCITTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA
AAAATTTATTAGAGAAAATCCAAATAGTCAAATCCTTTCAATTTGGTTGTG
GACTTGATACAAGGTTTGAAGAGTTCGATAAAGGACAAATTAGGTGGTAT
AACCTTGATTTGCCAGAGTTTATGGAGATAAGAAAATTTATTTTGAAGA
GCATGAAAGAGTTACTAATATAGCAAAATCAGCCATAGATGAACTTGGGA
CACGGGAGGTTAAATCCCAAAAATGCCCTTTTCTAATCGTGTGAGAAGGT
GTTTTAATGTTTTCTAAAAGAAAGATGACGTAGAGACTTTTCTTCAATCT
GACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTGCATAAGG
AAATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA
GAATTTCAAGTTGGTATCACAGATGGTCATGAGATTTGGATTTAGACC
TAAATTAAGCAAATAAATCTGATTAACCTTACAGATGAGATGAGCAAAT
TTGAGTTAGGCACACTTCGCTCTTACTTCCAACAATTCGTAATTTAATA
AATGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4910

STRAIN 1169NT

AAACATCCGATACTTAATGATCAAAAATCCTTAGCAAT
TTGTTGAACAGATAGAATATGATTTTGATAAATTCGATAATTCAGAAGCTT

Table 49: Comparative Sequences related to SAG1502

CTTTTTATGCAACATTAGCTAGAAATTCGCGTTATGGATAGAGAAATCAAA
AAATTTATTAGAGAAAAATCCAAATAGTCATATCCTTTTCIATGGTTGTGG
ACTTGATACAAGGTTTGAAGAGTCGATAATGGACAAATAGGTGGTATA
ACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGAG
CATGAAAGAGTTACTAATATAGCAAATCAGCCCTAGATGAAACTTGGAC
ACAGGAGGTAATCCCAAAATGCCCTTTTCTGATCGTGTGAGAGGTTG
TTTTAATGTTTCTAAAAGAGATGACGTAGAGACTTTTCTCATATCCCG
ACAAATTCATTTAGCCAATTTATGGCACAATTTGATTGTGTGAGAAAGGA
AATGATTAATAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG
AAATTCAGTTTGGTATCACAGATGGTCATGAAATTTGGATTAGACCCCT
AAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT
TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAATA
ATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4911
STRAIN JM9130013

AGCAATGTGTGAACAGATAGAATATGATT
TTGATAAATTCGATAATTCAGAAGCTTCTTTTTATGCAACATTAGCTAGA
ATTTCGCGTTATGGATAGAGAAATCAAAAATTTATTAGAGAAAAATCCAAA
TAGTCATATCCTTTCAATTTGGCTGTGGACTTGATACAAGGTTTGAAGAG
TCGATAATGGACAAATAGGTGGTATAACCTTGATTTGCCAGAGGTTATG
GAGATAAGAAAAATTTATTTTGAAGAGCATGAAGAGTTACTAATATAGC
AAAATCAGCCCTAGATGAAACTTGGACACGGGAGGTAATCCCAAAATG
CCCTTTTCTAATCGTGTGAGAGGTTGTTTAAATGTTTCTAAAAGAAAGAT
GACGTAGAGACTTTTCTCATATCCTGACAAAATTCATTTAGCCAATTTAT
GGCACAATTTGATTGTGTGAGAGGAAATGATTAATAAAGGAAAGCAAC
ATGATACAGTAAAGTATATGGATACAGAATTTGAGTTTGGTATCACAGAT
GGTCATGAAATTTGGATTAGACCCCTAAATTAAGCAAATAAATCTGAT
TAACTTTACAGATGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCT
TACTTCCAACAATTCGTAATTTAATAATTTGTTAGGTGTGTACGAATAT
AAAGCATC

PRETTY of: /biotmp/msa42193.2{*} January 21, 2003 05:04 ..

msa42193.2{176_090} 1 50
msa42193.2{176_CJB110} AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
msa42193.2{176_18RS21} -AACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
msa42193.2{176_2603} AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
msa42193.2{176_A909} AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
msa42193.2{176_COH1} AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
msa42193.2{176_M732} AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
msa42193.2{176_M781} AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
msa42193.2{176_H36B} AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
msa42193.2{176_JM9130013} msa42193.2{176_1169NT}
msa42193.2{176_1169NT} AAACATCCGA TACTtaatga tcaaaaatcc ttAGCAATG TTGAACAGAT
Consensus *****

msa42193.2{176_090} 51 100
msa42193.2{176_CJB110} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_18RS21} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_2603} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_A909} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_COH1} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_M732} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_M781} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_H36B} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_JM9130013} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
msa42193.2{176_1169NT} AGAATATGAT TTtGATAAAAT TCGATAATTC AGAAGCTTCT TTTTATGCAA
Consensus *****

msa42193.2{176_090} 101 150
msa42193.2{176_CJB110} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_18RS21} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_2603} CATTAGCTAG AwTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_A909} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_COH1} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_M732} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_M781} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_H36B} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_JM9130013} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
msa42193.2{176_1169NT} CATTAGCTAG AaTTCGCGTT ATGGATAGAG AAATCAAAAA ATTTATTAGA
Consensus *****

msa42193.2{176_090} 151 200
msa42193.2{176_CJB110} GAAAATCCAA ATAGTCAaAT CCTTTCaAIT GGtTGTGGAC TTGATACAAG
msa42193.2{176_18RS21} GAAAATCCAA ATAGTCAaAT CCTTTCaAIT GGtTGTGGAC TTGATACAAG
msa42193.2{176_2603} GAAAATCCAA ATAGTCAaAT CCTTTCaAIT GGtTGTGGAC TTGATACAAG
msa42193.2{176_A909} GAAAATCCAA ATAGTCAaAT CCTTTCaAIT GGtTGTGGAC TTGATACAAG
msa42193.2{176_COH1} GAAAATCCAA ATAGTCAaAT CCTTTCaAIT GGtTGTGGAC TTGATACAAG

Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_M732}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_M781}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_H36B}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_JM9130013}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_1169NT}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
Consensus	*****	*****	*****	*****	*****
201					
msa42193.2{176_090}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_CJB110}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_18RS21}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_2603}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_A909}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_COH1}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_M732}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_M781}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_H36B}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_JM9130013}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_1169NT}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
Consensus	*****	*****	*****	*****	*****
251					
msa42193.2{176_090}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_CJB110}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_18RS21}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_2603}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_A909}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_COH1}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_M732}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_M781}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_H36B}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_JM9130013}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_1169NT}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
Consensus	*****	*****	*****	*****	*****
301					
msa42193.2{176_090}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_CJB110}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_18RS21}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_2603}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_A909}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_COH1}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_M732}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_M781}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_H36B}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_JM9130013}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_1169NT}	ACTAATATAG	CAAAATCAGC	CcTAGATGAA	ACTTGGACAC	gGGAGGTAAA
Consensus	*****	*****	*-*****	*****	-*****
351					
msa42193.2{176_090}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_CJB110}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_18RS21}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_2603}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_A909}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_COH1}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_M732}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_M781}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_H36B}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_JM9130013}	TCCCCAAAAT	GCCCCTTTTC	TaATCGTGTc	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_1169NT}	TCCCCAAAAT	GCCCCTTTTC	TgATCGTGTc	AGAAGGTGTT	TTAATGTTTC
Consensus	*****	*****	*-*****	*****	*****
401					
msa42193.2{176_090}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_CJB110}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_18RS21}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_2603}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_A909}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_COH1}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_M732}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_M781}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_H36B}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_JM9130013}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_1169NT}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
Consensus	*****	*****	*****	*****	*****
451					
msa42193.2{176_090}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaCaAGGAAA	TGATTAATAA
msa42193.2{176_CJB110}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaCaAGGAAA	TGATTAATAA
msa42193.2{176_18RS21}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaCaAGGAAA	TGATTAATAA
msa42193.2{176_2603}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaCaAGGAAA	TGATTAATAA
msa42193.2{176_A909}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaCaAGGAAA	TGATTAATAA

Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_COH1}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAT AAGGAAA	TGATTAATAA
msa42193.2{176_M732}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAT AAGGAAA	TGATTAATAA
msa42193.2{176_M781}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAT AAGGAAA	TGATTAATAA
msa42193.2{176_H36B}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAG AAGGAAA	TGATTAATAA
msa42193.2{176_JM9130013}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAG AAGGAAA	TGATTAATAA
msa42193.2{176_1169NT}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAG AAGGAAA	TGATTAATAA
Consensus	*****	*****	*****	***-*****	*****
501					
msa42193.2{176_090}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_CJB110}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_18RS21}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_2603}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_A909}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_COH1}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_M732}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_M781}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_H36B}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_JM9130013}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_1169NT}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
Consensus	*****	*****	*****	*****	*****-*
551					
msa42193.2{176_090}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_CJB110}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_18RS21}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_2603}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_A909}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_COH1}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_M732}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_M781}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_H36B}	GTATCACAGA	TGGTCATGaa	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_JM9130013}	GTATCACAGA	TGGTCATGaa	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
msa42193.2{176_1169NT}	GTATCACAGA	TGGTCATGaa	ATTGTGGATT	TAGACCCTAA	ATTAAGCAA
Consensus	*****	*****	*****	*****	*****
601					
msa42193.2{176_090}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_CJB110}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_18RS21}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_2603}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_A909}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_COH1}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_M732}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_M781}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_H36B}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_JM9130013}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_1169NT}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
Consensus	*****	*****	*****	*****	*****
651					
msa42193.2{176_090}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_CJB110}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_18RS21}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_2603}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_A909}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_COH1}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_M732}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_M781}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_H36B}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_JM9130013}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
msa42193.2{176_1169NT}	ACTTCGCTCT	TTACTTCCAA	CAATTCGTAA	ATTTAATAAT	TGTTTAGGTG
Consensus	*****	*****	*****	*****	*****
701					
msa42193.2{176_090}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_CJB110}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_18RS21}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_2603}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_A909}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_COH1}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_M732}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_M781}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_H36B}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_JM9130013}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_1169NT}	TGTACGAATA	TAAAGCATC			
Consensus	*****	*****			

SEQ ID NO: 4912
 STRAIN 2603 frame: 1
 KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARXRVMREIKKFIENPNNSQILSI
 CGGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWREVPNQY
 APFLIVSEGLMFLKEDDVETFLHLILNFSQFMAQFDLCHKEMINKGKHQDHTVKYMDTE

Table 49: Comparative Sequences related to SAG1502

FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4913
STRAIN 090 frame: 2
NDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIENPNQSILSIGCGLD
TRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSAIDETWTREVNPNQAPFLI
VSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTEFQFGI
TDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4914
STRAIN A909 frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIENPNQSILSI
GCGLDTRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4915
STRAIN H36B frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIENPNSHILSI
GCGLDTRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4916
STRAIN 18RS21 frame: 3
HPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIENPNQSILSIG
CGLDTRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
PFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4917
STRAIN M732 frame: 1
KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIENPNQSILSI
GCGLDTRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4918
STRAIN COH1 frame: 1
KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIENPNQSILSI
GCGLDTRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4919
STRAIN M781 frame: 1
KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIENPNQSILSI
GCGLDTRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4920
STRAIN CJB110 frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIENPNQSILSI
GCGLDTRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSAIDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4921
STRAIN 1169NT frame: 1
KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIENPNSHILSI
GCGLDTRFRERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTQEVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

SEQ ID NO: 4922
STRAIN JM9130013 frame: 2
AIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIENPNSHILSIGCGLDTRFRERV
DNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVNPNQAPFLIVSEGVL
MFLKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTEFQFGITDGHEI
VDLDPKPKQINLINFTDEMSKFELGTLRSLLEPTIRKFNCLGVYEYKA

PRETTY of: /biotmp/msa42204.2{*} January 21, 2003 05:05 ..

Table with 5 columns: sequence identifier, alignment markers, and sequence segments. Rows include msa42204.2{176_H36B}, msa42204.2{176_JM9130013}, msa42204.2{176_090}, msa42204.2{176_18RS21}, msa42204.2{176_2603}, msa42204.2{176_A909}, and msa42204.2{176_CJB110}.

Table 49: Comparative Sequences related to SAG1502

msa42204.2{176_COH1}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_M732}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_M781}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_1169NT}	khpilndqks	LAIVEQIEYD	fdKFDNSEAS	FYATLARiRV	MDREIKKFIR
Consensus	-----	*****	*****	*****	*****
51					
msa42204.2{176_H36B}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_JM9130013}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_090}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_18RS21}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_2603}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_A909}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_CJB110}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_COH1}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M732}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M781}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_1169NT}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
Consensus	*****	*****	*****	*****	*****
101					
msa42204.2{176_H36B}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_JM9130013}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_090}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_18RS21}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_2603}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_A909}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_CJB110}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_COH1}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_M732}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_M781}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
msa42204.2{176_1169NT}	TNIAKSALDE	TWTrEVNPFQ	APFLIVSEGV	LMFLKEDDVE	TFLHILLNSF
Consensus	*****	***-*****	*****	*****	*****
151					
msa42204.2{176_H36B}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_JM9130013}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_090}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_18RS21}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_2603}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_A909}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_CJB110}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_COH1}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_M732}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_M781}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_1169NT}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
Consensus	*****	-*****	*****	***-*****	*****
201					
msa42204.2{176_H36B}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_JM9130013}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_090}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_18RS21}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_2603}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_A909}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_CJB110}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_COH1}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_M732}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_M781}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
msa42204.2{176_1169NT}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVVEYKA	
Consensus	*****	*****	*****	*****	
239					

Table 50: Comparative Sequences relating to SAG 1024

SEQ ID NO. 5001
 STRAIN 2603
 ATGAAAAACAAAACTATTACTGCTTATTGGAGGCTTATTAATAATGATAATGATGACA
 GCATGTAAGGATTCAAAAATCCCGAAAAACCGCACAAGGAAGAGTACCAAGCTGAACAA
 AATTTTAAACCGTTTTTTGAGTTTTAGCACAAAAAGATAAAGATTTGAGCAAAATACAA
 AAATACTTACTATTAGTATCGGATTCAGGTGATGCATTAGATTTAGAATATTTCTATAGT
 ATTCAAGATTTAAAAAAAATAAGGATTTAGGGAAGTTGAAACAAGAAAAAGTCAAATA
 GAAAGCCGGTGGCTATAATGAGTTAGAAAATAAAGAGTCCCAITTTGAATATTTTAAA
 AATAATATAGTTTATCCAAAAGGAAAAACCGAATATTACATTTGATGACTTTATTATCGGA
 GCAATGGATACTAAAGAATTAAGAATTAATAAATAAATAAAGTAAAAAGTTATTATTA
 AAACATCCGGAACCTGAGTTGAAAGATATAACATATGAATTGCCGACACAGTCAAGCTT
 ATTAATAAAA

SEQ ID NO. 5002
 STRAIN 090
 TAAGGATTCAAAAATCCCGAAAAACCGCACAAGG
 GAAGGTACCAAGCTGAACAAAAATTTTAAACTGTTTTTTGAGTTTTTAGC
 ACAAAAATATAAAGATTTGAACAAAAATACAAAAATACCTTACTATTAGTAT
 CGGATTCAGGTGATGCATTAGATTTAGAATATTTCTATAGTATTTCAAGAT
 TTAAAAAAAATAAAGGATTTAGGGAAGTTTGAACAAGAAAAAGTCAAAT
 AGAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAAGAGTCCCAITTTG
 AATATTTTAAAAATAATATAGTTTATCCAAAAGGAAAAACCGAATATTACA
 TTTGATGACTTTTATTATCGGAGCAATGGATACTAAAGAATTAATAAATAA
 AAAAGTAAAAAGTTATTATTAATAACATCCGGAACCTGAGTTGAAAGATA
 TAACATATGAATTGCCGACACAGTCAAGCTTATTAAAAAAA

SEQ ID NO. 5003
 STRAIN 18RS21
 TAAGGATTCAAAAATCCCGAAAAACCGCACAAGGAAG
 AGTACCAAGCTGAACAAAAATTTTAAACCGTTTTTTGAGTTTTTAGCACA
 AAGATAAAGATTTGAGCAAAATACAAAAATACCTTACTATTAGTATCGGA
 TTCAGGTGATGCATTAGATTTAGAATATTTCTATAGTATTTCAAGATTTAA
 AAAAAATAAAGGATTTAGGGAAGTTTGAACAAGAAAAAGTCAAATAGAA
 AAGCCGGTGGCTATAATGAGTTAGAAAATAAAGAGTCCCAITTTGAATA
 TTTTAAAAATAATATAGTTTATCCAAAAGGAAAAACCGAATATTACATTTG
 ATGACTTTATTATCGGAGCAATGGATACTAAAGAATTAAGAATTAATAA
 GAATTAATAAATAAAGTAAAAAGTTATTATTAATAACATCCGGAAC
 TGAGTTGAAAGATAAACATATGAATTGCCGACACAGTCAAGCTTATTAA
 AAAAA

PRETTY of: /biotmp/msa212269.2(*) February 10, 2003 05:07 ..

	1				50
msa212269.2{184_090}	-----	-----	-----	-----	-----
msa212269.2{184_2603}	atgaaaaaac	aaaaactatt	actgcttatt	ggaggcttat	taataatgat
msa212269.2{184_18RS21}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa212269.2{184_090}	-----	-----TAAGG	ATTCAAAAAT	CCCAGAAAAC	CGCACAAAGG
msa212269.2{184_2603}	aatgatgaca	gcatgTAAGG	ATTCAAAAAT	CCCAGAAAAC	CGCACAAAGG
msa212269.2{184_18RS21}	-----	-----TAAGG	ATTCAAAAAT	CCCAGAAAAC	CGCACAAAGG
Consensus	*****	*****	*****	*****	*****
	101				150
msa212269.2{184_090}	AAGAGTACCA	AGCTGAACAA	AATTTTAAAC	tGTTTTTTGA	GTTTTTAGCA
msa212269.2{184_2603}	AAGAGTACCA	AGCTGAACAA	AATTTTAAAC	cGTTTTTTGA	GTTTTTAGCA
msa212269.2{184_18RS21}	AAGAGTACCA	AGCTGAACAA	AATTTTAAAC	cGTTTTTTGA	GTTTTTAGCA
Consensus	*****	*****	*****	-*****	*****
	151				200
msa212269.2{184_090}	CAAAAAtATA	AAGATTTGaa	CAAAATACAA	AAATACTTAC	TATTAGTATC
msa212269.2{184_2603}	CAAAAAGATA	AAGATTTGag	CAAAATACAA	AAATACTTAC	TATTAGTATC
msa212269.2{184_18RS21}	CAAAAAGATA	AAGATTTGag	CAAAATACAA	AAATACTTAC	TATTAGTATC
Consensus	*****-***	*****-	*****	*****	*****
	201				250
msa212269.2{184_090}	GGATTCAGGT	GATGCATTAG	ATTTAGAATA	TTTCTATAGT	ATTCAAGATT
msa212269.2{184_2603}	GGATTCAGGT	GATGCATTAG	ATTTAGAATA	TTTCTATAGT	ATTCAAGATT
msa212269.2{184_18RS21}	GGATTCAGGT	GATGCATTAG	ATTTAGAATA	TTTCTATAGT	ATTCAAGATT
Consensus	*****	*****	*****	*****	*****
	251				300
msa212269.2{184_090}	TAAAAAATAA	TAAGGATTTA	GGGAAGTTTG	AAACAAGAAA	AAGTCAAATA
msa212269.2{184_2603}	TAAAAAATAA	TAAGGATTTA	GGGAAGTTTG	AAACAAGAAA	AAGTCAAATA
msa212269.2{184_18RS21}	TAAAAAATAA	TAAGGATTTA	GGGAAGTTTG	AAACAAGAAA	AAGTCAAATA
Consensus	*****	*****	*****	*****	*****
	301				350
msa212269.2{184_090}	GAAAAGCCGG	GTGGCTATAA	TGAGTTAGAA	AATAAAGAGG	TCCCATTTGA
msa212269.2{184_2603}	GAAAAGCCGG	GTGGCTATAA	TGAGTTAGAA	AATAAAGAGG	TCCCATTTGA
msa212269.2{184_18RS21}	GAAAAGCCGG	GTGGCTATAA	TGAGTTAGAA	AATAAAGAGG	TCCCATTTGA
Consensus	*****	*****	*****	*****	*****

Table 50: Comparative Sequences relating to SAG 1024

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msa212269.2{184_090} 351
msa212269.2{184_2603} ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT 400
msa212269.2{184_18RS21} ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT
Consensus *****

msa212269.2{184_090} 401
msa212269.2{184_2603} TTGATGACTT TATTATCGGA GCAATGGATA CT.....
msa212269.2{184_18RS21} TTGATGACTT TATTATCGGA GCAATGGATA CT..... .aaagaatta
Consensus *****

msa212269.2{184_090} 451
msa212269.2{184_2603} AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTATTAA AACATCCGGA 500
msa212269.2{184_18RS21} AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTATTAA AACATCCGGA
Consensus *****

msa212269.2{184_090} 501
msa212269.2{184_2603} AACTGAGTTG AAAGATATAA CATATGAATT GCCGACACAG TCGAAGCTTA
msa212269.2{184_18RS21} AACTGAGTTG AAAGATATAA CATATGAATT GCCGACACAG TCGAAGCTTA
Consensus *****

msa212269.2{184_090} 551
msa212269.2{184_2603} TTAATAAAA
msa212269.2{184_18RS21} TTAATAAAA
Consensus *****

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SEQ ID NO. 5004
 STRAIN 2603 frame: 1
 MKKQKLLLLIGLLIMIMMTACKDSDKI PENRTKEEYQAEQNFKPFPEFLAQKDKDLSKI Q
 KYLLLVSDSGDALDLEYFYSIQDLKKNKDLGKFETRKSQIEKPGGYNELENKEVPEYFK
 NNIVYPKPKPNITFDDFIIGAMDTKELKELKELKLVKSYLLKHPETELKDITYELPTQSKL
 IKK

SEQ ID NO. 5005
 STRAIN 090 frame: 2
 KDSKIPENRTKEEYQAEQNFKPFPEFLAQKDKDLSKI QKYLKLVSDSGDALDLEYFYSI Q
 DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPEYFKNNIVYPKPKPNITFDDFIIGAM
 DTKELKELKELKELKLVKSYLLKHPETELKDITYELPTQSKLIKK

SEQ ID NO. 5006
 STRAIN 18RS21 frame: 2
 KDSKIPENRTKEEYQAEQNFKPFPEFLAQKDKDLSKI QKYLKLVSDSGDALDLEYFYSI Q
 DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPEYFKNNIVYPKPKPNITFDDFIIGAM
 DTKELKELKELKELKLVKSYLLKHPETELKDITYELPAQSKLIKK

PRETTY of: /biotmp/msa212547.2{*} February 10, 2003 05:11 ..

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msa212547.2{184_18RS21} 1
msa212547.2{184_2603} mkkqklllli ggllimimmt ackDSKIPEN RTKEEYQAEQ NFKpFFEFLA 50
msa212547.2{184_090} ----- --KSKIPEN RTKEEYQAEQ NFKLFFEFLA
Consensus *****

msa212547.2{184_18RS21} 51
msa212547.2{184_2603} QKdKDLsKI Q KYLLLVSDSG DALDLEYFY S IQDLKKNKDL GKFETRKSQI 100
msa212547.2{184_090} QKdKDLsKI Q KYLLLVSDSG DALDLEYFY S IQDLKKNKDL GKFETRKSQI
Consensus **-***-*** *****

msa212547.2{184_18RS21} 101
msa212547.2{184_2603} EKPGGYNELE NKEVPFEYFK NNIVYPKPKP NITFDDFIIG AMDTkelkel 150
msa212547.2{184_090} EKPGGYNELE NKEVPFEYFK NNIVYPKPKP NITFDDFIIG AMDT.....
Consensus *****

msa212547.2{184_18RS21} 151
msa212547.2{184_2603} KELKLVKVS YLLKHPETEL KDITYELPa Q SKLIKK 186
msa212547.2{184_090} KELKLVKVS YLLKHPETEL KDITYELPt Q SKLIKK
Consensus *****

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Table 51: Comparative Sequences relating to SAG0677

SEQ ID NO. 5101

STRAIN 2603

ttgaataataaagggtgtcgggtggcgatgggtgtccaaatattatcaatacta
tatcaaaatggacaacaataaaccttacttaagtcacaaagataagacta
ctgtagagaagttagaagatcgctggaaaaaat tactttcaaagttcag
gatactggcatatgggtttgaaagacgctttatcttcaatctgttaagtatgt
tgggtggggcaataaataatttagacctatcacacctccaggatttaaaa
aagaagataaaaaaagttgaaaaaccaaatttagaccgtccaccagggaatt
gatttaccagcaccaacttcaatgagaagtttgattattcaacccccacc
gggaaactaagccaagcaaacccaaagatagtttcaactctccaggtt
tcccagatttaaacacgcccggatgaaagcaccaaaggatagtaaaaaa
gacgctattgaagataaatcaggagcaat taaatagctaaagctcttca
acttagctttggtgatggccctattttagctagcaaaagtaaatggcaaaa
tattacaagtcgaatctgatggcaaat tagtcatctcctagaatgctttg
tcagctaatcaatttgatgacactagtcttaaaat ttagctaaataataa
tcgcaataaagaaat tactatcacaacagatttat tttgcagatacaaaa
atgtcaaatcacagcgggtgactatttgagcaatactacttttgagcaa
ttagctactgggtgaaacagtagattaccatgcccattgtattttcaagctt
tgctgctattaaagacaaggggtgtaagatttatgtaacgataaaatgca
aagaaactctcgtatagcgtttaaagataaaatctgtaagatttgattt
gaattaccaaatgatgtcagacataatgatagtttatctgctcgtcgttt
gaatgaggttaaaactgttgataaatcttgaaaaatgatgacaagaca
ttaactcagcaaaaacttaccaaat taaaatacaacccgacaaaatcgtcgt
ctagagtttactat taaataacataaactcaagttcagaaatcatgaccac
tttcaagatggaaagatgcccagaattgggtgaaacaaaagatggtttctt
tggatataaaacgatgagcaatgagtaagtttaaaactatctcagactgga
cgaagaggtctgaaatttaaggggacaacttatgcaaaaactggaacagt
tgaattagatattgtttttcaacaactctcaagaccagcttcaattatta
aaaaaatatcccttaccaaaatgggtggttccaaatgaattgaaaaaattt
gactctagttttgggttaactgaaagtcagatagatggatactatattta
taagatgcaattaaccttaatttaaat taaccagtggtgcaagctctta
aagttggtttataaagggcaagaagatccatagctcagaaagaagat
atgactaaaaaaggtgaaacagctcagctcattcaactcaagccaatgaaaa
tacagcaaaaagtaacctttgctaatatgactgggtcacaattatagtaagg
ttactgtgaaatggaaaaagaagttggttaaaggtagtgagttacctttaact
aaaggatggacaacatttgtat tacaataaacagaaaaat tcaataaagt
taaaaagttgattatggagacgggtagtgtaagtaagaaagt tcaacaac
ttcctttaagtcctagatttatctaaaaat aagcatatgagggatagctta
cttactatgcaaaaagattcagcgtat tcaagaaacaagtgacagctcagct
ccttcgaattaatctcactgacagatactaaacttaattttaatgctgta
aaggagcagtgctcttactgaaaaatgatgatgagacagtttgagctt
gctggaccacaagatgacctgttagtgaaacataaataccatcagttat
tctcttaactcctgctctattggaaactgctagtgaggcaactc taaatg
tgaagaaaatcacagcatctggtattatcgggtcacatcaaggatgggtgat
aaaagcaagcatggtgaaagtcaaaatgggtgaaatggagacatgct
aggaaccctgttatattcaaggtaaagacttgactaatcgacaacaaac
cattaatgagtggaagcgtagagtaactttatgcccgttaacaatagagttc
cgggctaaattaccacttagtcgttttaacacttggattagggttgaagtt
ggttaacagaagcaggagagaagcaagatattggtcgtcgcagttctttg
accaatcagttccagagcttaaacacagcagttgctaaacgtgatttgatg
tctgatactgctcttatccacatcgttggcaaaagatgactctctaaaact
aaaaattatcaagatgat tcaattacttgaatctggttgataaaacccggtc
ttttagttttagaatgggtgtagaaatcactaaagatagacagtaacca
ctagaatttgagatataatatttaagttatctgctgttgacttatcaaaa
ttatcgtcgttaatgagacccttcatatctatagaacccggttttgatgta
aagcaagccaaaatgacagctgacaaaggagctaaagtaactgtggatattg
ttgatgaagcacttagttgttccagaatggcaggagcttatacattaac
aatcgacgaagctccaaacacaaaatgaaatcaggaatggttaacaaacgcta
aagttatcgattcattatgtaaatgggtgggttgataaagttgatgttccg
at taaagtagttgacttagaagctattcgtaaagctgaagaagcagtaaa
agctgaagaagcagctaaagctgaagaagcagtaaaagctgaagagggac
ataaaaacccaagaagcacctatagttgaagaaggtcacaaggttaataaac
gttcatcaaaactgatactacagtttaaagcgtctgatttaccaaagactaa
gacagtttccgcagttcatatggctagaacagacaataaacagataaactt
cacatcagacacatgttgaaaaaacaaat taaaaat acattgcatccact
gggtgacagcaaacgtgggtattatattactcactggaaaggctatcgttatgct
gagtgatttatttagtttagctaaaaagtttaaaagcaaatat

SEQ ID NO. 5102

STRAIN A909

TTGAATAATAAAGGTGTCGGTGGCGAT

GGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTA
CTTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGA
AAAAAATTACTTTCAAAGTTTCAAGATACCTGGCATTTGGTTTGAAGACGTT
TATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAAATTTAGACCT
TATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAA
AATTAGACCGTCCACCAGGAATTTGATTTACCAACCAACTTCAATGAGA
AGTTTGTGATTTATCAACCCACCGGGAATTAAGCCAAGCAACCCAAAGA
TAGTTTATCAACTCTCCAGGTTTCCAGATTTAAACACGCCGCCGATG
AAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCA
ATTAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCTATTTT
AGCTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAA
TAGTCATTCCTAGAAATGCTTTGTGAGCTAAATCAATTTGATGACACTAGT

Table 51: Comparative Sequences relating to SAG0677

CTTAAAATTTATCGTAATAATAATCGCAATAAAGAAATTAAGTATCACAAAC
 AGATTATTTTGCAGATACAAAAATATGTCATATCACAGCGGTTGACTATT
 TGAGCAATCTACTTTTGAGCAATTAGTACTGGTGAAACAGTAGATTAC
 CATGCCATTGTATTTCAAGCTTTGCTGCTATTAAGACAAGGGTGGTAA
 GATTTATGTTAACGATAAATGCAAGAAACTTCTCGTATAGCGCTTAAAG
 ATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATT
 GATAGTTTATCTGTTCTGTTGAAATGAGGTTAAACTGTTGATAATAT
 CTTGAAAAATGATGAACAAGACATTAACTCTCAGCAAACTTACCAATTA
 AATACAAACCCGACAAATCGTCTAGAGTTTACTATTAAATAACATTAAC
 TCAAGTTGAGAAATCATGACCACTTCAAAGATGGAAAGATGCCAGAATT
 GGTTGaaCAAAAAGATGTTCTTTGGATATAaCGATATGGACATGAGTA
 AGTTTAAAACCTATTGACTTTGGACGAAAGGATTCTGAATTTAAGGACAA
 CTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACATC
 TCAAGACCCAGCTTCAATTTAAAAAATATACCTTATCCAAAATGGTG
 TTCCAAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGT
 CAGATAGATGGATATATATTTATAAAGATGCAATTAACCTTAAATTTAA
 ATTAACCAGTGGTGCAGTCTTAAAGTGTGTTATAAAGGGCAAGAAGATC
 CATATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGT
 CATTTCACTCAAGCCAATGAAAATACAGCAAAAGTAACTTTGCTAATAT
 TGACTGGTCACTTATAGTAAGTTACTGTGAATGGAAAAGAAGTTGGTA
 AAGGTAGTGAGTTACTTTAACTAAAGGATGGACAACATTTGATTACAT
 AAAACAGAAAATTCATTAATGTTAAAGTTTGAATTTGGAGACGGGTAG
 TGTAAAGTAAGAAAGTTCAACAACCTTCTTTAAGTCTAGATTATCTAAAA
 ATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTAT
 TACGAAaCAAGTGAAGTCTAGTCTCGAATTAATCTCACTGACAGATAC
 TAAACTTAATTTAATGCTGTTAAAGGAGCGAGTCTTACTGAAAATA
 TGATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGT
 GAACATAAATACCCATCAGTATTTCTTAACTCCTGCTTATTTGGAAAC
 TGCTAGTGAGGCACTCTAAATGGTAAGGAATCACAGCATCTGGTATTA
 TCCGCTCACATCAAGGATGGTGAATAAAGCAAGCATGTTGAAGTCAAAATG
 GTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTTCAAGGTAA
 AGACTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTT
 ATGCCGGTAAACAATATGAGTTCCGGCTAAATTAACCACTTAGTCTGTTTT
 AACACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAAGCAAG
 TATGTTCTGTCGCTGCTTCTTTGACCAATCAGTCCAGAGCTTAAACACAG
 CAGTTGCTAAACGATTTGACTTCTGATCTGCTCTTATCCACATCGTT
 GCCAAGATGACTCTCTAAAACAAAATTAATCAAGATGATTCAATTA
 TGAATCTGTTGATAAAACCGGTCTTTATAGTTTTTAGAAATGGTGTAGAAA
 TCACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATATTAAG
 TTAATCTGCTGTTGACTTATCAAAATTAATCGTCTGTAATGAGACCCCTTATAT
 CTATAGAAAACCGTTTGTATGTTAAAGCAAGCAAAATGACAGCTGACAAAG
 GAGCTAAAGTAACTGTTGATATGTTGATGAAGCACTTAGTTGTTCCAGAA
 ATGGCAGGAGCTTATACATTACAATCGACGAAGATCCAACACAARTGA
 ATCAGGAATGTTAAACAAACGCTAAAGATCGATTCAATATGTAATGGTGT
 GTGTTGATAAAGTTGATGTTCCGATTAAGTAGTTGACTTGAAGACTTATT
 CGTAAAGCTGAAGAAGCATAAAGCTGACGAAGCAGCTAAAGCTGAAGA
 AGCAGCTAAAGCTGAAGAAGCAGCTAAAGCTGAAGAAGCAGTAAAGCTG
 AAGAGGGACATaAAAACCAAGAAGCACCTATAGTTGAAGAAGGCTACAAG
 GTTAATAACGTTTCACTAACTGATCTACAGTTAAAGCGTCTGATTTACC
 AAAGACTAAGACAGTTTCCGAGTTTCAATGGCTAGAACAGACAAATAAAC
 AGATAACTTCAATCAGACACATGTTGAAAAACAATTTAAAATA

SEQ ID NO. 5103

STRAIN H3B8

TGGTGTCCAAATTTATCAACTATATCAAAATGGACAACAATAAACCTT
 ACITTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGaaGATCGCTGG
 AAAAAAATTACTTTCAAAGTTCCAGGATACTGGCATTGGTTTGAAGACGT
 TTAATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACC
 TTAATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCA
 AAATTAGACCCGTTCCACCAGGAATGATTTACCAGCACCAACTTCAATGAG
 AAGTTTGTATTATTCAACCCACCGGAACTAAGCCAAGCAAACCCAAAG
 ATAGTTTATCAACTCTCCAGGTTTCCAGATTTAAACACCGCCGGAT
 GAAGCATAAAGGATAGTAAAAAAGACGCTATGAAAGATAAATCAGGAGC
 AATTAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCCTATT
 TAGCTAGCAAAGTAAATGGCAAAATATTAAGTGAATCTGATGGCAAA
 TTAGTCATTCTTGAATGCTTTGTCAGCTAATCAATTTGATGACACTAG
 TCTTAAAATTTATCGTAATAATAATCGCAATAAAGAAATTaCTATCACAA
 CAGATTATTTTGCAGATACAAAAATATGTCATATCACAGCGGTTGACTAT
 TTGAGCAATACTACTTTTGGACATTAGCTACTGGTGAaaCAGTAGATTA
 CCATGCCATTGTAeTTTCAAGCTTTGCTGCTATTAAGAACAAGGGTGGTA
 AGATTTATGTCAACGATAAATGCAAGAAACTTCTCGTATAGCGCTTAAA
 GATAAATCTGTTAAGATTTGATTTGAATTAACCAATGATGTCAGACATAT
 TGATAGTTTATCTGTTCTGTTGAAATGAGGTTAAACTGTTGATAATA
 TCTTGAAAAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTA
 AAATACAACCCGACAAATCGTCTAGAGTTTACTATTAAATAACATTA
 CTCAAGTTGAGAAATCATGACCACTTCAAAGATGGAAAGATGCCAGAAAT
 TGGTTGAACAAAAGATGTTCTTTGGATATAAACGATATGGACATGAGT
 AAGTTTAAAACCTATTGACTTTGGACGAAAGGATTCTGAATTTAAGGGACA
 ACTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACAT
 CTCAAGACCCAGCTTCAATTTAAAAAATATACCTTATCCAAAATGGT
 GTTCCAAATGAATGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAG
 TCAGATAGATGGATATATATTTATAAAGATGCAATTAACCTTAAATTTA
 AATTAACCAGTGGTGCAGTCTTAAAGTTGTTATAAAGGGCAAGAAGAT

Table 51: Comparative Sequences relating to SAG0677

CCATATAGtCATCAGAAAGAAGATATGACTAAAAAGGTGAACAGCTCAG
TCATTCAACTCAAGCCAATGAAAAACAGCAAAAGTAACCTTTGCTAATA
TTGACTGGTCCATTTATAGTAAGGTACTGTGAATGGAAAAGAAGTTGGT
AAAGGTAGTGAAGTACCTTTAACTAAAGGATGGACAACATTTGTATTACA
TAAAAACAGAAAATTCATTAATGTTAAAAAGTTTGATTTATGGAGACGGGTA
GTGTAAGTAAGAAGTTCAACAACCTCCCTTAAAGTCTTAGATTATCTAAA
AATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTACAGCGTA
TTACGAAACAAGTGACAGTCTAGTCCCTCGAATTAATCTCACTGCAGATA
CTAAACTTAATTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAT
ATGATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAG
TGAAACATAAATACCCATCAGTATTTCTCTAACTCCTGCCTTATTGGAAA
CTGCTAGTGAAGCaACTCTAATGGTAAGGAAATCACAGCATCTGGTATT
ATCGGTCACATCAAGGATGGtGATAAAAGCAAGCATGTTGAAGTCAAAT
GGTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTA
AAGACTTGACTAATCGAACAAAACCTTAAAGTGGAGCTAGAGTACTT
TATGCCGGTAAACAATATGAGTTCGGGGCTAAATTACCACCTTAGTCGTTT
TAACaCTTGGATTAGGGTTGAAGTGGTAACAGAACAGGAGAGAAAGCAA
GTATTGTTTCGTCGCATGTTCTTTGACCAATCAGTTCAGAGCTTAAACA
GCAGTTGCTAAACCTGATTTGACTTCTGATACTGCTCTTATCCACATCGT
TGCCAAAGATGACTCTCTAAAACATAAAATATATCAAGATGATTCAATAC
TTGAATCTGTTGATAAAACCGGCTTTTATAGTTTGAAGAAATGGTGTAGAA
ATCACTAAAGATATGACAGTACCCTAGAATTTGGAGATAATATTACTAA
GTATCTGCTGTTGACTTATCAAATTATCGTCTGTAATGAGACCCCTCATA
TCTATAGAAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAA
GGAGCTAAAGTAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGA
AATGGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATG
AATCAGGAATGTTAAACAACCGCTAAAGTATCGATTCAATTTATGTAATGGT
GGTGTGATAAAGtGATGTTCCGATTAAGTAGTTGACTTGAAGCTAT
TCGTTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAG
AAGCACGTAAGCTGACGAAGCACATAAAGCTGAAGAAGTACGTAAGCT
GAAGAAGCACATAAAGCTGAAGAAGCAGTAAAGCTGAAGAGGGACATAA
AACCCAAGAAGCACCTATAGTTGAAGAAGCTACAAGTTAATAACGTTT
ATCAAACTGATACTACAGTTAAAGCGTCTGATTTACCAAGACTAAGACA
GTTTCCGAGTTCATATGGCTAGAACAGACAATAAACAGATAAATTCACA
TCAGACACATG

SEQ ID NO. 5104
STRAIN 18RS21

TTGAATAATAAAGGTGTCGGTGGCGATGGTGTCCAA
ATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAGTCC
CAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAATTA
CTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAGACGTTTATCTTCAA
TCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACACC
TCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAATTAGACC
GTCCACCAGGAATTGATTTACCAGCACCAACTCAATGAGAAGTTTGTAT
TATTCACCCACCAGGAACTAAGCCAAAGCAAAACCAAAGATAGTTTATC
AACTCCTCCAGGTTTCCCAGATTTAAACACCGCCGCGGgTGAAGCACCAA
AGGATAGTAAAAAAGACCGCTATTGAAGATAAATCAGGAGCAATTAATAT
GCTAAGTCTCTCAACTTAGCTTTGTTGATGACCCATTTTAGCTAGCAA
AGTAAATGGCAAATATTAACAAGTGAATCTGATGGCAAATTAGTCATTC
CTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCTTAAATTT
TATCGTAATAATAATCGCAATAAAGAAATTAATCTCACAAACAGATTTATTT
TGACAGTACAAAATATGTCATATCACAGCGTTGACTATTTGAGCAATA
CTACTTTGAGCAATTAGCTACTGGTGAACAGTAGATTACCATGCCATT
GTATTTCAAGCTTTGCTGCTATTAAGACAAAGGTTGGTAAGATTTATGT
TAACGATAAATTGCAAGAAaACTTCTGTTATAGCGCTTAAAGTAAATCTG
TTAAGATGGTATTGAATTAACCAATGATGTGACACATATGATAGTTTA
TCTGTTCTGTCGTTTGAATGAGGTTAAACTGTTGATAATATCTTGAAAAA
TGATGAACAAGCATTAAATCTCAGCAAaACTTACCAATTAATAACAAACC
CGCAAATCGTCTGCTAGAGTTTACTATTAATAACATTAATCAAGTTCA
GAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAATTGGTTGAACA
AAAAGATGTTCTTTGGATATaAACGATATGGACATGAGTAAGTTTAAAA
CTATTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAACCTTATTGCA
AAAACCTGGAACAGTTGAATTAGATATGTTTTCAACAATCTCAAGACCC
AGCTTCAATTTATTAATAAATAATACCTTATCCAAATGGTGTTCCAAATG
AATTTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAAGATAGAT
GGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAAATTAACCAG
TGGTGCAAGTCTTAAAGTGTTTTATAAAGGGCAAGAAGATCCATATAGTC
ATCAGAAAGAAGATGACTAAAAAAGGTGAACAGCTCAGTCATTCAACT
CAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTGGTC
ACATTATAGTAAGGTTACTGTGAATGGAAGAAGTTGTTAAAGGTAGTG
AGTTACCTTTAACTAAAGGATGGACAACATTTGTAATTACATAAAACAGAA
AATTCATTAATGTTAAAGTTTGGATTATGGAGACGGGTAGTGAAGTAA
GAAAGTTCAACAACCTCCTTAAAGTCTTAGATTATCTAAAAAATAGCATA
TGAGGGATATGCTACTTACTATGCAAAAAGATTACGCGTATTACGAAACA
AGTGACAGTCTAGTCTTTCGAATTAATCTCACTGCAGATACTAACTTAA
TTTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAATATGATGATGA
GACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGAACATAAA
TACCCATCAGTATTTCTTAACTCCTGCCTTATTGGAACTGCTAGTGA
GGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTCACA
TCAAGGATGGTATATAAAGCAAGCATGTTGAAGTCAAATGGTGAATGAA
AATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTAAGACTTGAC
TAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTTATGCCGGTA

Table 51: Comparative Sequences relating to SAG0677

AACAATATGAGTTCCGGGCTAAATTACCACTAGTCGTTTAACTTGG
 ATTAGGGTTGAAGTGGTAAACAGAAGCAGGAGAGAAAGCAAGTATTGTTCCG
 TCGCATGTTCTTTGACCAATCAGTTCAGAGCTTAACACAGCAGTTGCTA
 AACGTGATTTGACTTCGATAGTCTCTTATCCACATCGTTGCCAAAGAT
 GACTCTCTAAAACATAAATTATATCAAGATGATTCATTAACCTGAATCTGT
 TGATAAAACCGGCTTTTATAGTTTGAAGATGGTGTAGAAATCACTAAAG
 ATATGACAGTACCCTAAGAATTGGAGATAATATTAAGTTATCTGCT
 GTTGACTTATCAAATTATCGTCTAATGAGACCTTCATATCTATAGAAA
 CCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTAAAG
 TAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCAGGA
 GCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGGAAT
 GTTAACAACCGCTAAAGTATCGATTCAATATGTAAGTGGTGGTGTGATA
 AAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCGTAAGCT
 GAAGAAGCACGTAAGCTGAAGAAGCACGTAAGCTGAAGAGGGACATAA
 AACCCAAAGACCCCTATAGTTGAAGAAGGCTACAAGTTAATAACGTTT
 ATCAAATGATACTACAGTTAAGCGTCTGATTTACCAAAGACTAAGACA
 GTTTCCGAGTTCATATGGCTAGAACAGACAATAACAGATAACTTCACA
 TCAGACACATGTTGAA

SEQ ID NO. 5105

STRAIN M732

TTGAATAATAAAGGTGTCCGGTGGCGATGGTGTCC
 AAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAAGT
 CCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAAT
 TACTTCAAAGTTCAGGATACTGGCATTTGGTTGAAAGACGTTTATCTTC
 AATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACA
 CCTCCAGGATTTAAAAAGAAAGATAAAAAAGTTGAAAAACCAAAATTAGA
 CCGTCCaCAGGAATTGATTTACCAGCACCAACTCAATGAGAAGTTTTG
 ATTATTCAACCCACCGGAACTAAAGCCAAAGCAACCCAAAGATAGTTTA
 TCAAATCCTCCAGGTTTCCAGATTAAACACGCGCCGGATGAAGCCAC
 CAAGGATAGTAAAAAGACCGCTATTGAAGATAAATCAGGAGCAATTA
 TAGCTAAGTCTCTCAACTTAGCTTTGTTGATGACCCTATTTTAGCTAG
 CAAAGTAAATGGCAAAATATTAACAAGTCGAATCTGATGGCAAAATGATCA
 TTCTTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCTTAAA
 ATTTATCGTAATAATAATCGCAATAAAGAATTAATCAACAACAGATTA
 TTTTGCAGATACAAAATATGTCATATCACAGCGTTGACTATTTGAGCA
 ATACTACTTTTGAGCAATAGCTACTGGTGAACAGTAGATTACCATGCC
 ATTGATTTTTCAAGCTTTGCTGCTATTAAGACAAGGGTGGTAAGATTTA
 TGTTAAGATAAATGCAAGAACTTCTCGTATAGCGCTTAAAGATAAAT
 CTGTTAAGATTTGGTATTGAATTACCAATGATGTCAGACATATTGATAGT
 TTATCTGTTCTGCTGTTGAATGAGGTTAAAAGTGTGATAATATCTTGAA
 AATGATGAAACAAGCATTAATCTCAGCAAACTTACCAATTAATAATACA
 ACCGCAAAATCGTCTGCTAGAGTTTACTATTAATAACATTAATCAAGT
 TCAGAAATCATGACCACTTCAAAAGATGGAAGATGCCAGAAATGGTTGA
 ACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAGTTA
 AAACCTATTGCACTTTGGACGAAAGGATTTCTGAATTAAGGGACAACCTATT
 GCAAAAAGTGGAAACAGTTGAATTAGATATGTTTTCAAACTTCAAGA
 CCCAGCTTCAATTTAATAAAAAATATACCTTATCCAAATGGTGTTCCAA
 ATGAATGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATA
 GATGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAAATTAAC
 CAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATA
 GTCATCAGAAAGAAGATATGACTAAAAAAGTGAACAGCTCAGTCAATCA
 ACTCAAGCCAAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTG
 GTCACATTTATAGTAAAGTTACTGTGAATGGAAGAAGTTGGTAAAGGTA
 GTGAGTTACCTTTAACTAAAGGATGGACACATTTGTTATACATAAAACA
 GAAAATTCATTAATGTTAAAAGTTTGAATTTGGAGACCGGTAGTGTAG
 TAAGAAAGTTCAAACACTTCTTTAAGTCTTAGATTATCAAAAATAAGC
 ATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTACGAA
 ACAAGTGAAGTCTAGTCTTCAAAATTAATCTCACTGCAGATACTAACT
 TAATTTAATGCTGTTAAAGGAGCGAGTCTCTTACTGAAAATATGATGA
 TGAGACAGTTTGCAGTTGCTGGACCACAGATGATCCTGTTaGTGAACAT
 AAATACCCATCAGTATTCTCTTAACTCCTGCTTATTGGAAaCTGCTAG
 TGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTC
 ACATCAAGGATGGTATAAAGCAAGCATGTTGAAGTCAAAATGGTGAAT
 GAAAATGGAGACATGCTAGAACCCCTGTTATTATTCAAGGTAAGACTT
 GACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTATGCCG
 GTAACAATATGAGTTCCGGGCTAAAATACCACCTAGTCTGTTTTAACACT
 TGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGT
 TCGTGCATGTTCTTTGACCAATCAGTTCAGAGCTTAAACACAGCAGTTG
 CTAACCGTGAATTTGACTTCGATAGTCTCTTATCCACATCGTTGCCAAA
 GATGACTCTCTAAAACATAAATATATCAAGATGATTCATTACTTGAATC
 TGTTGATAAAAACCGGCTTTATAGTTTGAAGATGGTGTAGAAATCACTA
 AAGATATGACAGTACCCTAGAAATTTGGAGATAATATTAAGTTATCT
 GCTGTTGACTTATCAAATTTATCGTCTAATGAGACCTTCATATCTATAG
 AAACCGTTTTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTA
 AAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCA
 GGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGG
 AATGTTAACAAACGCTAAAGTATCGATTCAATATGTAAGTGGTGGTGTG
 ATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCGTAAA
 GCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAGCTGAAGAAGCACG
 TAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAGCTGAAGAAG
 CACATAAAGTCAAGAGCACGTAAGCTGAAGAGGGACATAAACC
 GAAGCACCTATAGTTGAAGAAGGCTACAAGTTAATAACGTTTATCAAC

Table 51: Comparative Sequences relating to SAG0677

TGATACTACAGTTAAAGCGTCTGATTTACCAAAGACTAAGACAGTTTCCG
CAGTTCATATGGCTAGAACAGACAAATAAACAGATAACTTCACATCAGACA
CATGTTGAAAA

SEQ ID NO. 5106

STRAIN COH1

TTGAATAATAAAGGTGTCGGTGGCGATGGT
GTCCAAATTTATCAATACTATATCAAATGGACAACAATAAACCTTACTT
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAGACGTTTAT
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT
CACACCTCCAGGATTTAAAAAGAAAGATAAAAAAGTTGAAAAACCAAAAT
TAGACCGTCCACCAGGAATGATTTACCAGCACCAACTTCAATGAGAAGT
TTTGATTTTCAACCCACCGGAACTAAGCCAAGCAACCCAAAGATAG
TTTATCAACTCCTCCAGGTTCCAGATTAAACACGCCGCCGGATGAAG
CCaCCAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT
TAAATATGCTAAGTCTTCAACTTAGCTTTGGTGTAGACCTATTTTAG
CTAGCAAAGTAAATGGCAAATATTAACAAGTCCGAATCTGATGGCAATTA
GTCAATCCTAGAAATGCTTTGTGAGCTAATCAATTTGATGACTAGTCT
TAAAAATTTATCGTAATAAATCGCAATAAAGAAATTAATCACAACAG
ATTATTTTGCAGATACAAATATGTCAATATCACAGCGTTGACTATTGG
AGCAATACTACTTTTGGAGCAATTAGCTACTGGTGAACAGTAGATTACCA
TGCCAITTGTATTTTCAAGCTTTGCTGCTATTTAAAGACAAGGGTGGTAAGA
TTTATGTTAAGCATAAATGCAAGAACTTCTCGTATAGCGCTTAAAGAT
AAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATTGA
TAGTTTATCTGTTTCGTCGTTTGAATGAGGTTAAACTGTTGATAATATCT
TGAAAAATGATGAAACAAGACTTAATCTCAGCAAACTTACCAATAAAA
TACAACCCGACAAAATCGTCTGCTAGAGTTTACTATTAATAAATTAATC
AAGTTTCAAGAAATCATGACCACTTCAAAGATGAAAGATGCCAGAAATGG
TTGAACAAAAAGATGTTCTTTGGATATAAACGATATGGACATGAGTAAG
TTTAAAACTATTGACTTGGACGAAAGGATCTGAATTTAAGGGCACAACT
TATTGCAAAAACCTGGAACTGAAATAGATATGTTTTCAAAACATCTC
AAGACCCAGCTTCAATTTAAAAAATAATACCTTATCCAAATGGTGT
CCAAATGAATGAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCA
GATAGATGATACTATATTTATAAAGATGCAATTAACCTTAAATTTAAAT
TAACCAAGTGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA
TATAGTCAATCAGAAAGAGATATGACTAAAAAAGGTGAACAGCTCAGTCA
TTCAACTCAAGCCAATGAAAAATACAGCAAAAGTAACCTTTGCTAATATTG
ACTGGTCACTTATAGTAAGGTTACTGTGAATGAAAGAGGTTGGTAAA
GGTAGTGAGTTACCTTTAACTAAAGGATGGCAACATTTGTATTACATAA
ACAGAAAAATTCATTAATGTTAAAGTTTGAATATGGAGACGGGTAGTG
TAAGTAAGAAAGTTCAACAACCTCCTTTAAGTCTTAGTATCTAAAAAT
AAGCATATGAGGGATATGCTACTTACTTATGCAAAAAGATTGAGCTATTA
CGAAACAAGTGACAGTCTAGTCTCGAATTAATCTCACTGCAGATACTA
AACTTAAATTTAATGCTGTTAAAGGAGCGAGTCTTACTGAAAAATATG
ATGATGAGACAGTTTGCAGTTGCTGGACCAAGATGATCCTGTTAGTGA
ACATAAATACCCATCAGTATTTCTTAACTCTGCCTTATTGGAAACTG
CTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATC
GGTCACTCAAGGATGGTATGATAAAGCAAGCATGTTGAAGTCAAATGGT
GAATGAAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG
ACTTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTTAT
GCCGGTAAACAATATGAGTTCCGGGCTAAATTAACCACTTAGTCTGTTTAA
CACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAGCAAGTA
TTGTTCTGTCGATGTTCTTTGACCAATCAGTTCCAGACTTAAACAGCA
GTTGCTAAACGCTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGC
CAAAGATGACTCTCTAAAaCTAAAAATATATCAAGATGATTCATTTAGT
AATCTGTTGATAAAACCGGCTTTATAGTTTGAAGAAATGGTGTAGAAATC
ACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAAATATTATTAAAGTT
ATCTGCTGTTGACTTATCAAATTTATCGTCTGTAATGAGACCTTCATATCT
ATAGAAACCGTTTGGATGTTAAAGCAAGCCAAATGACAGCTGACAAAAGGA
GCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT
GGCAGGAGCTTATACATTAACCAATCGACGAAGCTPCCAAACACAAATGAAT
CAGGAATGTTAAACAACGCTAAAGTATCGAATTCATATGTAATGGTGGT
GTTGATAAAGTTGATGTTCCGATTAAGTAGTTGACTTAGAAGCTATTCCG
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAGAAG
CAGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAGCTGAA
GAAGCACATAAAGTCAAGAAGCACGTAAGCTGAAGAGGGACATAAAAC
CCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAAGCTTCATC
AACTGATACTACAGTTAAAGCTCTGATTTACCAAGACTAAGACAGTT
TCCGAGTTTATATGGCTAGAACAGACAAATAAACAGATAAATTCACATCA
GACACATGT

SEQ ID NO. 5107

STRAIN M781

TTGAATAATAAAGGTGTCGGTGGCGATGGT
GTCCAAATTTATCAATACTATATCAAATGGACAACAATAAACCTTACTT
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAGACGTTTAT
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT
CACACCTCCAGGATTTAAAAAGAAAGATAAAAAAGTTGAAAAACCAAAAT
TAGACCGTCCACCAGGAATGATTTACCAGCACCAACTTCAATGAGAAGT
TTTGATTTTCAACCCACCGGAACTAAGCCAAGCAACCCAAAGATAG
TTTATCAACTCCTCCAGGTTTCCAGATTAAACACGCCGCCGGATGAAG

Table 51: Comparative Sequences relating to SAG0677

CCaCCAAAGGATAGTAAAAAGACGCTATGAAGATAAATCAGGAGCAAT
TAAATATGCTAAGTCTCTCAACTAGCTTTGGTGGATGACCCATATTTAG
CTAGCAAAGTAAATGGCAAAATATTAACAAGTCCAATCTGATGGCAAATTA
GTCATTCTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCT
TAAaATTTATCGTAATAATAATCGCAATAAAGAAATPaCTATCAACAACAG
ATTTATTTGAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTG
AGCAATACTACTTTTGAGCAATTAGCTACTGGTGAACAGTAGATTACCA
TGCCAITGTATTTTCAAGCTTTGCTGCTATTAAGACAAGGGTGGTAAGA
TTTATGTTAACGATAAATGCAAGAACTTCTCGTATAGCGCTTAAAGAT
AAATCTGTTAAGATTTGGTATTGAATTAACAAATGATGTCAGACATATTGA
TAGTTTATCTGTTGCTGCTTTGAATGAGGTTAAAACGTTGATAATATCT
TGAAAAATGATGAACAAGACATTAATCTCAGCAAAAACFFACCAATAAAA
TACAACCCGACAAAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTC
AAGTTCAGAAATCATGACCCTTTCAAAGATGGAAGATGCCAGAAATGG
TTGAACA AAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAG
TTTAAAACTATTGCACTTGGACGAAAGGATTTCTGAATTAAGGGCAACT
TATTGCAAAAACGAAACAGTTGAATTAGATATGTTTTTCAAACAATCTC
AAGACCCAGCTTCAATTTAAAAAATAATACCTTATCAAATGGTGT
CCAAATGAATTAAGAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCA
GATAGATGGATACTATAATTATAAAGATGCAATTAACCTTAAATTTAAAT
TAACCAAGTGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA
TATAGTCACTCAGAAAGAAGATATGACTTAAAAAGGTGAACAGCTCAGTCA
TTCAACTCAAGCCAATGAAAATACAGCAAAAGTAACTTTGCTAATATTG
ACTGGTCACTTATAGTAAGGTTACTGTGTAATGAAAAGAAGTTGGTAAA
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGATTTACATAA
AACAGAAAATTCATTAATGTTAAAGTTTGAATATGAGAGCGGGTAGTG
TAAGTAAGAAAAGTTCAACAACTTCTTTAAGTCTTAGATTATCTAAAAAT
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGACGGTATTA
CGAAACAAGTACAGTCTAGTCTTGAATTAATCTCACTGACAGATACTA
AACTTAAATTTTAAATGCTGTTAAAGGAGCGAGTCTTACTGAAAATATG
ATGATGAGACAGTTGCAAGTCTGGACCAAGATGATCTGTTAGTGA
ACATAAATACCCATCCATCAGTATTTCTTAACTCTGCTTATTGAAAATG
CTAGTGAGGCAACTCTAATGTTAAGAAAATCACAGCATCTGGTATTATC
GGTCACTCAAGGATGGTATAAAAGCAAGCATGTTGAAGTCAAATGGT
GAATGAAAATGGAGACATGCTAGGAAACCCCTGTTATTTCAAGGTAAAG
ACTTGACTAATCGAACAACCAATTAATGAGTGGACGTAGAGTACTTTAT
GCCGGTAAACAATATGAGTTCCGGGCTAAATTAACCACTTAGTCTGTTTTAA
CACTTGGATTAGGGTTGAAGTGGTAAACAGAACGAGGAGAAAAGCAAGTA
TTGTTGCTCGCATGTTCTTTGACCAATCAGTTCAGAGCTTAAACAGCA
GTTGCTAAACGTTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTG
CAAAGATGACTCTTAAACTTAAATTTATATCAAGATGATTCACTACTTG
AATCTGTTGATAAAAACCGGCTTTTATAGTTTTAGAAATGGTGTGAAATC
ACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAAATATTAAAGTT
ATCTGCTGTTGACTTATCAAATTTATCGTCTAATGAGACCCCTTCAATCT
ATAGAAAACCGTTTTGATGTTAAAGCAAGCAAAATGACAGCTGACAAAAGGA
GCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT
GGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAACAACAATGAAT
CAGGAATGTTAAACAACGCTAAGTATCGAATTCATTTATGTAATGGTGGT
GTTGATAAAGTTGATGTTCCGATTAAGTAGTTGACTTAGAAGCTATTCG
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAGCTGAAGAAG
CAGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAGCTGAA
GAAGCACATAAAGCTGAAGAAGCACCGTAAAGCTGAAGAAGGACATAAAA
CCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACCGTTTCA
CAAACCTGATACTACAGTAAAGCGTCTGATTTACCAAGACTAAGACAGT
TTCCGCAAGTTTCAATGGCTAGAACAGACAATAAACAGATAAATTCACATC
AGACACATGTTG

SEQ ID NO. 5109
STRAIN JM9130013

TGGTGTCCAAATTTATCAACTATATCAAATGGACAACAATAAAC
CTTACTTAAAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGC
TGGAAAAAATTTACTTTCAAAGTTCCAGGATCTGGCATTGGTTTGAAGA
CGTTTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAG
ACCTTATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAGTTGAAAAA
CCAAAATTTAGACCGTCCACCAGGAATTTGATTTACCAGCACCAACTTCAAT
GAGAAGTTTTGATTATTCACCCACCGGGAACCTAAGCCAAGCAACCCA
AAGATAGTTTATCAACTCTCCAGGTTTCCAGATTTAAACACGCGCCGG
GATGAAGCACCAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGG
AGCAATTAATATGCTAAGTCTCTCAACTTAGCTTTGTTGATGACCCTA
TTTTAGCTAGCAAAGTAAATGGCAAAATATTACAAGTCCAATCTGATGGC
AAATTAGTCATTCTTAGAATGCTTTGTGAGCTAATCAATTTGATGACAC
TAGTCTTAAAATTTATCGTAATAATAATCGCAATAAAGAAATTAATATCA
CAACAGATTTATTTGAGATACAAAATATGTAATATCACAGCGGTTGAC
TATTTGAGCAaTACTACTTTTGAGCAATTTAGCTACTGGTGAACAGTAGA
TTACCATGCCATTGTATTTTCAAGCTTTGCTGCTATTAAGACAAGGTTG
GTAAGATTTATGTTAACGATAAATGCAAGAAACTTCTCGTATAGCGCTT
AAAGATAAATCTGTTAAGATTTGGTATTGAATTAACAAATGATGTCAGACA
TATTGATAGTTTATCTGTTGCTGCTTTGAATGAGGTTAAAACGTTGATA
ATATCTGAAAATGATGAACAAGACATTAATCTCAGCAAAAACCTTACCAA
TTAAAATACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAATAACAT
TAACTCAAGTTTCAAGAAATCATGACCCTTTCAAAGATGGAAGATGCCAG
AATGGTTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATG
AGTAAGTTTAAAACATTTCCAGCTTGGACGAAGGATTTGAAATTAAGGG

Table 51: Comparative Sequences relating to SAG0677

ACAACCTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTTCAAAC
AATCTCAAGAGACCAGCTTCAATTATTAATAAATAATACCTTATCCAAAAT
GGTGTTCCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGA
AAGTCAGATAGATGGATACATATATTAATAAGATGCAATTAACCTTAAT
TTAAATTAACCAAGTGGTGCAAGTCTTAAAGTTGTTTATAAGGGCAAGAA
GATCCATATAGTCATCAGAAGAGATATGACTAAAAAAGGTGACAGCT
CAGTCATTCAACTCAAGCCAATGAAAAATACAGCAAAAGTAACTTTGCTA
ATATTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAGTT
GGTAAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTGTATT
ACATAAAAACAGAAAATTCATTAAATGTTAAAAGTTTGATTATGGAGACGG
GTAGTGTAAAGTAAGAAAGTTCAACAACTTCCTTTAAGTCCTAGATTATCT
AAAAATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGC
GTATTACGAAACAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAG
ATACTAAACTTAATTTAATGCTGTAAAAGGAGCGAGTCTCTTACTGAA
AATATGATGATGAGACAGTTTGCAGTGTCTGGACCACAAGATGATCCTGT
TAGTGAACATAAATACCCATCAGTATTTCTTAACTCCTGCCTTATTGG
AAACTGCTAGTGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGT
ATTATCGGTCACATCAAGGATGGTGATAAAAGCAAGCATGTGAAGTCAA
AATGGTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATATTCAAAG
GTAAGAAGCTTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTA
CTTTATGCCGGTAAACAATATGAGTTCCGGGCTAAAATACCCTTAGTTCG
TTTTAACACTTGGATTAGGGTTGAAGTGGTAAACAGAACGAGGagaGaaag
cAaGTATTGTTTCGTCGCATGTTCTTTGCCAATCAGTCCAGAGCTTAAC
ACAGCAGTTGCTAAACCTGATTTGACTTCTGTACTGCTCTTATCCACAT
CGTTGCCAAAGATGACTCTTAAACTAAAATATATCAAGATGATTCAT
TACTTGAATCTGTGATAAAACCCGGTCTTTATAGTTTGAAGATGGTGA
GAAATCACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATTAT
TAAGTTATCTGCTGTTGACTTATCAAATTTATCGTCTGTAATGAGACCCCTC
ATATCTATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGAC
AAAGGAGCTAAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCC
AGAAATGGCAGGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAA
ATGAATCAGGAATGTTAACAAACGCTAAAGTATCGATTCAATTTGTAAT
GGTGGTGTGATAAAGTTGATGTTCCGATTAAGTAGTTGACTTAGAAGC
TATTCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTG
AAGAAGCACGTTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAA
GCTGAAGAAGCACATAAAGCTGAAGAAGCACCGTAAAGCTGAAGAAGGAC
ATAAAACCCAAAGACACCTATAGTTGAAGAAGGCTACAAGTTAATAAC
GTTCACTAAACTGATACTACAGTTAAAGCGTCTGATTTACCAAGACTAA
GACAGTTCCGCACTCATATGGCTAGAACAGACAATAAACAGATAACTT
CACATCAGACACATGTTG

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa235280.2{*} December 10, 2002 05:12 ..

1 50
msa235280.2{195_COH1} ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
msa235280.2{195_M732} ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
msa235280.2{195_M781} ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
msa235280.2{195_H36B} -----TGGT GTCCAAATTT ATCAATACTA
msa235280.2{195_JM9130013} -----TGGT GTCCAAATTT ATCAATACTA
msa235280.2{195_18RS21} ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
msa235280.2{195_2603} ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
msa235280.2{195_A909} ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA
Consensus -----*****

51 100
msa235280.2{195_COH1} TATCAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA
msa235280.2{195_M732} TATCAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA
msa235280.2{195_M781} TATCAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA
msa235280.2{195_H36B} TATCAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA
msa235280.2{195_JM9130013} TATCAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA
msa235280.2{195_18RS21} TATCAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA
msa235280.2{195_2603} TATCAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA
msa235280.2{195_A909} TATCAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA
Consensus *****

101 150
msa235280.2{195_COH1} CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
msa235280.2{195_M732} CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
msa235280.2{195_M781} CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
msa235280.2{195_H36B} CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
msa235280.2{195_JM9130013} CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
msa235280.2{195_18RS21} CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
msa235280.2{195_2603} CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
msa235280.2{195_A909} CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG
Consensus *****

151 200
msa235280.2{195_COH1} GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
msa235280.2{195_M732} GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
msa235280.2{195_M781} GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT
msa235280.2{195_H36B} GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_JM9130013}	GATACTGGCA	TTGGTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_18RS21}	GATACTGGCA	TTGGTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_2603}	GATACTGGCA	TTGGTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_A909}	GATACTGGCA	TTGGTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
Consensus	*****	*****	*****	*****	*****
	201				250
msa235280.2{195_COH1}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M732}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M781}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_H36B}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_JM9130013}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_18RS21}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_2603}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_A909}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
Consensus	*****	*****	*****	*****	*****
	251				300
msa235280.2{195_COH1}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M732}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M781}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_H36B}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_JM9130013}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_18RS21}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_2603}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_A909}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
Consensus	*****	*****	*****	*****	*****
	301				350
msa235280.2{195_COH1}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_M732}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_M781}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_H36B}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_JM9130013}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_18RS21}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_2603}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
msa235280.2{195_A909}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACC
Consensus	*****	*****	*****	*****	*****
	351				400
msa235280.2{195_COH1}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M732}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M781}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_H36B}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_JM9130013}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_18RS21}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_2603}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_A909}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
Consensus	*****	*****	*****	*****	*****
	401				450
msa235280.2{195_COH1}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M732}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M781}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_H36B}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACtAAAGG	ATAGTAAAAA
msa235280.2{195_JM9130013}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_18RS21}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_2603}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_A909}	TCCCAGATTT	AAACACGCCG	CCGGATGAAG	.CACtAAAGG	ATAGTAAAAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa235280.2{195_COH1}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M732}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M781}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_H36B}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_JM9130013}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_18RS21}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_2603}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_A909}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
Consensus	*****	*****	*****	*****	*****
	501				550
msa235280.2{195_COH1}	AACTTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M732}	AACTTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M781}	AACTTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_H36B}	AACTTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_JM9130013}	AACTTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_18RS21}	AACTTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_2603}	AACTTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_A909}	AACTTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
Consensus	*****	*****	*****	*****	*****

Table 51: Comparative Sequences relating to SAG0677

		551			600	
msa235280.2	{195_COH1}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAATGCTTT
msa235280.2	{195_M732}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAATGCTTT
msa235280.2	{195_M781}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAATGCTTT
msa235280.2	{195_H36B}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAATGCTTT
msa235280.2	{195_JM9130013}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAATGCTTT
msa235280.2	{195_18RS21}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAATGCTTT
msa235280.2	{195_2603}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAATGCTTT
msa235280.2	{195_A909}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAATGCTTT
	Consensus	*****	*****	*****	*****	*****
		601			650	
msa235280.2	{195_COH1}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2	{195_M732}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2	{195_M781}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2	{195_H36B}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2	{195_JM9130013}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2	{195_18RS21}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2	{195_2603}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2	{195_A909}	GTCAGCTAAT	CAATTTGATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
	Consensus	*****	*****	*****	*****	*****
		651			700	
msa235280.2	{195_COH1}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2	{195_M732}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2	{195_M781}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2	{195_H36B}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2	{195_JM9130013}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2	{195_18RS21}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2	{195_2603}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2	{195_A909}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
	Consensus	*****	*****	*****	*****	*****
		701			750	
msa235280.2	{195_COH1}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2	{195_M732}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2	{195_M781}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2	{195_H36B}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2	{195_JM9130013}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2	{195_18RS21}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2	{195_2603}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2	{195_A909}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
	Consensus	*****	*****	*****	*****	*****
		751			800	
msa235280.2	{195_COH1}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT
msa235280.2	{195_M732}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT
msa235280.2	{195_M781}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT
msa235280.2	{195_H36B}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT
msa235280.2	{195_JM9130013}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT
msa235280.2	{195_18RS21}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT
msa235280.2	{195_2603}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT
msa235280.2	{195_A909}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAAGCT
	Consensus	*****	*****	*****	*****	*****
		801			850	
msa235280.2	{195_COH1}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2	{195_M732}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2	{195_M781}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2	{195_H36B}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2	{195_JM9130013}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2	{195_18RS21}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2	{195_2603}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2	{195_A909}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
	Consensus	*****	*****	*****	*****	*****
		851			900	
msa235280.2	{195_COH1}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2	{195_M732}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2	{195_M781}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2	{195_H36B}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2	{195_JM9130013}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2	{195_18RS21}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2	{195_2603}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2	{195_A909}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
	Consensus	*****	*****	*****	*****	*****
		901			950	
msa235280.2	{195_COH1}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2	{195_M732}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2	{195_M781}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2	{195_H36B}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2	{195_JM9130013}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_18RS21}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_2603}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_A909}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
Consensus	*****	*****	*****	*****	*****
	951				1000
msa235280.2{195_COH1}	TGAATGAGGT	TAAAACGTGT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M732}	TGAATGAGGT	TAAAACGTGT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M781}	TGAATGAGGT	TAAAACGTGT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_H36B}	TGAATGAGGT	TAAAACGTGT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_JM9130013}	TGAATGAGGT	TAAAACGTGT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_18RS21}	TGAATGAGGT	TAAAACGTGT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_2603}	TGAATGAGGT	TAAAACGTGT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_A909}	TGAATGAGGT	TAAAACGTGT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa235280.2{195_COH1}	ATTAATCTCA	GCAAACTTA	CCAATTAATA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M732}	ATTAATCTCA	GCAAACTTA	CCAATTAATA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M781}	ATTAATCTCA	GCAAACTTA	CCAATTAATA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_H36B}	ATTAATCTCA	GCAAACTTA	CCAATTAATA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_JM9130013}	ATTAATCTCA	GCAAACTTA	CCAATTAATA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_18RS21}	ATTAATCTCA	GCAAACTTA	CCAATTAATA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_2603}	ATTAATCTCA	GCAAACTTA	CCAATTAATA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_A909}	ATTAATCTCA	GCAAACTTA	CCAATTAATA	TACAACCCGA	CAAATCGTCG
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa235280.2{195_COH1}	TCTAGAGTTT	ACTATTAATA	ACATTAACFC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M732}	TCTAGAGTTT	ACTATTAATA	ACATTAACFC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M781}	TCTAGAGTTT	ACTATTAATA	ACATTAACFC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_H36B}	TCTAGAGTTT	ACTATTAATA	ACATTAACFC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_JM9130013}	TCTAGAGTTT	ACTATTAATA	ACATTAACFC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_18RS21}	TCTAGAGTTT	ACTATTAATA	ACATTAACFC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_2603}	TCTAGAGTTT	ACTATTAATA	ACATTAACFC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_A909}	TCTAGAGTTT	ACTATTAATA	ACATTAACFC	AAGTTCAGAA	ATCATGACCA
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa235280.2{195_COH1}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M732}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M781}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_H36B}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_JM9130013}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_18RS21}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_2603}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_A909}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
Consensus	*****	*****	*****	*****	*****
	1151				1200
msa235280.2{195_COH1}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACCTA	TTCGACTTGG
msa235280.2{195_M732}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACCTA	TTCGACTTGG
msa235280.2{195_M781}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACCTA	TTCGACTTGG
msa235280.2{195_H36B}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACCTA	TTCGACTTGG
msa235280.2{195_JM9130013}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACCTA	TTCGACTTGG
msa235280.2{195_18RS21}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACCTA	TTCGACTTGG
msa235280.2{195_2603}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACCTA	TTCGACTTGG
msa235280.2{195_A909}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACCTA	TTCGACTTGG
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa235280.2{195_COH1}	ACGAAAGGAT	TCTGAATTTA	AGGGACAACCT	TATTGC AAAA	ACTGGAACAG
msa235280.2{195_M732}	ACGAAAGGAT	TCTGAATTTA	AGGGACAACCT	TATTGC AAAA	ACTGGAACAG
msa235280.2{195_M781}	ACGAAAGGAT	TCTGAATTTA	AGGGACAACCT	TATTGC AAAA	ACTGGAACAG
msa235280.2{195_H36B}	ACGAAAGGAT	TCTGAATTTA	AGGGACAACCT	TATTGC AAAA	ACTGGAACAG
msa235280.2{195_JM9130013}	ACGAAAGGAT	TCTGAATTTA	AGGGACAACCT	TATTGC AAAA	ACTGGAACAG
msa235280.2{195_18RS21}	ACGAAAGGAT	TCTGAATTTA	AGGGACAACCT	TATTGC AAAA	ACTGGAACAG
msa235280.2{195_2603}	ACGAAAGGAT	TCTGAATTTA	AGGGACAACCT	TATTGC AAAA	ACTGGAACAG
msa235280.2{195_A909}	ACGAAAGGAT	TCTGAATTTA	AGGGACAACCT	TATTGC AAAA	ACTGGAACAG
Consensus	*****	*****	*****	*****	*****
	1251				1300
msa235280.2{195_COH1}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M732}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M781}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_H36B}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_JM9130013}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_18RS21}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_2603}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_A909}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
Consensus	*****	*****	*****	*****	*****
	1301				1350

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_COH1}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_M732}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_M781}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_H36B}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_JM9130013}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_18RS21}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_2603}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
msa235280.2{195_A909}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT
Consensus	*****	*****	*****	*****	*****
	1351				1400
msa235280.2{195_COH1}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_M732}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_M781}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_H36B}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_JM9130013}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_18RS21}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_2603}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
msa235280.2{195_A909}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT
Consensus	*****	*****	*****	*****	*****
	1401				1450
msa235280.2{195_COH1}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT
msa235280.2{195_M732}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT
msa235280.2{195_M781}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT
msa235280.2{195_H36B}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT
msa235280.2{195_JM9130013}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT
msa235280.2{195_18RS21}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT
msa235280.2{195_2603}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT
msa235280.2{195_A909}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT
Consensus	*****	*****	*****	*****	*****
	1451				1500
msa235280.2{195_COH1}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_M732}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_M781}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_H36B}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_JM9130013}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_18RS21}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_2603}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
msa235280.2{195_A909}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA
Consensus	*****	*****	*****	*****	*****
	1501				1550
msa235280.2{195_COH1}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA
msa235280.2{195_M732}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA
msa235280.2{195_M781}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA
msa235280.2{195_H36B}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA
msa235280.2{195_JM9130013}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA
msa235280.2{195_18RS21}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA
msa235280.2{195_2603}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA
msa235280.2{195_A909}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA
Consensus	*****	*-*****	*****	*****	*****
	1551				1600
msa235280.2{195_COH1}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_M732}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_M781}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_H36B}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_JM9130013}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_18RS21}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_2603}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
msa235280.2{195_A909}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG
Consensus	*****	*****	*****	*****	*****
	1601				1650
msa235280.2{195_COH1}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_M732}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_M781}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_H36B}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_JM9130013}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_18RS21}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_2603}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
msa235280.2{195_A909}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC
Consensus	*****	*****	*****-****	*****	*****
	1651				1700
msa235280.2{195_COH1}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_M732}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_M781}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_H36B}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_JM9130013}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_18RS21}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_2603}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAATG
msa235280.2{195_A909}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAATG
Consensus	*****	*****	*****	*****	*****
	1701				1750
msa235280.2{195_COH1}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_M732}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_M781}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_H36B}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_JM9130013}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_18RS21}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_2603}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_A909}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
Consensus	*****	*****	*****	*****	*****
	1751				1800
msa235280.2{195_COH1}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M732}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M781}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_H36B}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_JM9130013}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_18RS21}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_2603}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_A909}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
Consensus	*****	*****	*****	*****	*****
	1801				1850
msa235280.2{195_COH1}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M732}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M781}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_H36B}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_JM9130013}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_18RS21}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_2603}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_A909}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
Consensus	*****	*****	*****	*****	*****
	1851				1900
msa235280.2{195_COH1}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M732}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M781}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_H36B}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_JM9130013}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_18RS21}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_2603}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_A909}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
Consensus	*****	*****	*****	*****	*****
	1901				1950
msa235280.2{195_COH1}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_M732}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_M781}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_H36B}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_JM9130013}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_18RS21}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_2603}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_A909}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
Consensus	*****	*****	*****	*****	*****
	1951				2000
msa235280.2{195_COH1}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M732}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M781}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_H36B}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_JM9130013}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_18RS21}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_2603}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_A909}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
Consensus	*****	*****	*****	*****	*****
	2001				2050
msa235280.2{195_COH1}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M732}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M781}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_H36B}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_JM9130013}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_18RS21}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_2603}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_A909}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
Consensus	*****	*****	*****	*****	*****
	2051				2100
msa235280.2{195_COH1}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M732}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_M781}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_H36B}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_JM9130013}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_18RS21}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_2603}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_A909}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
Consensus	*****	*****	*****	*****	*****
	2101				2150
msa235280.2{195_COH1}	TAAAAGCAAG	CATGTTGAAG	TCAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M732}	TAAAAGCAAG	CATGTTGAAG	TCAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M781}	TAAAAGCAAG	CATGTTGAAG	TCAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_H36B}	TAAAAGCAAG	CATGTTGAAG	TCAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_JM9130013}	TAAAAGCAAG	CATGTTGAAG	TCAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_18RS21}	TAAAAGCAAG	CATGTTGAAG	TCAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_2603}	TAAAAGCAAG	CATGTTGAAG	TCAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_A909}	TAAAAGCAAG	CATGTTGAAG	TCAAATGGT	GAATGAAAAT	GGAGACATGC
Consensus	*****	*****	*****	*****	*****
	2151				2200
msa235280.2{195_COH1}	TAGGAACCCC	TGTTATTATT	CAAGGTAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_M732}	TAGGAACCCC	TGTTATTATT	CAAGGTAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_M781}	TAGGAACCCC	TGTTATTATT	CAAGGTAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_H36B}	TAGGAACCCC	TGTTATTATT	CAAGGTAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_JM9130013}	TAGGAACCCC	TGTTATTATT	CAAGGTAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_18RS21}	TAGGAACCCC	TGTTATTATT	CAAGGTAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_2603}	TAGGAACCCC	TGTTATTATT	CAAGGTAAG	ACTTGACTAA	TCGAACAAAA
msa235280.2{195_A909}	TAGGAACCCC	TGTTATTATT	CAAGGTAAG	ACTTGACTAA	TCGAACAAAA
Consensus	*****	*****	*****	*****	*****
	2201				2250
msa235280.2{195_COH1}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M732}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M781}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_H36B}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_JM9130013}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_18RS21}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_2603}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_A909}	CCATTAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
Consensus	*****	*****	*****	*****	*****
	2251				2300
msa235280.2{195_COH1}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_M732}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_M781}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_H36B}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_JM9130013}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_18RS21}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_2603}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
msa235280.2{195_A909}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACTTGGATT	AGGGTTGAAG
Consensus	*****	*****	*****	*****	*****
	2301				2350
msa235280.2{195_COH1}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTCTGCG	CATGTTCTTT
msa235280.2{195_M732}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTCTGCG	CATGTTCTTT
msa235280.2{195_M781}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTCTGCG	CATGTTCTTT
msa235280.2{195_H36B}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTCTGCG	CATGTTCTTT
msa235280.2{195_JM9130013}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTCTGCG	CATGTTCTTT
msa235280.2{195_18RS21}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTCTGCG	CATGTTCTTT
msa235280.2{195_2603}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTCTGCG	CATGTTCTTT
msa235280.2{195_A909}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTCTGCG	CATGTTCTTT
Consensus	*****	*****	*****	*****	*****
	2351				2400
msa235280.2{195_COH1}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M732}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M781}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_H36B}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_JM9130013}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_18RS21}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_2603}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_A909}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
Consensus	*****	*****	*****	*****	*****
	2401				2450
msa235280.2{195_COH1}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M732}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M781}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_H36B}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_JM9130013}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_18RS21}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_2603}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_A909}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
Consensus	*****	*****	*****	*****	*****
	2451				2500
msa235280.2{195_COH1}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_M732}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_M781}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_H36B}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_JM9130013}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_18RS21}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_2603}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_A909}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
Consensus	*****	*****	*****	*****	*****
	2501				2550
msa235280.2{195_COH1}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_M732}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_M781}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_H36B}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_JM9130013}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_18RS21}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_2603}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_A909}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
Consensus	*****	*****	*****	*****	*****
	2551				2600
msa235280.2{195_COH1}	ACTAGAATTT	GGAGATAATA	TTA:TAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_M732}	ACTAGAATTT	GGAGATAATA	TTA:TAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_M781}	ACTAGAATTT	GGAGATAATA	TTA:TAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_H36B}	ACTAGAATTT	GGAGATAATA	TTA:TAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_JM9130013}	ACTAGAATTT	GGAGATAATA	TTA:TAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_18RS21}	ACTAGAATTT	GGAGATAATA	TTA:TAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_2603}	ACTAGAATTT	GGAGATAATA	TTA:TAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_A909}	ACTAGAATTT	GGAGATAATA	TTA:TAAGTT	ATCTGCTGTT	GACTTATCAA
Consensus	*****	*****	***_*****	*****	*****
	2601				2650
msa235280.2{195_COH1}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_M732}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_M781}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_H36B}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_JM9130013}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_18RS21}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_2603}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_A909}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
Consensus	*****	*****	*****	*****	*****
	2651				2700
msa235280.2{195_COH1}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_M732}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_M781}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_H36B}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_JM9130013}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_18RS21}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_2603}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_A909}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
Consensus	*****	*****	*****	*****	*****
	2701				2750
msa235280.2{195_COH1}	GTTGATGAAG	CACITAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_M732}	GTTGATGAAG	CACITAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_M781}	GTTGATGAAG	CACITAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_H36B}	GTTGATGAAG	CACITAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_JM9130013}	GTTGATGAAG	CACITAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_18RS21}	GTTGATGAAG	CACITAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_2603}	GTTGATGAAG	CACITAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_A909}	GTTGATGAAG	CACITAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
Consensus	*****	*****	*****	*****	*****
	2751				2800
msa235280.2{195_COH1}	CAATCGACGA	AGcTCCAAC	ACAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_M732}	CAATCGACGA	AGcTCCAAC	ACAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_M781}	CAATCGACGA	AGcTCCAAC	ACAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_H36B}	CAATCGACGA	AGcTCCAAC	ACAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_JM9130013}	CAATCGACGA	AGcTCCAAC	ACAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_18RS21}	CAATCGACGA	AGcTCCAAC	ACAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_2603}	CAATCGACGA	AGcTCCAAC	ACAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_A909}	CAATCGACGA	AGcTCCAAC	ACAATGAAT	CAGGAATGTT	AACAAACGCT
Consensus	*****	***_*****	*****	*****	*****
	2801				2850
msa235280.2{195_COH1}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_M732}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M781}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_H36B}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_JM9130013}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_18RS21}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_2603}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_A909}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
Consensus	*****	*****	*****	*****	*****
2851					
msa235280.2{195_COH1}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M732}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M781}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_H36B}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_JM9130013}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_18RS21}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..
msa235280.2{195_2603}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..
msa235280.2{195_A909}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
Consensus	*****	*****	*****	*****	*****
2901					
msa235280.2{195_COH1}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M732}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M781}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_H36B}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_JM9130013}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_18RS21}CGTAAAGC	TGAaGAAGCA
msa235280.2{195_2603}cgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_A909}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
Consensus	-----	-----	-----	-----	-----
2950					
2951					
msa235280.2{195_COH1}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M732}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M781}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_H36B}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_JM9130013}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_18RS21}	CgTAAAGCTG	AAGAAGcA..
msa235280.2{195_2603}	CgTAAAGCTG	AAGAAGcA..
msa235280.2{195_A909}	CgTAAAGCTG	AAGAAGcA..
Consensus	*-*****	*****-*	-----	-----	-----
3001					
msa235280.2{195_COH1}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M732}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M781}	agcacCGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_H36B}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_JM9130013}	agcacCGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_18RS21}CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_2603}CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_A909}CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
Consensus	-----	*****	*****	*****	*****
3051					
msa235280.2{195_COH1}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_M732}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_M781}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_H36B}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_JM9130013}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_18RS21}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_2603}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_A909}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
Consensus	*****	*****	*****	*****	*****
3101					
msa235280.2{195_COH1}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M732}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M781}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_H36B}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_JM9130013}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_18RS21}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_2603}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_A909}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
Consensus	*****	*****	*****	*****	*****
3150					
3151					
msa235280.2{195_COH1}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGT	-----
msa235280.2{195_M732}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGT	TGAAAA----
msa235280.2{195_M781}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGT	TG-----
msa235280.2{195_H36B}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGT	-----
msa235280.2{195_JM9130013}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGT	TG-----
msa235280.2{195_18RS21}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGT	TGAA-----
msa235280.2{195_2603}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGT	TGAAAAACAA
msa235280.2{195_A909}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGT	TGAAAAACAA

Table 51: Comparative Sequences relating to SAG0677

Consensus	*****	*****	*****	*****	*****
	3201				3250
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	ATTAAAAATA	cattgccatc	cactgggtgac	agcaaacgtg	gttattatat
msa235280.2{195_A909}	ATTAAAAATA	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3251				3300
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	cactggaatg	gctatcgta	tgctgagtgt	attatttagt	ttagctaaaa
msa235280.2{195_A909}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3301	3317			
msa235280.2{195_COH1}	-----	-----			
msa235280.2{195_M732}	-----	-----			
msa235280.2{195_M781}	-----	-----			
msa235280.2{195_H36B}	-----	-----			
msa235280.2{195_JM9130013}	-----	-----			
msa235280.2{195_18RS21}	-----	-----			
msa235280.2{195_2603}	agttaaaag	caaatat			
msa235280.2{195_A909}	-----	-----			
Consensus	*****	*****			

SEQ ID NO. 5110

STRAIN 2603 frame: 1

LNNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDQVY
LQSVKYVGGGNNLIDLITPPGFKKEDKVKPKLDRPPGIDLPAPTSMRSFDYSTPPGPK
PSKPKDLSLTPPGFPDLNTPPDEAPKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNI TAV
DYLNTTPEQLATGETVDYHAI VFSSFAAIKDGGKIYVNDKLQETSRIALKDKSVKIGI
ELPNDVRHIDLSVRLNEVKTVDNLIKNDQDINLSKTYQLKYNPTNRRLEFTINNINS
SSEIMTTFKDGKMPPELVEQKDVSLDINDMDSKFKTIRLGRKDESEFKQLIAKTGTVELD
MFFKQSDPASI IKKIYLIQNGVPELKKFDSSFGLTESQIDGYYIYKDAINLKFCLTSG
ASLVVYKQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANI DWSHYSKVTVNGKE
VVGKSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVVQQLPLSPRLSKNKHMRDML
LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
HKYPSVFLTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMNVNENGDMGLTGP
VI IQGKDLNTRTKPLMSGRRVLVYAGKQYEFRAKPLSRFNTWIRVEVVTEAGEKASIVRR
MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLYQDDSLLESVDKTLGYSFRNG
VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAQVTVDM
LMKHLVVPPEMAGAYTITIDEAPNTNESGMLTNAKVISIHVNGGVDKVDVPIKVDLEAIR
KAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARK
AVHMARTDNKQITSHQTHVEKQIKNTLPSTGDSKRGYITGMAIVMLSVLFLSLAKKFKSK
Y

SEQ ID NO. 5111

STRAIN A909 frame: 1

LNNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDQVY
LQSVKYVGGGNNLIDLITPPGFKKEDKVKPKLDRPPGIDLPPPTSMRSFDYSTPPGPK
PSKPKDLSLTPPGFPDLNTPPDEALKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNI TAV
DYLNTTPEQLATGETVDYHAI VFSSFAAIKDGGKIYVNDKLQETSRIALKDKSVKIGI
ELPNDVRHIDLSVRLNEVKTVDNLIKNDQDINLSKTYQLKYNPTNRRLEFTINNINS
SSEIMTTFKDGKMPPELVEQKDVSLDINDMDSKFKTIRLGRKDESEFKQLIAKTGTVELD
MFFKQSDPASI IKKIYLIQNGVPELKKFDSSFGLTESQIDGYYIYKDAINLKFCLTSG
ASLVVYKQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANI DWSHYSKVTVNGKE
VVGKSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVVQQLPLSPRLSKNKHMRDML
LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
HKYPSVFLTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMNVNENGDMGLTGP
VI IQGKDLNTRTKPLMSGRRVLVYAGKQYEFRAKPLSRFNTWIRVEVVTEAGEKASIVRR
MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLYQDDSLLESVDKTLGYSFRNG
VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAQVTVDM
LMKHLVVPPEMAGAYTITIDEAPNTNESGMLTNAKVISIHVNGGVDKVDVPIKVDLEAIR
KAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARK
KASDLPKTKTVSAVHMARTDNKQITSHQTHVEKQIKN

SEQ ID NO. 5112

STRAIN H36B frame: 2

GVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDQVY
LQSVKYVGGGNNLIDLITPPGFKKEDKVKPKLDRPPGIDLPAPTSMRSFDYSTPPGPK
PSKPKDLSLTPPGFPDLNTPPDEALKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNI TAV
DYLNTTPEQLATGETVDYHAI VFSSFAAIKDGGKIYVNDKLQETSRIALKDKSVKIGI
ELPNDVRHIDLSVRLNEVKTVDNLIKNDQDINLSKTYQLKYNPTNRRLEFTINNINS
SSEIMTTFKDGKMPPELVEQKDVSLDINDMDSKFKTIRLGRKDESEFKQLIAKTGTVELD
MFFKQSDPASI IKKIYLIQNGVPELKKFDSSFGLTESQIDGYYIYKDAINLKFCLTSG
ASLVVYKQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANI DWSHYSKVTVNGKE
VVGKSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVVQQLPLSPRLSKNKHMRDML
LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
HKYPSVFLTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMNVNENGDMGLTGP
VI IQGKDLNTRTKPLMSGRRVLVYAGKQYEFRAKPLSRFNTWIRVEVVTEAGEKASIVRR
MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLYQDDSLLESVDKTLGYSFRNG
VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAQVTVDM
LMKHLVVPPEMAGAYTITIDEAPNTNESGMLTNAKVISIHVNGGVDKVDVPIKVDLEAIR
KAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARKAEARK
KASDLPKTKTVSAVHMARTDNKQITSHQTHVEKQIKN

Table 51: Comparative Sequences relating to SAG0677

DGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNIATAVDYLSNTTFFE
QLATGETVDYHAIVFSSFAAIKDKGGKIYVNDKLOETSRIALKDKSVKIGIELPNDVRHI
DLSVRRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINSSEIMTTFK
DGKMPLEVEQKDVSLDINDMDMSKFKTIRLGRKDESEFKGQLIAKTGTVELDMFFKQSDP
ASIIKKIYLIQNGVFNELKKFDSSFGLETESQIDGYIYKDAINLKFKLTSGLSKVYK
QEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTAFANIDWSHYSKVTVNGKEVKGSELPL
TKGWTFVLHKTENSLNVKSLIMETGSVSKVQQLPLSPRLSKNKHMRDMLTMQKDSAY
YETSLSVLRLINLTADTKLNFNAVGASALTENMMMRQFAVAGPQDDPVSEHKYPSVFL
LPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDMGLTGPVIOGKDLT
NRTKPLMSGRRVLYAGKQYEFRAKPLSRFNTWIRVEVVTAGEKASIVRRMFFDQSVPE
LNTAVAKRDLTSDTALIHIVAKDDSLKLYQDDSLLESVDKTLGYSFRNGVEITKDMTV
PLEFGDNITKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAQVTVDMMLKHLVPE
MAGAYTLTIDEAPTNEGMLTNAKVSIHVNGGVKVDVPIKVVLEAIRKAEAEHAKAD
EARKAEAEARKADEAHKAEVEARKAEAEHAKAEHGHKTQEPAVEEGYKVVNVNHQTD
TTVKASDLPKTKTVAHVHMARTDNKQITSHQTH

SEQ ID NO. 5113

STRAIN 18RS21 frame: 1
LNNKGVGGDGVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD
VYLSQSVKYVGGGNNLDDLTIPPGFKKEDKVEKPKLDRPPGIDLPAPTSMRSDYSTPPG
TKPSKPKDLSLTPPGFPDLNTPPEAPKDSKDAIEDKSGAIKYAKSLQLSFDVDDPILASK
VNGKILQVESDGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNI
ATAVDYLSNTTFFEQLATGETVDYHAIVFSSFAAIKDKGGKIYVNDKLOETSRIALKDK
SVKIGIELPNDVRHIDLSVRRRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLE
FTINNINSSEIMTTFKDGKMPLEVEQKDVSLDINDMDMSKFKTIRLGRKDESEFKGQL
IAKTGTVELDMFFKQSDPASIKKIYLIQNGVFNELKKFDSSFGLETESQIDGYIYKDA
INLKFKLTSGLSKVYKQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTAFANIDWSH
YSKVTVNGKEVKGSELPLTKGWTFVLHKTENSLNVKSLIMETGSVSKVQQLPLSPRLS
KNKHMRDMLTMQKDSAYYETSLSVLRLINLTADTKLNFNAVGASALTENMMMRQFAVA
GAPQDDPVSEHKYPSVFLTTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVK
MVNENGDMGLTGPVIOGKDLTNRNTPKPLMSGRRVLYAGKQYEFRAKPLSRFNTWIR
VEVVTAGEKASIVRRMFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLYQDD
SLLESVDKTLGYSFRNGVEITKDMTVPLEFGDNITKLSAVDLSNYRRNETLHIYRNR
FDVKASQMTADKGAQVTVDMMLKHLVPEMAGAYTLTIDEAPTNEGMLTNAKVSIHV
NGGVKVDVPIKVVLEAIRKAEAEHAKADEAHKAEVEARKAEAEHGHKTQEPAVEEGY
KVVNVNHQTDTTVKASDLPKTKTVAHVHMARTDNKQITSHQTH

SEQ ID NO. 5114

STRAIN M732 frame: 1
LNNKGVGGDGVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD
VYLSQSVKYVGGGNNLDDLTIPPGFKKEDKVEKPKLDRPPGIDLPAPTSMRSDYSTPPG
TKPSKPKDLSLTPPGFPDLNTPPEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS
KWQNTSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYHNRFLFCRYKICQYHSG
.LFEQYIF.AISYW.NSRLPCHCIFKLCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY
.ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQONLPIKIQDPKSSSRVY..H.L
KFRNHDFQRWKDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.I.GTYCKNWN.S.IR
YVFQTIISRPSFNY.KNIPYKWC.SK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW
CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSSQ.KYSKSNLC.Y.LVTL..GYCEWKR
SW.R..VTFN.RMDNICIT.NRKFIC.KFDYGDG.CK.ESSSTSFKS.II.K.AYEGYA
TYAKRFSVLRNK.QSSPSN.SHCYR.T.F.CC.RSECSY.KYDDETVCSWTR.SC..
T.IPISISLNSCLIGNC..GNSKW.GNHSIWYRSHQGW..KQAC.SQNGE.KWRHARNP
CYYSR.RLD.SNKTINEWT.STLCR.TI.VPG.I.TT.SF.HLD.G.SGNRSRRESKYCSS
HVL.PISSRA.HSSC.T.FDF.YCSYPHRCOR.LSKTKIISR.FIT.IC..NRSL.F.KW
CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPNDS.QRS.SNCGY
VDEALSCSRNGRSLSYINNRSSKHK.IRNVNKR.SIDSLCKWWC..S.CSD.SS.LRSYS
.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRRST.S.RGT.NPRSTYS.RRL
QS..RSSN.YS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC.K

SEQ ID NO. 5115

STRAIN COH1 frame: 1
LNNKGVGGDGVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD
VYLSQSVKYVGGGNNLDDLTIPPGFKKEDKVEKPKLDRPPGIDLPAPTSMRSDYSTPPG
TKPSKPKDLSLTPPGFPDLNTPPEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS
KWQNTSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYHNRFLFCRYKICQYHSG
.LFEQYIF.AISYW.NSRLPCHCIFKLCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY
.ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQONLPIKIQDPKSSSRVY..H.L
KFRNHDFQRWKDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.I.GTYCKNWN.S.IR
YVFQTIISRPSFNY.KNIPYKWC.SK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW
CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSSQ.KYSKSNLC.Y.LVTL..GYCEWKR
SW.R..VTFN.RMDNICIT.NRKFIC.KFDYGDG.CK.ESSSTSFKS.II.K.AYEGYA
TYAKRFSVLRNK.QSSPSN.SHCYR.T.F.CC.RSECSY.KYDDETVCSWTR.SC..
T.IPISISLNSCLIGNC..GNSKW.GNHSIWYRSHQGW..KQAC.SQNGE.KWRHARNP
CYYSR.RLD.SNKTINEWT.STLCR.TI.VPG.I.TT.SF.HLD.G.SGNRSRRESKYCSS
HVL.PISSRA.HSSC.T.FDF.YCSYPHRCOR.LSKTKIISR.FIT.IC..NRSL.F.KW
CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPNDS.QRS.SNCGY
VDEALSCSRNGRSLSYINNRSSKHK.IRNVNKR.SIDSLCKWWC..S.CSD.SS.LRSYS
.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRRST.S.RGT.NPRSTYS.RRL
QS..RSSN.YS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC

SEQ ID NO. 5116

STRAIN M781 frame: 1
LNNKGVGGDGVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD
VYLSQSVKYVGGGNNLDDLTIPPGFKKEDKVEKPKLDRPPGIDLPAPTSMRSDYSTPPG
TKPSKPKDLSLTPPGFPDLNTPPEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS
KWQNTSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYHNRFLFCRYKICQYHSG
.LFEQYIF.AISYW.NSRLPCHCIFKLCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY
.ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQONLPIKIQDPKSSSRVY..H.L
KFRNHDFQRWKDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.I.GTYCKNWN.S.IR
YVFQTIISRPSFNY.KNIPYKWC.SK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW
CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSSQ.KYSKSNLC.Y.LVTL..GYCEWKR
SW.R..VTFN.RMDNICIT.NRKFIC.KFDYGDG.CK.ESSSTSFKS.II.K.AYEGYA
TYAKRFSVLRNK.QSSPSN.SHCYR.T.F.CC.RSECSY.KYDDETVCSWTR.SC..
T.IPISISLNSCLIGNC..GNSKW.GNHSIWYRSHQGW..KQAC.SQNGE.KWRHARNP
CYYSR.RLD.SNKTINEWT.STLCR.TI.VPG.I.TT.SF.HLD.G.SGNRSRRESKYCSS
HVL.PISSRA.HSSC.T.FDF.YCSYPHRCOR.LSKTKIISR.FIT.IC..NRSL.F.KW
CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPNDS.QRS.SNCGY
VDEALSCSRNGRSLSYINNRSSKHK.IRNVNKR.SIDSLCKWWC..S.CSD.SS.LRSYS
.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRRST.S.RGT.NPRSTYS.RRL
QS..RSSN.YS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC

Table 51: Comparative Sequences relating to SAG0677

	201				250
msa235427.2{195_H36B}	sanqfddtsl	kiyrnnrnk	eitittdyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_JM9130013}	sanqfddtsl	kiyrnnrnk	eitittdyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_18RS21}	sanqfddtsl	kiyrnnrnk	eitittdyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_2603}	sanqfddtsl	kiyrnnrnk	eitittdyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_A909}	sanqfddtsl	kiyrnnrnk	eitittdyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_COH1}	vs.si..h.s	.nls...sq.	rnyyhrlFc	ryKicqyhsq	.lfeqyyF.a
msa235427.2{195_M732}	vs.si..h.s	.nls...sq.	rnyyhrlFc	ryKicqyhsq	.lfeqyyF.a
msa235427.2{195_M781}	vs.si..h.s	.nls...sq.	rnyyhrlFc	ryKicqyhsq	.lfeqyyF.a
	Consensus	-----	-----*	-----*	-----*
	251				300
msa235427.2{195_H36B}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_JM9130013}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_18RS21}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_2603}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_A909}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_COH1}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
msa235427.2{195_M732}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
msa235427.2{195_M781}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
	Consensus	-----	-----*	-----*	-----*
	301				350
msa235427.2{195_H36B}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_JM9130013}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_18RS21}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_2603}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_A909}	elpndvrhid	slsvrrlnev	ktvdniLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_COH1}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
msa235427.2{195_M732}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
msa235427.2{195_M781}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
	Consensus	-----	-----*	-----*	-----*
	351				400
msa235427.2{195_H36B}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd	mskfktirlg
msa235427.2{195_JM9130013}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd	mskfktirlg
msa235427.2{195_18RS21}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd	mskfktirlg
msa235427.2{195_2603}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd	mskfktirlg
msa235427.2{195_A909}	leftinnins	sseimttFkd	gKmpelveqK	dvslldindmd	mskfktirlg
msa235427.2{195_COH1}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
msa235427.2{195_M732}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
msa235427.2{195_M781}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
	Consensus	-----*	-----*	-----*	-----*
	401				450
msa235427.2{195_H36B}	rKdsefkGql	iaKtgtveld	mfFkqsqDpa	siikKiyliq	ngvvpnelkKf
msa235427.2{195_JM9130013}	rKdsefkGql	iaKtgtveld	mfFkqsqDpa	siikKiyliq	ngvvpnelkKf
msa235427.2{195_18RS21}	rKdsefkGql	iaKtgtveld	mfFkqsqDpa	siikKiyliq	ngvvpnelkKf
msa235427.2{195_2603}	rKdsefkGql	iaKtgtveld	mfFkqsqDpa	siikKiyliq	ngvvpnelkKf
msa235427.2{195_A909}	rKdsefkGql	iaKtgtveld	mfFkqsqDpa	siikKiyliq	ngvvpnelkKf
msa235427.2{195_COH1}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
msa235427.2{195_M732}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
msa235427.2{195_M781}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
	Consensus	-----*	-----*	-----*	-----*
	451				500
msa235427.2{195_H36B}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_JM9130013}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_18RS21}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_2603}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_A909}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_COH1}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
msa235427.2{195_M732}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
msa235427.2{195_M781}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
	Consensus	-----	-----	-----	-----
	501				550
msa235427.2{195_H36B}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_JM9130013}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_18RS21}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_2603}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_A909}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_COH1}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
msa235427.2{195_M732}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
msa235427.2{195_M781}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
	Consensus	-----*	-----*	-----*	-----*
	551				600
msa235427.2{195_H36B}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_JM9130013}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_18RS21}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_2603}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl

Table 51: Comparative Sequences relating to SAG0677

msa235427.2{195_A909}	kgwtffvlhk	tenslnvksl	imetGavskk	vqqlplsprl	sknhkhrdml
msa235427.2{195_COH1}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M732}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M781}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
Consensus	-----	-----	-----*	-----	-----
601					
msa235427.2{195_H36B}	lTmqkdsayy	etsdsvlri	Nltadtklnf	navkgaSalt	enmmmrqfav
msa235427.2{195_JM9130013}	lTmqkdsayy	etsdsvlri	Nltadtklnf	navkgaSalt	enmmmrqfav
msa235427.2{195_18RS21}	lTmqkdsayy	etsdsvlri	Nltadtklnf	navkgaSalt	enmmmrqfav
msa235427.2{195_2603}	lTmqkdsayy	etsdsvlri	Nltadtklnf	navkgaSalt	enmmmrqfav
msa235427.2{195_A909}	lTmqkdsayy	etsdsvlri	Nltadtklnf	navkgaSalt	enmmmrqfav
msa235427.2{195_COH1}	aTyyakrfsv	lrnk.qssps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M732}	aTyyakrfsv	lrnk.qssps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M781}	aTyyakrfsv	lrnk.qssps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
Consensus	-*-----	-----	*-----	-----*	-----
651					
msa235427.2{195_H36B}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_JM9130013}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_18RS21}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_2603}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_A909}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_COH1}	scwttr.sc.	.t.ipisisl	nsclignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M732}	scwttr.sc.	.t.ipisisl	nsclignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M781}	scwttr.sc.	.t.ipisisl	nsclignc..	gnskw.gnhS	iwyrrshqGw
Consensus	-----	-----	-----*	-----*	-----*
701					
msa235427.2{195_H36B}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_JM9130013}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_18RS21}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_2603}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_A909}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_COH1}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M732}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M781}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
Consensus	--*-----	*-----	-----	-----	-----
751					
msa235427.2{195_H36B}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_JM9130013}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_18RS21}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_2603}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_A909}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_COH1}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M732}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M781}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
Consensus	-----	-----	-----*	-----	-----
801					
msa235427.2{195_H36B}	sdtalihiva	kddsLkIkly	qddslllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_JM9130013}	sdtalihiva	kddsLkIkly	qddslllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_18RS21}	sdtalihiva	kddsLkIkly	qddslllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_2603}	sdtalihiva	kddsLkIkly	qddslllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_A909}	sdtalihiva	kddsLkIkly	qddslllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_COH1}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
msa235427.2{195_M732}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
msa235427.2{195_M781}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
Consensus	-----	-----*	-----	-----	-----
851					
msa235427.2{195_H36B}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_JM9130013}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_18RS21}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_2603}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_A909}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_COH1}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.snec
msa235427.2{195_M732}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.snec
msa235427.2{195_M781}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.snec
Consensus	-----	-----	-----*	-----*	-----
901					
msa235427.2{195_H36B}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_JM9130013}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_18RS21}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_2603}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_A909}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_COH1}	yvdealscsr	nGrsllyinnr	rsakhk.irn	vNkr.SIdsl	ckwcc..s.c
msa235427.2{195_M732}	yvdealscsr	nGrsllyinnr	rsakhk.irn	vNkr.SIdsl	ckwcc..s.c
msa235427.2{195_M781}	yvdealscsr	nGrsllyinnr	rsakhk.irn	vNkr.SIdsl	ckwcc..s.c
Consensus	-----	-----*	-----	-----*	-----

Table 51: Comparative Sequences relating to SAG0677

		951			1000
msa235427.2{195_H36B}	ikvvdleair	kaeeahkade	arkaeearka	deahkaeevr	kaeeahkvee
msa235427.2{195_JM9130013}	ikvvdleair	kaeeahkade	arkaeearka	eeahkaeevr	kaeeahkvee
msa235427.2{195_18RS21}	ikvvdlea..	...irkaee	arkaeearka	eeghktqeap	iveegykvnn
msa235427.2{195_2603}	ikvvdleair	kaeearkae	arkaeearka	eeghktqeap	iveegykvnn
msa235427.2{195_A909}	ikvvdleair	kaeeahkade	arkaeearka	eearkaeear	kaeeeghktqe
msa235427.2{195_COH1}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.s.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M732}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.s.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M781}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.s.	s.rst.s.rs	t.s.rst.sr
	Consensus	-----	-----	-----	-----
		1001			1050
msa235427.2{195_H36B}	arkaeeeghkt	qeapiveegy	kvnnvhqtdt	tvkasdlpkt	ktvsavhmar
msa235427.2{195_JM9130013}	ap.s.rgt.n	prstys.rrl	gg.rssn.y	ys.sv.ftkd	.dsfrssyg.
msa235427.2{195_18RS21}	vhqtdttvka	sdlpktktvs	avhmardnk	qitshqthve	-----
msa235427.2{195_2603}	vhqtdttvka	sdlpktktvs	avhmardnk	qitshqthve	kqikntlps
msa235427.2{195_A909}	apiveegykv	nnvhqtdttv	kasdlpktkt	vsavhmard	nkqitshqth
msa235427.2{195_COH1}	rst.s.rgt.	nprstys.rr	lqs.rssn.	yys.sv.ftk	d.dsfrssyg
msa235427.2{195_M732}	rst.s.rgt.	nprstys.rr	lqs.rssn.	yys.sv.ftk	d.dsfrssyg
msa235427.2{195_M781}	rstvklkrdi	kpkkhl.lkk	atklitfikl	ilqlkrllyq	rlrqfpqfiw
	Consensus	-----	-----	-----	-----
		1051		1081	
msa235427.2{195_H36B}	tdnkqitshq	th-----	-----	-----	~
msa235427.2{195_JM9130013}	nrq.tdnfts	dtc-----	-----	-----	~
msa235427.2{195_18RS21}	-----	-----	-----	-----	~
msa235427.2{195_2603}	gdskrgyyit	gmaivmlsvl	fslakkfksk	y	
msa235427.2{195_A909}	vekqikn---	-----	-----	-----	~
msa235427.2{195_COH1}	.nrq.tdnft	sdTC-----	-----	-----	~
msa235427.2{195_M732}	.nrq.tdnft	sdTC.k---	-----	-----	~
msa235427.2{195_M781}	leqtinr.lh	irhml-----	-----	-----	~
	Consensus	-----	-----	-----	~
		-----	*****	*****	*

Table 52: Comparative Sequences relating to SAG 1823

SEQ ID NO. 5201

STRAIN 090

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA
CAATGCTATCACTAAAACAGATAAAAACAACAGAAATTATTTCCAACCAGA
CAACAAGCCAAACTGGGCAAATGTCCTTTTGGAAAACTAACACCAGCA
CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
CGGCGATCAAAAATGCGCTCCTTGATTTGGACAATCCGCGTAGAAGGCG
TTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT
CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
TATTGCCAAATATAAAGATGCTACTCCGGCAGAAATAGAGAAAAACCAA
ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT
TATTTTGACTCACAACAACATCGAGCAAAAATGGATATGATGGCaGCGAA
TGTTGTCAAACAAGAGATACTTTGGCAAGAAATATCGTCTCTGTGTAAG
TGCTCATTGAAGATAAATACTAAATCTAATTGAAAAATTTGGTTGGAGTTATT
GCTTATTGAATCGAGTCAAGCCGAGGCTGCTAATCGTGCAAGCCACTT
ACAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATTA
AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAG
CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC
ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG
GCATGTTACGTCGAAAATACCATTCACAACATGAAACTCTCAATCGCTCAG
TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT
TGTCAACGCTAATAATGCGCATTGCGAGTGTGGCTGAAACTAGTAAAG
AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCTGTTTCTATT
AAATCTGTCACCTAGCTGAAAGCTTAGTGGCTCAAAAATAATGGTATT
TATCGCTGCCATAGACAAGGACGTAAGGAACGTGCCCAATTGGAACTCG
CTGTTATTAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT
AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAA
AGTTGATGAGTCT

SEQ ID NO. 5202

STRAIN A909

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA
CAATGCTATCACTAAAACAGATAAAAACAACAGAAATTATTTCCAACCAGA
CAACAAGCCAAACTGGGCAAATGTCCTTTTGGAAAACTAACACCAGCA
CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
CGGTGACCAAAATGCGCTCCTTGATTTGGACAATCCGCGTAGAAGGCG
TTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT
CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
TATTGCCAAATATAAAGATGCTACTCCGGCAGAAATAGAGAAAAACCAA
ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT
TATTTTGACTCACAACAACATCGAGCAAAAATGGATATGATGGCAGCGAA
TGTTGTCAAACAAGAGATACTTTGGCAAGAAATATCGTCTCTGTGTAAG
TGCTCATTGAAGATAAATACTAAATCTAATTGAAAAATTTGGTTGGAGTTAWT
GCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTT
ACAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATTA
AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAG
CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC
ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAACTTG
GCATGTTACGTCGAAAATACCATTCACAACAATGAAACTCTCAATCGCTCAG
TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT
TGTCAACGCTAATAATGCGCATTGCGAGTGTGGCTGAAACTAGTAAAG
AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCTGTTTCTATT
AAATCTGTCACCTAGCTGAAAGCTTAGTGGCTCAAAAATAATGGTATT
TATCGCTGCCATAGACAAGGACGTAAGGAACGTGCCCAATTAGAACTCG
CTGTTATTAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT
AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAA
AGTTGATGAGTCT

SEQ ID NO. 5203

STRAIN H36B

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC
AATGCTATCACTAAAACAGATAAAAACAACAGAAATTATTTCCAACCAGAC
AACAAGCCAAACTGGGCAAATGTCCTTTTGGAAAACTAACACCAGCAC
AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGTG
GGTGACCAAAATGCGCTCCTTGATTTGGACAATCCGCGTAGAAGGCGT
TAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC
CTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
ATTGCCAAATATAAAGATGCTACTCCGGCAGAAATAGAGAAAAACCAA
CTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTT
ATTTTGACTCACAACAACATCGAGCAAAAATGGATATGATGGCAGCGAAT
GTTGTCAAACAAGAGATACTTTGGCAAGAAATATCGTCTCTGTGAAAT
GCTCATTGAAGATAAATACTAAATCTAATTGAAAAATTTGGTTGGAGTTATTG
CTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
CAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATTA
AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAGC
AACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCA
CAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAACTTGG
CATGTTACGTCGAAAATACCATTCACAACAATGAAACTCTCAATCGCTCAGT
TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
GTCAACGCTAATAATGCGCATTGCGAGTGTGGCTGAAACTAGTAAAGA
AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCTGTTTCTATTAA
AATCTGTCACCTAGCTGAAAGCTTAGTGGCTCAAAAATAATGGTATT
ATCGCTGCCATAGACAAGGACGTAAGGAACGTGCCCAATTAGAACTCTGC

Table 52: Comparative Sequences relating to SAG 1823

TGTTATTAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATa
AAAAATAGTTGAAGCCTTACTCAaCGAAGGTaAATCTACCCAAGAAAA
GTTGATGAGTCT

SEQ ID NO. 5204

STRAIN 18RS21

TTTTGATATTGACCAAATTCAGACAATGCTATCACTAAAACAGATAAAA
CAACAGAAATTAATTTCCAACCAGACAACAAGCCAACTGGGCAAATTGCC
TTTTTTGAAAAAATAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAC
ACCAGCTTTGGTAGATACTTTTGTGGCGATCAAATGCGCTCCTTGATT
TTGGACAATCCGAGTAGAAGCGTTAATACCACCTGTTAATCATATCTTG
CTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC
CGCAGAAATAGAGAAAAAACCAACTTGATTCAAAAATTAATCAAAACA
AGCAAGACCTCGCTACAGGAATTTATTTTGAATCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCGAATGTTGTCAAACAAGAAATACCTTTGG
CAAGAAATATCGTCTCTGCTGAAATGCTCATTGAAGATAATCTAAATCT
ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCTAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA
GCCAAACGCTCCGAGTATCAAATTAAGAATACCAATTAGCTCGAATGACT
GAAGTTATCAATACCTCGAACAGCAACATCCTGAATATGTCAGCCGCTCT
CTACGTTGCAATGGCAACAACACCACAGATGCGAACTTGGTCAAGTAT
GTCAGATATGCGTCAAGAACTTGGCATGTTACGTCGAAATACCAATCCA
ACAAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AGATGCTGGCTGAACTAGTAAAGAAGCGATTCGGATGTTAGAGAAGACC
GCACAAGCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
AGGAACGTGCCCaATTGGAATCTGCTGTATTAAATCGGCTGAAACAATC
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
CGAAGTAAATCTACCCAAGAAAAGTTGATGAGTCT

SEQ ID NO. 5205

STRAIN M732

AGCGATACCTTTAATTTTGATATTGACCAAATTCAGAC
AATGCTATCACTAAAACAGATAAAAACAAGAAATTAATTTCCAACCAGAC
AACAGCCAACTGGGCAAATTCCTTTTGGAAAACTAACACCAGCAC
AAAAGTCTGCTATCTCTGAAAAAACCAGCTTTGGTAGATACTTTTGT
GGTAGCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCGT
TAATACTACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC
CTCAAGTTGATGATTTACTAAAAATGCTAATCGCGAACTAAATGGATTT
ATTGCCAAATATAAAGATGCTACTCCGGCAGAAATAGAGAAAAAACC
CTTGATTCAAATAATTAATCAAACAAGCAAGACCTCGCTACAGGAATTTT
ATTTTGAATCAAAAACATCGAGCAAAAATGGATATGATGGCAGCAAAT
GTTGTCAAACAAGAAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAAT
GCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTG
CTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
CAACAAGAAATTCCTAGCATTAGATAGCCAAACGTCGGAATATCAAATTA
AAGTAACCAATTAGCCCAATGACTGAAGTTATCAATACCTCGAACAGC
ACATACGGAATATGTCAGCCGCTCTACGTTGCTGAGGCAACAACACCA
CAGATGCGAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTGG
TAGTTACGTCGAAATACCAATCCAACAATGAAACTCTCAATCGCTCAGT
TAGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
GTCACCGCTAATAATGTCAGCATTGCAAAATGCTGGCTGAAACTAGTAAAGA
AGCAATTCGATGTTAGAGAAGACCCGCAACAAGCCCACTGTTTCTATTA
AATCTGTCAGTATTAGCTGAAAGCTTAGTGGCTCAAATAATGGTATT
ATCGCTGCCATAGACAAAGGACGTAAGGAACGTCGCCAATTAGAATCTGC
GTTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGCTGATA
AAAAATAGTTGAAGCCTTACTCAACGAAGTAAATCTACCCAAGAAAA
G

SEQ ID NO. 5206

STRAIN COH1

CTAAAACAGATAAAAACAAGAAATTAATTTCCAACCAGACAACAAGCCAA
ACTGGGCAAATTCCTTTTGGAAAACTAACACCAGCACAAAAGTCTGC
TWTCTGAAAAAACCAGCTTTGGTAGATACTTTTGTGGTAGACCAAA
ATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCGTTAATACTACT
GTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGA
TGATTTACTAAAAATGCTAATCGCGAACTAAATGGATTTATTGCCAAAT
ATAAAGATGCTACTCCGGCAGAAATAGAGAAAAAACCAACTTGATTCAA
AAATTAATCAAACAAGCAAGACCTCGCTACAGGAATTTTATTGACTC
ACAAAACATCGAGCAAAAATGGATATGATGGCAGCAAATGTTGTCAAAC
AAGAAGTACTTTGGCAAGAAATATCGTCTGCTGAAATGCTATTGAA
GATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGA
ATCGAGTCAAGCCGAGGCTGCCAATCGTGCAGCCACTTACAACAAGAAA
TTCTAGCaATTAGATAGCCAAACGTCGGAATATCAAATTAAGAATACCA
TTAGCCCGAATGACTGAAATTATCAaTaCCCTPCGAACAGCAACATACGGA
aATGTCAGCCGCTCTACGTTGCTGAGGCAACAACACCAGATGCGAA
ACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTGGTATGTTACGT
CGAAATACCAATCCAACAATGAAACTCTCAATCGCTCAGTTAGGCATGAT
GCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATTGTCAACGCTA
ATAATGAGCATTGCAAAATGCTGGCTGAAACTAGTAAAGAAGCGATTCCG
ATGTTAGAGAAGACCCGCAACAAGCCCACTGTTTCTATTAAATCTGTCAC

Table 52: Comparative Sequences relating to SAG 1823

TGCATTAGCTGAAAAGCTTAGTGGCTCAAATAATGGTATTATCGCTGCCA
TAGACAAAAGGACGTAAGGAACGTGCCCAATTAGAATCTGCTGTATTAAA
TCGGCTGAAAACAATCAATGATTCTGTCAAATTCGTGATAAAAAAATAGT
TGAAGCCTTACTCAaCGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGT
CT

SEQ ID NO. 5207
STRAIN M781

TTTTGATATGACCAAATTCAGACAATGCTATCACTAAAAACAGATAAAA
CAACAGAAATTAATTTCCAACCAGACAACAAGCCAAACTGGGCAAAATGCC
TTTTTTGAAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAC
ACCAGCTTTGGTAGATACTTTTGTGGTACCAAAATGCGCTCCTTGATT
TTGGACAATCCGCAAGTAGAAGGCGTTAATACTACTGTAATCATATCTTG
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTATTGCAAAATATAAGATGCTACTC
CGGCAGAATTAGAGAAAAACCAAACCTTGATTCAAAAATTATCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCAAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATTCGTCTCTGCTGAAATGCTCATGAAGATAAATACTAAATCT
ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCCAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA
GCCAAACGTCGGAATATAAATTAAGTAACCAATTAGCCGAAATGACT
GAAGTTATCAATAACCCCTCGAACAGCAACATACGGAATATGTCAGCCGCT
CTACGTTGATGGGCAACAACACCACAGATGCGAAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAAACTTGGTATGTTACGTCGAAATACCATCCA
ACAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AAATGCTGGCTGAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCACTGTTTCTAATAAATCTGTCACTGCATTAGCTGAAAG
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAGGACGTA
AGGAACGTGCCCAATTAGAATCTGCTGTTATTAATCGGCTGAAACAATC
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5208
STRAIN CJB110

TTTTGATATGACCAAATTCAGACAATGCTATCACTAAAAACAGATAAAA
CAACAGAAATTAATTTCCAACCAGACAACAAGCCAAACTGGGCAAAATGCC
TTTTTTGAAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAC
ACCAGCTTTGGTAGATACTTTTGTGGTACCAAAATGCGCTCCTTGATT
TTGGACAATCCGCAAGTAGAAGGCGTTAATACTACTGTAATCATATCTTG
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTATTGCAAAATATAAGATGCTACTC
CGGCAGAATTAGAGAAAAACCAAACCTTGATTCAAAAATTATCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCGAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATTCGTCTCTGCTGAAATGCTCATGAAGATAAATACTAAATCT
ATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCTAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA
GCCAAACGTCGAGTATCAAATTAAGTAACCAATTAGCTCGAATGACT
GAAGTTATCAATAACCCCTCGAACAGCAACATACGGAATATGTCAGCCGCT
CTACGTTGATGGGCAACAACAACACCACAGATGCGAAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAAACTTGGCATGTTACGTCGAAATACCATCCA
ACAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AGATGCTGGCTGAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCACTGTTTCTAATAAATCTGTCACTGCATTAGCTGAAAG
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAGGACGTA
AGGAACGTGCCCAATTAGAATCTGCTGTTATTAATCGGCTGAAACAATC
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5209
STRAIN 1169NT

GCAGACAATGCTATCACTAAAAACAGATAAAAACAAGAAATTAATTTCCA
CCAGACAACAAGCCAAACTGGGCAAAATGCTTTTTGAAAAACTAACAC
CAGCACAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACT
TTTGTGGTACCAAAATGCGCTCCTTGATTTTGGACAATCCGCAAGTAGA
AGGCGTTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTC
AAATTCCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAAT
GGATTATTGCAAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAAA
ACCAAACCTTGATCCAAAATTAATTCAAACAAGCAAGACCTCACTACAGG
AATTTATTTGACTCACAAAACATCGAGCAAAAATGGATATGATGGCA
CAAAATGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGC
TGAATGCTCATGAAGATAAATACTAAATCTATTGAAAATTTGGTTGGAG
TTATTGCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTCAAGC
CACTTACAACAAGAAATCTAGCATTAGATAGCCAAACCTCCGAGTATCA
AATTAAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCCTCG
AaCAGCAACATACTGAATAATGTCAGCCGCTCTACGTTGCATGGGCAACA
aCACCAAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAA
ACTTGGCATGTTACGTCGAAATACCAATTCACCAAAATGAAACTCTCAATCG
CTCAGTTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGAT
GCTATTGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAG

Table 52: Comparative Sequences relating to SAG 1823

TAAAGAAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTT
CTATTAATCTGTCACTGCATTAGCTGAAAGCTTAGTGCGCTCAAATAAT
GGTATTATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCAATTAGA
ATCTGCTGTTATTAATCGGCTGAAACAAATCAATGATTCTGTCAAATTC
GTGATAAAAAAATAGTTGAGCCTTACTCAACGAAGGTAAATCTACCCAA
GAAAAAGTTGATGAGTCT

SEQ ID NO. 5210

STRAIN JM9130013

AGCGATACCTTTAATTTTGATATTGACCAAATTCAGAC
AATGCTATCACTAAAACAGATAAAAACACAGAAATTTTCCAACCGAC
AACAGCCAAACTGGGCAAAATTCCTTTTTTGA AAAACTAACACCAGCAC
AAAAGTCTGCTATCTCTGAAAAAACACCAAGCTTTGGTAGATACTTTTGT
GGTGACCAAAATCGCTCCTTGTATTTGGACAATCCGACGTAGAAAGCGT
TAATACCACGTGTTAATCAATATCTTGTCTGAGCAGAAAAAATCAAATTC
CTCAAGTTGATGATTACTAAAAATGCTAATCGCGAACTAATGGATTT
ATTGCCAAATATAAAGATGCTACTCCGGCAGAATTAGAGAAAAAACAAA
CTTTGATCAAATAATTAATCAAACAAGCAAGACCTCGCTACAGGAATTTT
ATTTTGA CTCAAAAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT
GTTGTCAAACAAGAAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAAT
GCTCAITGAAGATAATACTAATCTATTGAAAAATTTGGTTGGAGTTAATG
CTTTTATGAAATcGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
CAACAAGAAATCTAGCATTAGATAGCCAAACGTCGGAGTATCAAATTA
AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCCTCGAACAGC
AACATACTGAATATGTAGCGCTCTCTACGTTGATGGCAACAACACCA
CAGATGCGAACTTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTTGG
CATGTTAGCTCGAAATACCAATCAAACAATGAACTCTCAATCGCTCAGT
TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAAT
GTCAACGCTAATAATGACGATGTCAGATGCTGGCTGAAACTAGTAAAGA
AGCGATTCCGATGTTAGAGAAGACCCGCAAAAGCCCCACTGTTTCTATTA
AATCTGTCACTGATTAGCTGAAAGCTTAGTGGCTCAAAAATATGTTAT
ATCGCTGCCATAGACAAAGGACGTAAGGAACGTCGCCAATTAGAATCTGC
TGTATTAAATCCGGCTGAAACAAATCAATGATTCTGTCAAATTCGTTGATA
AAAAAATAGTTGAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA
GTTGATGAGTCT

SEQ ID NO. 5211

STRAIN 2603

agcgatacctttaattttgatattgaccaaattgcagacaatgctatcac
taaaacagataaaaacaacagaaattatccaaccagacaacaagccaaa
ctgggcaaatgcctttttgaaaaactaacaccagcacaagaagtctgct
atctctgaaaaaacaccagctttggtagatactttgtcggcgatcaaaa
tgcgctccttgattttggacaatccgcagtagaaggcgttaataccactg
ttaatcatatctgtctgagcagaaaaaaatccaattcctcaagttgat
gatttactaaaaaatgctaatcggaactaaatggatttattgccaata
taaaagtgctactccggcagaattagagaaaaaaccaacttgatcaaa
aattattcaaacaaagcaagacctcgctacaggaattttattttgactca
caaacatcgagcaaaaaatggatgatggcagcgaatggtgcaaca
agaagatactttggcaagaatatacgtctctgctgaaatgctcattgaag
ataaactaaatctattgaaaatttggttggagtattgctttatttgaa
tcgagtcgaagccgaggtgctaatcgtgcaagccactacaacaagaaat
tctagcatttagatagccaaacgtccgagatcaaataaaagtaaccaat
tagctcgaatgactgaagttatcaataccctcgaacagcaacatcctgaa
tatgtcagcctctctacgttgcatgggcaacaacacacagatgcaaaa
cttgggtcaaaatgctcagatagcgtcagaaacttggcatgttacgtc
gaaataccattccaacaatgaaactctcaatcgctcagttaggcatgatg
caacaatctgtcaaatccgggtgctcactgctgatgctattgtcaacgctaa
taatgcagcattgcagatgctggctgaaactagtaagaagcagattccga
tgtagagaagaccgcacaagccccactgtttctataaatctgtcact
gcattagctgaaagcttagtggctcaaaaataatggattatcgctgccaat
agacaagggacgtaaggaacgtgcccattggaatctgctgttataaat
cggtgaaacaatcaatgatctgtcaaaatctggtgataaaaaaatagtt
gaagccttactcaacgaaggttaactcaccgaagaaaagttgatgagtc
t

PRETTY of: /biotmp/msa13607.2{*} April 22, 2002 03:55 ..

Table with 5 columns: sequence identifier, alignment position 1, alignment position 50, and consensus sequence. Rows include various strain identifiers like msa13607.2{201_COH1} and a final consensus line with asterisks.

Table 52: Comparative Sequences relating to SAG 1823

	51				100
msa13607.2{201_COH1}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_M781}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_090}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_CJB110}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_18RS21}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_2603}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_A909}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_H36B}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_JM9130013}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_1169NT}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_M732}	TAAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
Consensus	*****	*****	*****	*****	*****
	101				150
msa13607.2{201_COH1}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_M781}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_090}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_CJB110}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_18RS21}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_2603}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_A909}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_H36B}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_JM9130013}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_1169NT}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_M732}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
Consensus	*****	*****	*****	*****	*****
	151				200
msa13607.2{201_COH1}	wTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_M781}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_090}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GcGAtCAAAA
msa13607.2{201_CJB110}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GcGAtCAAAA
msa13607.2{201_18RS21}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GcGAtCAAAA
msa13607.2{201_2603}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GcGAtCAAAA
msa13607.2{201_A909}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_H36B}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_JM9130013}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_1169NT}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_M732}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
Consensus	-*****	*****	*****	*****	*-***-*****
	201				250
msa13607.2{201_COH1}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACtACTG
msa13607.2{201_M781}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACtACTG
msa13607.2{201_090}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACcACTG
msa13607.2{201_CJB110}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACcACTG
msa13607.2{201_18RS21}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACcACTG
msa13607.2{201_2603}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACcACTG
msa13607.2{201_A909}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACcACTG
msa13607.2{201_H36B}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACcACTG
msa13607.2{201_JM9130013}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACcACTG
msa13607.2{201_1169NT}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACcACTG
msa13607.2{201_M732}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATACtACTG
Consensus	*****	*****	*****	*****	*****-*****
	251				300
msa13607.2{201_COH1}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_M781}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_090}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_CJB110}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_18RS21}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_2603}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_A909}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_H36B}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_JM9130013}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_1169NT}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
msa13607.2{201_M732}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTC	TCAAGTTGAT
Consensus	*****	*****	*****	*****	*****
	301				350
msa13607.2{201_COH1}	GATTTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M781}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_090}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_CJB110}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_18RS21}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_2603}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_A909}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_H36B}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_JM9130013}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_1169NT}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_M732}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
Consensus	*****	*****	*****	*****	*****
	351				400
msa13607.2{201_COH1}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_M781}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_090}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_CJB110}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_18RS21}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_2603}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_A909}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_H36B}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_JM9130013}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_1169NT}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
msa13607.2{201_M732}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAA
Consensus	*****	*****	*****	*****	*****
	401				450
msa13607.2{201_COH1}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M781}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_090}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_CJB110}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_18RS21}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_2603}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_A909}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_H36B}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_JM9130013}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_1169NT}	AATTATTC	ACAAAGCAAG	ACCTCaCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M732}	AATTATTC	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
Consensus	*****	*****	*****	*****	*****
	451				500
msa13607.2{201_COH1}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M781}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_090}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_CJB110}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_18RS21}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_2603}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_A909}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_H36B}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_JM9130013}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_1169NT}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M732}	CAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
Consensus	*****	*****	*****	*****	*****
	501				550
msa13607.2{201_COH1}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M781}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_090}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_CJB110}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_18RS21}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_2603}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_A909}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_H36B}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_JM9130013}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_1169NT}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M732}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa13607.2{201_COH1}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTA tTGC	TTTTATTGAA
msa13607.2{201_M781}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTA tTGC	TTTTATTGAA
msa13607.2{201_090}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTA tTGC	TTTTATTGAA
msa13607.2{201_CJB110}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTA tTGC	TTTTATTGAA
msa13607.2{201_18RS21}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTA tTGC	TTTTATTGAA

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_2603}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_A909}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAWTGC	TTTTATTGAA
msa13607.2{201_H36B}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_JM9130013}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_1169NT}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M732}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
Consensus	*****	*****	*****	*****-***	*****
	601				650
msa13607.2{201_COH1}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M781}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_090}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_CJB110}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_18RS21}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_2603}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_A909}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_H36B}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_JM9130013}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_1169NT}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M732}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
Consensus	*****	*****	-*****	*****	*****
	651				700
msa13607.2{201_COH1}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_M781}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_090}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_CJB110}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_18RS21}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_2603}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_A909}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_H36B}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_JM9130013}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_1169NT}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
msa13607.2{201_M732}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaA	AGTAACCAAT
Consensus	*****	*****	*****-**	*****	*****
	701				750
msa13607.2{201_COH1}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_M781}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_090}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_CJB110}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_18RS21}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_2603}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_A909}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_H36B}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_JM9130013}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_1169NT}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_M732}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
Consensus	****-*****	*****	*****	*****	****-***
	751				800
msa13607.2{201_COH1}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M781}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_090}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_CJB110}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_18RS21}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_2603}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_A909}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_H36B}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_JM9130013}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_1169NT}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M732}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
Consensus	*****	*****	*****	*****	*****
	801				850
msa13607.2{201_COH1}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_M781}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_090}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_CJB110}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_18RS21}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_2603}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_A909}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_H36B}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aAAACTTGGc	ATGTTACGTC
msa13607.2{201_JM9130013}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aAAACTTGGc	ATGTTACGTC
msa13607.2{201_1169NT}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aAAACTTGGc	ATGTTACGTC
msa13607.2{201_M732}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
Consensus	*****	*****	*****	-*****-	*****
	851				900
msa13607.2{201_COH1}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M781}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_090}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_CJB110}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_18RS21}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_2603}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_A909}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_H36B}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_JM9130013}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_1169NT}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M732}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
Consensus	*****	*****	*****	*****	*****
	901				950
msa13607.2{201_COH1}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M781}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_090}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_CJB110}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_18RS21}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_2603}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_A909}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_H36B}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_JM9130013}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_1169NT}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M732}	CAACAATCTG	TCAAATCCGG	TGTCACTGCT	GATGCTATTG	TCAACGCTAA
Consensus	*****	*****	*****	*****	*****
	951				1000
msa13607.2{201_COH1}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M781}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_090}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_CJB110}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_18RS21}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_2603}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_A909}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_H36B}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_JM9130013}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_1169NT}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M732}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
Consensus	*****	*****-****	*****	*****	*****
	1001				1050
msa13607.2{201_COH1}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M781}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_090}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_CJB110}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_18RS21}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_2603}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_A909}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_H36B}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_JM9130013}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_1169NT}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M732}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa13607.2{201_COH1}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_M781}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_090}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_CJB110}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_18RS21}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_2603}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_A909}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_H36B}	GCATTAtCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_JM9130013}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_1169NT}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M732}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
Consensus	*****-***	*****	*****	*****	*****
	1101				1150
msa13607.2{201_COH1}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M781}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_090}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_CJB110}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_18RS21}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_2603}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_A909}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_H36B}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_JM9130013}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_1169NT}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M732}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
Consensus	*****	*****-****	*****	-*****	*****
	1151				1200
msa13607.2{201_COH1}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M781}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_090}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_CJB110}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_18RS21}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_2603}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_A909}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_H36B}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_JM9130013}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_1169NT}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M732}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa13607.2{201_COH1}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M781}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_090}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_CJB110}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_18RS21}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_2603}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_A909}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_H36B}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_JM9130013}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_1169NT}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M732}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
Consensus	*****	*****	*****	*****	-----
	1251				
msa13607.2{201_COH1}	t				
msa13607.2{201_M781}	t				
msa13607.2{201_090}	t				
msa13607.2{201_CJB110}	t				
msa13607.2{201_18RS21}	t				
msa13607.2{201_2603}	t				
msa13607.2{201_A909}	t				
msa13607.2{201_H36B}	t				
msa13607.2{201_JM9130013}	t				
msa13607.2{201_1169NT}	t				
msa13607.2{201_M732}	-				
Consensus	-				

SEQ ID NO. 5212

STRAIN_090 frame: 1
SDTFNFDIDQIADNAITKTDKTTTEIISNQTTTSQTGQIAFFEKLTTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTIVNHLISEQKKIQIPQVDDLLKQANRELNGFIAKYKDA
TPAELEKPNLQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQEQEILALDSQTSYQIKSNQLARMTEV
INTLEQQHTYVSRLLVAVATTQPMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAI VVANNALQMLAETSKEAI PMLKTAQSPTVSIKSVTALAESLVAQN
NGI IAAIDKGRKERQALES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 52013

STRAIN_A909 frame: 1
SDTFNFDIDQIADNAITKTDKTTTEIISNQTTTSQTGQIAFFEKLTTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTIVNHLISEQKKIQIPQVDDLLKQANRELNGFIAKYKDA
TPAELEKPNLQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM

Table 52: Comparative Sequences relating to SAG 1823

LI EDNTKSIENLVGVXAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVAWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESASVAKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5214

STRAIN H36B frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIKYKDA
TPAELEKKNLQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNI VSAEM
LI EDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVAWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESASVAKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5215

STRAIN 18RS21 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTPAQKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIKYKDATPAEL
EKKPNLQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNI VSAEMLI EDN
TKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHPEYVSRLYVAVAWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESASVAKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5216

STRAIN M732 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIKYKDA
TPAELEKKNLQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNI VSAEM
LI EDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVAWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESASVAKSAETINDSVKIRDKKIVEALLNEGKSTQEK

SEQ ID NO. 5217

STRAIN COH1 frame: 3

KTDKTEIISNQTTCTGTGQIAFFEKLTPAQKSAXSEKTPALVDTFVGDQNALLDGQSAV
EGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIKYKDATPAELEKKNLQKLFK
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNI VSAEMLI EDNTKSIENLVGVIA
FIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV
AWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAVNAN
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ
LESASVAKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5218

STRAIN COH1 frame: 3

KTDKTEIISNQTTCTGTGQIAFFEKLTPAQKSAXSEKTPALVDTFVGDQNALLDGQSAV
EGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIKYKDATPAELEKKNLQKLFK
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNI VSAEMLI EDNTKSIENLVGVIA
FIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV
AWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAVNAN
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ
LESASVAKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5219

STRAIN M781 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTPAQKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIKYKDATPAEL
EKKPNLQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNI VSAEMLI EDN
TKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHTEYVSRLYVAVAWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESASVAKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5220

STRAIN CJB110 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTPAQKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIKYKDATPAEL
EKKPNLQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNI VSAEMLI EDN
TKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHTEYVSRLYVAVAWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLESASVAKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5221

STRAIN 1169NT frame: 1

ADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTPAQKSAISEKTPALVDTFVGDQNALLD
FGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIKYKDATPAELEKKNL
QKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNI VSAEMLI EDNTKSIEN
LVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEY
VSRLYVAVAWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTAD
AVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGR

Table 52: Comparative Sequences relating to SAG 1823

KERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5222
STRAIN JM9130013 frame: 1
SDTFNFDIDQIADNAITKTDKTEIISNQTTSTQGTQIAFFFEKLTTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5223
STRAIN 2603 frame: 1
SDTFNFDIDQIADNAITKTDKTEIISNQTTSTQGTQIAFFFEKLTTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFKQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

PRETTY of: /biotmp/msa28369.2{*} April 22, 2002 04:27 ..

1 50
msa28369.2{201_090} sdtfnfdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_1169NT} ----- -adnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_A909} sdtfnfdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_JM9130013} sdtfnfdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_COH1} -----KTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_CJB110} -----fdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_M781} -----fdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_2603} sdtfnfdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_H36B} sdtfnfdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_18RS21} -----fdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
msa28369.2{201_M732} sdtfnfdidq iadnaitKTD KTEIISNQTTSTQGTQIAFF EKLTPAQKSA
Consensus -----*****

51 100
msa28369.2{201_090} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_1169NT} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_A909} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_JM9130013} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_COH1} xSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_CJB110} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_M781} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_2603} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_H36B} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_18RS21} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
msa28369.2{201_M732} iSEKTPALVD TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVD
Consensus -*****

101 150
msa28369.2{201_090} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_1169NT} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_A909} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_JM9130013} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_COH1} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_CJB110} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_M781} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_2603} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_H36B} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_18RS21} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
msa28369.2{201_M732} DLLKKNANREL NGFIAKYKDA TPAELEKKPNLIQKLFKQSKTSLQEFYFDS
Consensus *****

151 200
msa28369.2{201_090} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE
msa28369.2{201_1169NT} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE
msa28369.2{201_A909} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE
msa28369.2{201_JM9130013} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE
msa28369.2{201_COH1} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE
msa28369.2{201_CJB110} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE
msa28369.2{201_M781} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE
msa28369.2{201_2603} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE
msa28369.2{201_H36B} QNIEQKMDMM AANVVKQEDTLARNIVSAEM LIEDNTKSIENLVGVIAFIE

Table 52: Comparative Sequences relating to SAG 1823

msa28369.2{201_18RS21}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M732}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
Consensus	*****	*****	*****	*****	*****-****
201					
msa28369.2{201_090}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_1169NT}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_A909}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_JM9130013}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_COH1}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_CJB110}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M781}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_2603}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHpe
msa28369.2{201_H36B}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_18RS21}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHpe
msa28369.2{201_M732}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
Consensus	*****	*****	*****	*****	*****-_*
251					
msa28369.2{201_090}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_1169NT}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_A909}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_JM9130013}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_COH1}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_CJB110}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_M781}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_2603}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_H36B}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_18RS21}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
msa28369.2{201_M732}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLSTIAQLGMM
Consensus	*****	*****	*****	*****	*****
301					
msa28369.2{201_090}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_1169NT}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_A909}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_JM9130013}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_COH1}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_CJB110}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M781}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_2603}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_H36B}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_18RS21}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M732}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
Consensus	*****	*****	*****	*****	*****
351					
msa28369.2{201_090}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_1169NT}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_A909}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_JM9130013}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_COH1}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_CJB110}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M781}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_2603}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_H36B}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_18RS21}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M732}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
Consensus	**-*****	*****	*****	*****	*****
401					
msa28369.2{201_090}	EALLNEGKST	QEKvdes			
msa28369.2{201_1169NT}	EALLNEGKST	QEKvdes			
msa28369.2{201_A909}	EALLNEGKST	QEKvdes			
msa28369.2{201_JM9130013}	EALLNEGKST	QEKvdes			
msa28369.2{201_COH1}	EALLNEGKST	QEKvdes			
msa28369.2{201_CJB110}	EALLNEGKST	QEKvdes			
msa28369.2{201_M781}	EALLNEGKST	QEKvdes			
msa28369.2{201_2603}	EALLNEGKST	QEKvdes			
msa28369.2{201_H36B}	EALLNEGKST	QEKvdes			
msa28369.2{201_18RS21}	EALLNEGKST	QEKvdes			
msa28369.2{201_M732}	EALLNEGKST	QEKvdes			
Consensus	*****	***----			

Table 53: Comparative Sequences relating to SAG 0755

SEQ ID NO. 5301

STRAIN 2603

acaaaactttgaaaaaagaattagttgaagctaaaaagacaattccatc
cgtaaaagcttcaaaagtaccgcaaaaatcaacatcatcgaaagataaag
agtttggtcttaaacgattatcgatgtctctgggtggcaacttccaaag
gagattgat tacgatacgccttcaaaaaatattcagggtgtgttatctg
tgtctttgggtggatcaaagatctcaagactaataacgcgtcttatcaaa
ctggaaatcgataaaatcgtttaagaccatatacaagaattcaaaaagcga
aatatcccagtagctgtctacagttatgcacttgggttcaagtggttaaga
aatgaaagaagaggctcagatattttataagaatgcagctccttacaaac
caactttttattggattgacgtagaagaggagacaatgtctaacatgaat
aaaggtgtccaagcattccgaaaagaattaaaaagacttgggtgctaaaaa
tggttggtatctacatgggtacttactttatgactgagcaaggcatctctg
taaaaaggatttgacgctgtttggattccaacttatggtagcgtatctgga
tactatgaagcggctccgcaaaactgaacttaaatcagatttacaccaata
cacctctcaaggttatctaccaggawtcaatcaaccgcttgatttaaatc
aaatgcagttataaagacaagaagaaaacttatgagaactttttgga
aaagtaaaaagag

SEQ ID NO. 5302

STRAIN 090

ACAAATACTTTGAAAAAGAATTAG
TTGAAGCTAAAAAGACAATCCATCCGTAAAAGCTTCAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA
TGTCTCTGGTTGGCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTT CAGGTGTGTGTATTCTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACCGCTGCTTATACAACTGGAATCGATAAAATCGTTAAGAC
CCATATCAAAGAAATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTT
ATGCACCTTGGTTCAAGTGTAAAGAAAATGAAAGAAGAGGCTCAGATATTT
TATAAGAATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG
AATTA AAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTA AAAAGGATTGACGCTGTTGGAT
TCCAACCTTATGGTAGCGAATTCTGGATACTATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTAAATCAAATTCAGTTAATAAAGACAAGAA
GAAAACCTTATGAGAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5303

STRAIN A909

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAAA
AGACAATTCATCCGTAAAAGCTTCAAAGTACCGCAAAATCAACATCA
TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTG
GCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAA AAAATATTT CAG
GTGTGTATTATCTGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAAC
GCTGCTTATACAACTGGAATCGATAAAATCGTTAAGACCCATATCAAAGA
ATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCATTTGGTT
CAAGTGTAAAGAAAATGAAAGAAGAGGCTCAGATATTTTATAAGAATGCA
GCCTCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAAT
GTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAATTA AAAAGAC
TTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAG
CAAGGCATCTCTGTA AAAAGGATTGACGCTGTTGGATTCCAACCTTATGG
TAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACTTAAATACG
ATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTC AATCAACCG
CTTGATTAAATCAAATTCAGTTAATAAAGACAAGAAGAAAACCTTATGA
GAAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5304

STRAIN H36B

ACAAATACTTTGAAAAAGAATTAG
TTGAAGCTAAAAAGACAATCCATCCGTAAAAGCTTCAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA
TGTCTCTGGTTGGCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTT CAGGTGTGTGTATTCTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACCGCTGCTTATACAACTGGAATCGATAAAATCGTTAAGAC
CCATATCAAAGAATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTT
ATGCACCTTGGTTCAAGTGTAAAGAAAATGAAAGAAGAGGCTCAGATATTT
TATAAGAATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG
AATTA AAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTA AAAAGGATTGACGCTGTTGGAT
TCCAACCTTATGGTAGCGAATTCTGGATACTATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTAAATCAAATTCAGTTAATAAAGACAAGAA
GAAAACCTTATGAGAACTTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5305

STRAIN 18RS21

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAAA
GACAATTCATCCGTAAAAGCTTCAAAGTACCGCAAAATCAACATCAT
CGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTGG
CAACTTCTTAAGGAGATTGATTACGATACGCTTTCAA AAAATATTT CAGG
TGTTGTATTCTGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAACG

Table 53: Comparative Sequences relating to SAG 0755

CTGCTTATACAACCTGGAATFCGATAAATCGTTTAAAGACCCATATCAAAGAA
TTTCAAAGCGAAATATCCCAGTAGCTGTCTACAGTTATGCACCTGGTTC
AAGTGTAAAGAAATGAAGAAGAGGGCTCAGATAATTTATAAGAAATGCAG
CTCCTTACAACCAACTTTTATTTGGATTGACGTAGAAGAGGAGACAATG
TCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAATTAAGAACT
TGGTGTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAGC
AAGGCATCTCTGTAAGAGGATTTGACGCTGTTGGATTCCAACCTTATGGT
AGCGAATCTCGGATACTATGAAGCGGCTCCGCAAACTGAACCTAATACGA
TTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGC
TTGATTTAAATCAAATGCAGTTAATAAAGACAAGAAGAAAACCTATGAG
AAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5306
STRAIN M732

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA
AAGACAATCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC
ATCGAAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT
GGCAACTTCCTAAGGAGATTGATTACGATACGCTTCAA AAAATATTTCA
GGTGTGTTTATTTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAA
CGCTGCTTATACAACCTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG
AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACCTTGGT
TCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAATGC
AGCTCCTTACAAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA
TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAGA
CTTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA
GCAAGGTATCTCTGTAAAAGGATTTGACGCTGTTGGATTCCAACCTTATG
GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACCTAAATAC
GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC
GCTTGATTTAAATCAAATGCAGTTAATAAAGACAAGAAGAAAACCTTATG
AGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5307
STRAIN COH1

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA
AGACAATCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATCA
TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTG
GCAACTTCCTAAGGAGATTGATTACGATACGCTTCAA AAAATATTTCA
GTGTTGTTATTTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAAC
GCTGCTTATACAACCTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGA
AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACCTTGGTT
CAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAATGCA
GCTCCTTACAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAT
GTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAGAC
TTGGTGTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAG
CAAGGTATCTCTGTAAAAGGATTTGACGCTGTTGGATTCCAACCTTATGG
TAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACCTAATACG
AATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG
CTTGATTTAAATCAAATGCAGTTAATAAAGACAAGAAGAAAACCTTATGA
GAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5308
STRAIN M781

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA
AAGACAATCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC
ATCGAAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT
GGCAACTTCCTAAGGAGATTGATTACGATACGCTTCAA AAAATATTTCA
GGTGTGTTTATTTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAA
CGCTGCTTATACAACCTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG
AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACCTTGGT
TCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAATGC
AGCTCCTTACAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA
TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAGA
CTTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA
GCAAGGTATCTCTGTAAAAGGATTTGACGCTGTTGGATTCCAACCTTATG
GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACCTAATAC
GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC
GCTTGATTTAAATCAAATGCAGTTAATAAAGACAAGAAGAAAACCTTATG
AGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5309
STRAIN CJB110

AAATACTTTGAAAAAGAATTAGTTGAAGCTAAAAGACAATCCATCCG
TAAAAGCTTCAAAGTACCGCAAAAATCAACATCATCGAAAAGATAAAGAG
TTTGTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCCTAAGGA
GATTTGATTACGATACGCTTCAA AAAATATTTCAAGGTGTTGTTATTTCGTG
TCTTTGGTGGATCAAAGATATCTAAGACTAATAACGCTGCTTATACAACCT
GGAATCGATAAATCGTTTAAAGACCCATATCAAAGAAATTTCAAAGCGAAA
TATCCAGTAGCTGTCTACAGTTATGCACCTTGGTTCAAGTGTAAAGAAA
TGAAGAAGAGGCTCAGATATTTATAAGAATGCAGCTTCTTACAACCA
ACTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATGAATAA
AGGTCTCCAGCATTCGAAAAGAATTAAGAAGACTTGGTGTAAAAATG
TTGGTATCTACATTTGGTACTTACTTTATGACTGAGCAAGGCATCTCTGTA
AAAGGATTTGACGCTGTTGGATTCCAACCTTATGGTAGCGATTCTGGATA

Table 53: Comparative Sequences relating to SAG 0755

CTATGAAGCGGCTCCGCAAACTGAACTTAAATACGATTTACACCAATACA
CCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAAATCAA
ATTACAGTTAATAAAGACAAGAAGAAAACCTTATGAGAAAACTTTTGGAAA
AGTAAAAGAG

SEQ ID NO. 5310

STRAIN 1169NT

ACAAATACTTTGAAAAAGAATTAGTTGAAAGCTAAAAAGACAATTCC
ATCCGTAAGCTTCAAAGTACCGCAAAAATCAACATCATCGAAAGATA
AAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTGGCACTTCCCT
AAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCAAGTGTGTTAT
TCGTGTCTTTGGTGGATCAAGATATCTAAGACTAATAACGCTGCTTATA
CAACTGGAATCGATAAATCCTTTAAGACCATATCAAGAATTTCAAAAG
CGAAATATCCAGTAGCTGTCTACAGTTATGCCTTTGGTTCAAGTGTAA
AGAAATGAAAGAAGAGGCTCAGATATTTATAAGAAATGCAGCTCCTTACA
AACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAATGCTTAAACATG
AATAAAGGTGTCGAAGCATTCCGAAAAGAATTAAAAAGACTTGGCGCTAA
AAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAGCAAGGTATCT
CTGTAAAAGGATTTGACGCTGTTTGGATTCCAACCTATGGTAGCGATTCT
GGATACATGAAAGCAGCTCCGCAAACTGAACTTAAATACGATTTACACCA
ATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAA
ATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATGAGAAAACTTTT
GGAAAAGTAAAAGAG

SEQ ID NO. 5311

STRAIN JM9130013

ACAAATACTTTGAAAAAGAATTAG
TTGAAAGCTAAAAAGACAATTCCATCCGTAAGCTTCAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA
TGTCTCTGGTTGGCACTTCTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTTCAAGTGTGTTATTCTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGC
CCATATCAAAGAATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTT
ATGCACCTGGTTCAAGTGTAAAGAAATGAAAAGAAGAGGCTCAGATATTT
TATAAGAAATGCAGCTCCTTACAAACCACTTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCGAAGCATTCCGAAAAG
AATTAATAAGACTTGGTGTCTAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTAAGGATTTGACGCTGTTTGGAT
TCCAACCTATGGTAGCGATTCTGATACTATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAA
GAAAACCTTATGAGAAAACTTTTGGAAAAGTAAAAGAG

PRETTY of: /biotmp/msa21441.2{*} January 20, 2003 03:46 ...

msa21441.2{206_090} 1 acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC 50
msa21441.2{206_18RS21} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_2603} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_A909} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_H36B} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_JM9130013} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_CJB110} --AAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_COH1} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_M732} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_M781} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
msa21441.2{206_1169NT} acAAATACTT TGAAAAAGA ATTAGTTGAA GCTAAAAAGA CAATCCATC
Consensus --*****

msa21441.2{206_090} 51 CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG 100
msa21441.2{206_18RS21} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_2603} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_A909} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_H36B} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_JM9130013} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_CJB110} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_COH1} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_M732} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_M781} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
msa21441.2{206_1169NT} CGTAAAAGCT TCAAAGTAC CGCAAAAATC AACATCATCG AAAGATAAAG
Consensus *****

msa21441.2{206_090} 101 AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG 150
msa21441.2{206_18RS21} AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
msa21441.2{206_2603} AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
msa21441.2{206_A909} AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
msa21441.2{206_H36B} AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
msa21441.2{206_JM9130013} AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
msa21441.2{206_CJB110} AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
msa21441.2{206_COH1} AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG
msa21441.2{206_M732} AGTTTGTCT TAAACCGATT ATCGATGTCT CTGGTTGGCA ACTTCCTAAG

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M781}	AGTTTGTCT	TAAACCGATT	ATCGATGCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_1169NT}	AGTTTGTCT	TAAACCGATT	ATCGATGCT	CTGGTTGGCA	ACTTCCTAAG
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_18RS21}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_2603}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_A909}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_H36B}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_JM9130013}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_CJB110}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_COH1}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_M732}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_M781}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
msa21441.2{206_1169NT}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTCAGGTG	TTGTTATTCC
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_18RS21}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_2603}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_A909}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_H36B}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_JM9130013}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_CJB110}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_COH1}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_M732}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_M781}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_1169NT}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
Consensus	*-*****	*****	*****	*****	*****
msa21441.2{206_090}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_18RS21}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_2603}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_A909}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_H36B}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_JM9130013}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_CJB110}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_COH1}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_M732}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_M781}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
msa21441.2{206_1169NT}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATF	TCAAAAGCGA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_18RS21}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_2603}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_A909}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_H36B}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_JM9130013}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_CJB110}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_COH1}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_M732}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_M781}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_1169NT}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_18RS21}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_2603}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_A909}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_H36B}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_JM9130013}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_CJB110}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_COH1}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_M732}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_M781}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_1169NT}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_18RS21}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_2603}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_A909}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_H36B}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_JM9130013}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_CJB110}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_COH1}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M732}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_M781}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_1169NT}	CAACTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
Consensus	*****	*****	*****	*****	*****
	451				500
msa21441.2{206_090}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_18RS21}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_2603}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_A909}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_H36B}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_JM9130013}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_CJB110}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_COH1}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_M732}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_M781}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_1169NT}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GcGCTAAAAA
Consensus	*****	*****	*****_***	*****	*_*****
	501				550
msa21441.2{206_090}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_18RS21}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_2603}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_A909}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_H36B}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_JM9130013}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_CJB110}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_COH1}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_M732}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_M781}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_1169NT}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
Consensus	*****	*****_****	*****	*****	**_*****
	551				600
msa21441.2{206_090}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_18RS21}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_2603}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_A909}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_H36B}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_JM9130013}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_CJB110}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_COH1}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_M732}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_M781}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_1169NT}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
Consensus	*****	*****	*****	*****	*****
	601				650
msa21441.2{206_090}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_18RS21}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_2603}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_A909}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_H36B}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_JM9130013}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_CJB110}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_COH1}	TACTATGAAG	CaGCTCCaCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_M732}	TACTATGAAG	CaGCTCCaCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_M781}	TACTATGAAG	CaGCTCCaCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_1169NT}	TACTATGAAG	CaGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
Consensus	*****	*_*****_**	*****	*****	*****
	651				700
msa21441.2{206_090}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_18RS21}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_2603}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_A909}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_H36B}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_JM9130013}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_CJB110}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_COH1}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_M732}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_M781}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
msa21441.2{206_1169NT}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTTAAATC
Consensus	*****	*****	*****_****	*****	*****
	701				750
msa21441.2{206_090}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_18RS21}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_2603}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_A909}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_H36B}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_JM9130013}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_CJB110}	AAATTaCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_COH1}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACITTTTGGG
msa21441.2{206_M732}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACITTTTGGG
msa21441.2{206_M781}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACITTTTGGG
msa21441.2{206_1169NT}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACITTTTGGG
Consensus	*****-**** ***** **
	751 762
msa21441.2{206_090}	AAAGTAAAAG AG
msa21441.2{206_18RS21}	AAAGTAAAAG AG
msa21441.2{206_2603}	AAAGTAAAAG AG
msa21441.2{206_A909}	AAAGTAAAAG AG
msa21441.2{206_H36B}	AAAGTAAAAG AG
msa21441.2{206_JM9130013}	AAAGTAAAAG AG
msa21441.2{206_CJB110}	AAAGTAAAAG AG
msa21441.2{206_COH1}	AAAGTAAAAG AG
msa21441.2{206_M732}	AAAGTAAAAG AG
msa21441.2{206_M781}	AAAGTAAAAG AG
msa21441.2{206_1169NT}	AAAGTAAAAG AG
Consensus	***** **

SEQ ID NO. 5312

STRAIN 2603 frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVFLKPI IDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHI KEFQKRNI PVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAQFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHQQYTSQGYLPGFNQPLDLNQLI AVNKG
KKKTYEKLFGKVKE

SEQ ID NO. 5313

STRAIN 090 frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVFLKPI IDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHI KEFQKRNI PVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAQFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHQQYTSQGYLPGFNQPLDLNQLI AVNKG
KKKTYEKLFGKVKE

SEQ ID NO. 5314

STRAIN A909 frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVFLKPI IDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHI KEFQKRNI PVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAQFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHQQYTSQGYLPGFNQPLDLNQLI AVNKG
KKKTYEKLFGKVKE

SEQ ID NO. 5315

STRAIN H36B frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVFLKPI IDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHI KEFQKRNI PVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAQFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHQQYTSQGYLPGFNQPLDLNQLI AVNKG
KKKTYEKLFGKVKE

SEQ ID NO. 5316

STRAIN 18RS21 frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVFLKPI IDVSGWQLPKEIDYDTLSKN
ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHI KEFQKRNI PVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAQFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHQQYTSQGYLPGFNQPLDLNQLI AVNKG
KKKTYEKLFGKVKE

SEQ ID NO. 5317

STRAIN M732 frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVFLKPI IDVSGWQLPKEIDYDTLSKN
ISGVVIRIFGGSKI SKTNNAAYTTGIDKSFKTHI KEFQKRNI PVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAQFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHQQYTSQGYLPGFNQPLDLNQLI AVNKG
KKKTYEKLFGKVKE

SEQ ID NO. 5318

STRAIN COH1 frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVFLKPI IDVSGWQLPKEIDYDTLSKN
ISGVVIRIFGGSKI SKTNNAAYTTGIDKSFKTHI KEFQKRNI PVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAQFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHQQYTSQGYLPGFNQPLDLNQLI AVNKG
KKKTYEKLFGKVKE

SEQ ID NO. 5319

STRAIN M781 frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVFLKPI IDVSGWQLPKEIDYDTLSKN
ISGVVIRIFGGSKI SKTNNAAYTTGIDKSFKTHI KEFQKRNI PVAVYSYALGSSVKEMKE
EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAQFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHQQYTSQGYLPGFNQPLDLNQLI AVNKG
KKKTYEKLFGKVKE

Table 53: Comparative Sequences relating to SAG 0755

SEQ ID NO. 5320
STRAIN CJB110 frame: 2
NTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVLPKI IDVSGWQLPKEIDYDTLSKNI
ISGVVIRVFGGSKISKTNNAAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKEE
AQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGI YIGTYFMTEQG
ISVKGDFDAVWIPTYGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQTIVNKDK
KKTYEKLFGKVKE

SEQ ID NO. 5321
STRAIN 1169NT frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVLPKI IDVSGWQLPKEIDYDTLSKNI
ISGVVIRVFGGSKISKTNNAAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKEE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGI YIGTYFMTEQ
GISVKGDFDAVWIPTYGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQTIVNKDK
KKTYEKLFGKVKE

SEQ ID NO. 5322
STRAIN JM9130013 frame: 1
TNTLKKELVEAKKTI PSVKASKVPQKSTSSKDKFVLPKI IDVSGWQLPKEIDYDTLSKNI
ISGVVIRVFGGSKISKTNNAAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKEE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGI YIGTYFMTEQ
GISVKGDFDAVWIPTYGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQTIVNKDK
KKTYEKLFGKVKE

PRETTY of: /biotmp/msa21641.2{*} January 20, 2003 03:59 ..

1 50
msa21641.2{206_090} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_1169NT} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_18RS21} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_2603} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_A909} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_H36B} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_JM9130013} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_COH1} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_M732} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_M781} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
msa21641.2{206_CJB110} tNTLKKELVE AKKTIPSVKA SKVPQKSTSS KDKEFVLPKI IDVSGWQLPK
Consensus -*****

51 100
msa21641.2{206_090} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_1169NT} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_18RS21} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_2603} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_A909} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_H36B} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_JM9130013} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_COH1} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_M732} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_M781} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
msa21641.2{206_CJB110} EIDYDTLSKN ISGVVIRvFG GSKISKTNNA AYTGTIDKSF KTHIKEFQKR
Consensus *****

101 150
msa21641.2{206_090} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_1169NT} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_18RS21} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_2603} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_A909} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_H36B} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_JM9130013} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_COH1} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_M732} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_M781} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
msa21641.2{206_CJB110} NIPVAVYSYA LGSSVKEMKE EAQIFYKNAA PYKPTFYWID VEEETMSNMN
Consensus *****

151 200
msa21641.2{206_090} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_1169NT} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_18RS21} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_2603} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_A909} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_H36B} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_JM9130013} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_COH1} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_M732} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_M781} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
msa21641.2{206_CJB110} KGVQAFRKEL KRLGAKNVGI YIGTYFMTEQ GISVKGDFDAV WIPTYGSDSG
Consensus *****

Table 53: Comparative Sequences relating to SAG 0755

	201			250	
msa21641.2{206_090}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_1169NT}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_18RS21}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_2603}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGxNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_A909}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_H36B}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_JM9130013}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_COH1}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_M732}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_M781}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
msa21641.2{206_CJB110}	YYEAAPQTEL	KYDLHQYTSQ	GYLPGFNQPL	DLNQIaVNKD	KKKTYEKLFG
Consensus	*****	*****	*****	*****	*****
	251				
msa21641.2{206_090}	KVKE				
msa21641.2{206_1169NT}	KVKE				
msa21641.2{206_18RS21}	KVKE				
msa21641.2{206_2603}	KVKE				
msa21641.2{206_A909}	KVKE				
msa21641.2{206_H36B}	KVKE				
msa21641.2{206_JM9130013}	KVKE				
msa21641.2{206_COH1}	KVKE				
msa21641.2{206_M732}	KVKE				
msa21641.2{206_M781}	KVKE				
msa21641.2{206_CJB110}	KVKE				
Consensus	****				

Table 54: Comparative Sequences relating to SAG0949

SEQ ID NO. 5401
 STRAIN 2603
 TTGACTCACAAAAATATATTATTAACCATTATATTGGATTATTT
 ATGATTATATTTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATAATTGG
 GAACATTATCAAAGGAAAAGAAAATTAATCTATTGGATTGATAATACTTTTGTCCATG
 GGATTGAAAGTCGTTCTGGTGACTATACCGGCTTGATATTGATTTAGCTAATGCTGTT
 TTTAAGAATAACGGTATTTCAGTGAATGGCAGCCTATTAACGGGATATGAAAGAACT
 GAACTTAATAATGGTAAATAGACCTTATTGGAAATGGTTATTCAAAAACGGCAGAACGT
 GCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTTGTTACTAAA
 ACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG
 GGTTTATCTGGTTTGGATGCTTTAAACGCTAAACCTGATATTTTAAAAAAGTTTGTAAAA
 GGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGCTTTGATTTGATTTAAAAATAAC
 CGTATTGATGGTCTTTTGGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGA
 AATAATAAAGCTTATTAATTTGTTAAACCTGCTTATCAAGGAGAAAAATTTGTAGTAGGA
 GCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAAACAGCTTCAT
 AATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGTTTATAGTAAA
 GAA

SEQ ID NO. 5402
 STRAIN 090
 ATTGGGaaCATTATC
 AAAAGGAAAAGAAAATTAATCTATTGGATTGATAACTTTTTGTTCCTATG
 GGATTGAAAGCCGTTCTGGTGACTATACCGGCTTGATATTGATTTAGC
 TAATGCTGTTTTTAAAGAATACGGTATTTCAGTGAATGGCAGCCTATA
 ACTGGGATATGAAAGAACTGAACCTTAATAATGGTAAATAGACCTTATT
 TGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTTAC
 AAACCCATATATGAATAATCATCAAGTAATTTGTTACTAAAACCTCATCAC
 ATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG
 GGTTTATCTGGTTTTGATGCTTTTAAATGCTAAACCTGATATTTTAAAAA
 GTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGCTT
 TGATTGATTTAAAAATAACCGTATTGATGGTCTTTTGGATTGATGAAGTT
 TAGCTAACTATTATTTAAAGCAAGAAGGAATATAAAAAGCTTATTAATTT
 TGTAAAACCTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGCAAAG
 TTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAAACAGCTTCAT
 AATAAGGAAAATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGT
 TTATAGTAAAGAA

SEQ ID NO. 5403
 STRAIN A909
 ATTGGG
 aACATTATCAAAGGAAAAGAAAATTAATCTATTGGATTGATAACTTTTT
 GTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATAT
 TGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTGAATGGC
 AGCCTATAAATCGGATATGAAAGAACTGAACCTTAATAATGGTAAATATA
 GAACCTTATTGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGT
 CGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTTGTTACTAAAA
 CTTTCATCACATATTAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGA
 GCCAGTCGGGTTTCACTCTGGTTTTGATGCTTTTAAACGCTAAACCTGATAT
 TTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATACCTTCA
 CTAAGGCTTTGATTGATTTAAAAATAACCGTATTGATGGTCTTTTGGATT
 GATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAATATAAAAAGC
 TTATTATTTTGTAAAACCTGCTTATCAAGGAGAAAAATTTGTAGTAGGAG
 CTCGTAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAA
 CAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGG
 TGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5404
 STRAIN H36B
 ATTGGGAACATTATCAAAGGAAAAGAAAATTAATCTATTGGATT
 TGATAACTTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATA
 CCGGCTTTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATT
 TCAGTGAATGGCAGCCTATAAATCGGATATGAAAGAACTGAACCTAA
 TAATGGTAAATAGACCTTATTGGAAATGGTTATTCAAAAACGGCAGAAC
 GTGCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTA
 ATTGTTACTAAAACCTCATCACATATTAATAGTATTAAAGGATATGAAGGG
 GAAAAAATAGGAGCCAGTCGGGTTTCACTCTGGTTTTGATGCTTTTAAACG
 CTAACCTGATATTTTAAAAAAGTTTGTAAAAGGAAAAGAAGCAGTTCAA
 TACGATACCTTCACTCAGGCTTTGATTGATTTAAAAATAACCGTATTGA
 TGGTCTTTTGGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAG
 GAAATATAAAAAGCTTATTAATTTGTTAAAACCTGCTTATCAAGGAGAAAAT
 TTTGTAGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAACAAAGCTTTCAA
 CAAAGCTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTT
 ACAATGGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5405
 STRAIN 18RS21
 ATTGGGAACATTA
 TCAAAGGAAAAGAAAATTAATCTATTGGATTGATAACTTTTTGTTCCTA
 TGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTGATATTGATTTA
 GCTAATGCTGTTTTTAAAGAATACGGTATTTCAGTGAATGGCAGCCTAT
 TAACCTGGGATATGAAAGAACTGAACCTTAATAATGGTAAATAGACCTTA
 TTTGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTT
 ACAACCCATATATGAATAATCATCAAGTAATTTGTTACTAAAACCTTCAT

Table 54: Comparative Sequences relating to SAG0949

ACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCAGT
CGGGTTCATCTGGTTTTGATGCTTTAACGCTAAACCTGATATTTAAAA
AAGTTTGTAAAAGGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGC
TTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTGATTTGATGAAG
TTTATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAAGCTTATTAT
TTTGTAAAACCTGCTTATCAAGGAGAAAATTTTGTAGTAGGAGCTCGTAA
AGTTGATCGTAGACTAATTGAAAAGATTACAAAGCTTTCAAACAGCTTC
ATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGAT
GTTTATAGTAAAGAA

SEQ ID NO. 5406

STRAIN M732

ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAA
TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
TTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG
TAATATAGACCTTATTGGAAATGGTTATTCAAACCGGCAGAACCGTGCTA
AAAAGTCGCTTTTACAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAA
ACTAGGAGCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAAC
CTGATATTTTAAAAAAGTTTTGTAAGGAAAAGAAGCAGTTCAATACGAT
ACTTTCACTCAGGCTTTGATTTGATTTAAAAAATAACCGTATTGATGGTCT
TTTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATA
TAAAAGCTTATTATTTTGTAAAACCTGCTTATCAAGGAGAAAATTTTGT
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGC
TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5407

STRAIN COH1

ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAA
TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
TTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG
TAATATAGACCTTATTGGAAATGGTTATTCAAACCGGCAGAACCGTGCTA
AAAAGTCGCTTTTACAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAA
ACTAGGAGCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAAC
CTGATATTTTAAAAAAGTTTTGTAAGGAAAAGAAGCAGTTCAATACGAT
ACTTTCACTCAGGCTTTGATTTGATTTAAAAAATAACCGTATTGATGGTCT
TTTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATA
TAAAAGCTTATTATTTTGTAAAACCTGCTTATCAAGGAGAAAATTTTGT
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGC
TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5408

STRAIN M781

ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAA
ATACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
TTTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG
GAAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG
GTAATATAGACCTTATTGGAAATGGTTATTCAAACCGGCAGAACCGTGCT
AAAAGTCGCTTTTACAACCCATATATGAATAATCATCAAGTAATTGTT
TACTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAA
AACTAGGAGCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAA
CCTGATATTTTAAAAAAGTTTTGTAAGGAAAAGAAGCAGTTCAATACGA
TACTTTCACTCAGGCTTTGATTTGATTTAAAAAATAACCGTATTGATGGTCT
TTTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAAT
ATAAAAAGCTTATTATTTTGTAAAACCTGCTTATCAAGGAGAAAATTTTGT
AGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGC
CTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAA
TGGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5409

STRAIN CJB110

ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAA
ACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTT
TGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG
AATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGGT
AATAATAGACCTTATTGGAAATGGTTATTCAAACCGGCAGAACCGTGCTAA
AAAAGTCGCTTTTACAACCCATATATGAATAATCATCAAGTAATTGTTA
CTAAAACCTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAA
CTAGGAGCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAACC
TGATATTTTAAAAAAGTTTTGTAAGGAAAAGAAGCAGTTCAATACGATA
CTTTCACTCAGGCTTTGATTTGATTTAAAAAATAACCGTATTGATGGTCTT
TTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATAT
AAAAGCTTATTATTTTGTAAAACCTGCTTATCAAGGAGAAAATTTTGT
TAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGCT
TTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATG
GTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5410

Table 54: Comparative Sequences relating to SAG0949

STRAIN 1169NT
ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAA
TACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT
TTGATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCAAGTG
AAATGGCAGCCTATTAACTGGGATATGAAAAGAACTGAACTCAATAATGG
TAATATAGACCTTATTTGGAATGGTTATTCAAACCGGCAGAACGTCGTA
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAAACCTCATCACATATTAAATAGTATTAAGGATATGAAGGGGAAAAA
ACTAGGAGCCAGTCGGTTTCATCTGGTTTTGATGCTTTTAAAGTCAAAC
CTGACATTTTAAAAAAGTTTGTAAAAGGAAAAGAACGAGTTCATACAGAT
ACTTTCACTCAGGCTTTGATTTGATTTAAAAAATAACCGTATTGATGGTCT
TTTGATTTGATGAAGTTTATGCTAACATTTTAAAGCAAGAAGGAAATA
TAAAAGCTTATTATTGTTAAAACGCTTATCAAGGAGAAAATTTTGTGA
GTAGGAGCTCGAAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGC
TTTCAAACGCTTCATAATAGGGGAAATTTCAAATAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5411
STRAIN JM9130013
ATTGGGAACATTATC

AAAAGGAAAAGAAAATTACTATTTGGATTGATAACTTTTGTTCCTATG
GGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTTAGC
TAATGCTGTTTTTAAAGAATACGGTATTTCAAGTAAATGGCAGCCTATTA
ACTGGGATATGAAAAGAACTGAACTTAATAATGGTAATATAGACCTTATT
TGGAAATGGTTATTCAAACCGGCAGAACGTCGCTAAAAGTTCGCTTTTAC
AAACCCATATATGAATAATCATCAAGTAAATGTTACTFAAAACCTCATCAC
ATATTAAATAGTATTAAAGGATATGAAGGGGAAAAGAACTAGGAGCCAGTCG
GGTTCATCTGGTTTTGATGCTTTTAAACGCTAAACCTGATATTTAAAAAA
GTTTGTAAAAGGAAAAGAAAGCAAGTTCATACGATACTTTCACTCAGGCTT
TGATTTGATTTAAAAAATAACCGTATTGATGGTCTTTTGTGATGAAGTT
TATGCTAACTATTATTAAAGCAAGAAGGAAATATAAAAAGCTTATTATT
TGTAAAACGCTTATCAAGGAGAAAATTTGTAGTAGGAGCTCGTAAAG
TTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACGCTTCAT
AATAAGGGGAGATTCAAATAATCTCTTACAAATGGTTTGGTGAAGATGT
TTATAGTAAAGAA

PRETTY of: /biotmp/msa39314.2{*} February 18, 2003 11:01 ..

1 50
msa39314.2{225_18RS21} -----
msa39314.2{225_2603} ttgactcaca aaaatatatt attaaccatt atatttggat tatttatgat
msa39314.2{225_A909} -----
msa39314.2{225_CJB110} -----
msa39314.2{225_COH1} -----
msa39314.2{225_H36B} -----
msa39314.2{225_KM9130013} -----
msa39314.2{225_M732} -----
msa39314.2{225_M781} -----
msa39314.2{225_090} -----
msa39314.2{225_1169NT} -----
Consensus *****

51 100
msa39314.2{225_18RS21} -----
msa39314.2{225_2603} tatattatca gcatgtggta tgtctaataa ggaaatggct ggtattgata
msa39314.2{225_A909} -----
msa39314.2{225_CJB110} -----
msa39314.2{225_COH1} -----
msa39314.2{225_H36B} -----
msa39314.2{225_KM9130013} -----
msa39314.2{225_M732} -----
msa39314.2{225_M781} -----
msa39314.2{225_090} -----
msa39314.2{225_1169NT} -----
Consensus *****

101 150
msa39314.2{225_18RS21} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_2603} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_A909} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_CJB110} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_COH1} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_H36B} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_KM9130013} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_M732} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_M781} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_090} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
msa39314.2{225_1169NT} ATTGGGAACA TTATCAAAG GAAAAGAAAA TFACTATTGG ATTTGATAAT
Consensus *****

151 200
msa39314.2{225_18RS21} ACTTTTGTTC CTATGGGATT TGAAAGtCGI TCTGGTGACT ATACCGGCTT
msa39314.2{225_2603} ACTTTTGTTC CTATGGGATT TGAAAGtCGI TCTGGTGACT ATACCGGCTT

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_A909}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
msa39314.2{225_CJB110}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
msa39314.2{225_COH1}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
msa39314.2{225_H36B}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
msa39314.2{225_KM9130013}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
msa39314.2{225_M732}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
msa39314.2{225_M781}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
msa39314.2{225_090}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
msa39314.2{225_1169NT}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCCGGCTT
Consensus	*****	*****	*****	*****	*****

msa39314.2{225_18RS21}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_2603}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_A909}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_CJB110}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_COH1}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_H36B}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_KM9130013}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_M732}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_M781}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_090}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
msa39314.2{225_1169NT}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCACTGA
Consensus	*****	*****	*****	*****	*****

msa39314.2{225_18RS21}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_2603}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_A909}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_CJB110}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_COH1}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_H36B}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_KM9130013}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_M732}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_M781}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_090}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
msa39314.2{225_1169NT}	AATGGCAGCC	TATTAACCTG	GATATGAAAG	AAACTGAACT	CAATAATGGT
Consensus	*****	*****	*****	*****	*****

msa39314.2{225_18RS21}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_2603}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_A909}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_CJB110}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_COH1}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_H36B}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_KM9130013}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M732}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M781}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_090}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_1169NT}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
Consensus	*****	*****	*****	*****	*****

msa39314.2{225_18RS21}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_2603}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_A909}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_CJB110}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_COH1}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_H36B}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_KM9130013}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M732}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M781}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_090}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_1169NT}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
Consensus	*****	*****	*****	*****	*****

msa39314.2{225_18RS21}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_2603}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_A909}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_CJB110}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_COH1}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_H36B}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_KM9130013}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M732}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M781}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_090}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_1169NT}	CTAAAACCTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
Consensus	*****	*****	*****	*****	*****

msa39314.2{225_18RS21}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
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Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_18RS21}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_2603}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_A909}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_CJB110}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_COH1}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_H36B}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_KM9130013}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M732}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M781}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_090}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_1169NT}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
Consensus	*****	*****	***-**-****	*****	*****

	801	828	
msa39314.2{225_18RS21}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_2603}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_A909}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_CJB110}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_COH1}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_H36B}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_KM9130013}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_M732}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_M781}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_090}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
msa39314.2{225_1169NT}	GTTTGGTGAA	GATGTTTATA	GTAAGAA
Consensus	*****	*****	*****

SEQ ID NO. 5412

STRAIN 2603 frame: 1

LTHKNILLTIIFGLFMIILSACGMSNEMAGIDNWEHYQKEKKITIGFDNTFVPMGFESR
SGDYTGFDIDLNAVFKYEGISVKWQPINWDMKETELNNGNIDLIWNGYSKTAERAKKVA
FTNPNMNHQVIVTKTSSHINSIKDMKGKLGKLAQSGSSGFDAFNAKPDILKRFVKGKEAV
QYDTFTQALIDLKNNRIDGLLIDEVYANYLQKEGNIKAYYFVKTAQGENFVVGARKVDR
RRLIEKINKAFKQLHNGKRFQKISYKWFGEDEVYSKE

SEQ ID NO. 5413

STRAIN 090 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKYEGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPNMNHQVIVTKTSSHINSIKDMKGKLGKLAQ
SGSSGFDAFNAKPDILKRFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNGKRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5414

STRAIN A909 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKYEGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPNMNHQVIVTKTSSHINSIKDMKGKLGKLAQ
SGSSGFDAFNAKPDILKRFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNGKRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5415

STRAIN H36B frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKYEGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPNMNHQVIVTKTSSHINSIKDMKGKLGKLAQ
SGSSGFDAFNAKPDILKRFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNGKRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5416

STRAIN 18RS21 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKYEGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPNMNHQVIVTKTSSHINSIKDMKGKLGKLAQ
SGSSGFDAFNAKPDILKRFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNGKRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5417

STRAIN M732 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKYEGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPNMNHQVIVTKTSSHINSIKDMKGKLGKLAQ
SGSSGFDAFNAKPDILKRFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNGKRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5418

STRAIN COH1 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKYEGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPNMNHQVIVTKTSSHINSIKDMKGKLGKLAQ
SGSSGFDAFNAKPDILKRFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNGKRFQKISYKWFGEDEVYS
KE

Table 54: Comparative Sequences relating to SAG0949

SEQ ID NO. 5419
STRAIN M781 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKKEYGISVKWQPINWDMKE
TELNNGNIDLINWNGYSKTAERAKKVAFTNPMNNHQVIVTKTSSHINSIKDMKGGKLGAAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDFTQALIDLKNNRIDGLLIDEVYANYLKKQE
GNIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHKNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5420
STRAIN CJB110 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKKEYGISVKWQPINWDMKE
TELNNGNIDLINWNGYSKTAERAKKVAFTNPMNNHQVIVTKTSSHINSIKDMKGGKLGAAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDFTQALIDLKNNRIDGLLIDEVYANYLKKQE
GNIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHKNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5421
STRAIN 1169NT frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKKEYGISVKWQPINWDMKE
TELNNGNIDLINWNGYSKTAERAKKVAFTNPMNNHQVIVTKTSSHINSIKDMKGGKLGAAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDFTQALIDLKNNRIDGLLIDEVYANYLKKQE
GNIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHKNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5422
STRAIN JM9130013 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLNAVFKKEYGISVKWQPINWDMKE
TELNNGNIDLINWNGYSKTAERAKKVAFTNPMNNHQVIVTKTSSHINSIKDMKGGKLGAAQ
SGSSGFDAFNAKPDILKKFVKGKEAVQYDFTQALIDLKNNRIDGLLIDEVYANYLKKQE
GNIKAYYFVKTAAYQGENFVVGARKVDRRLIEKINKAFKQLHKNKGRFQKISYKWFGEDEVYS
KE

PRETTY of: /biotmp/msa45901.2{*} February 19, 2003 03:09 ..

1 50
msa45901.2{225_090} -----WEHYQK EKKITIGFDN
msa45901.2{225_1169NT} -----WEHYQK EKKITIGFDN
msa45901.2{225_18RS21} -----WEHYQK EKKITIGFDN
msa45901.2{225_2603} lthknillti ifglfmiils acgmsnkema gidnWEHYQK EKKITIGFDN
msa45901.2{225_A909} -----WEHYQK EKKITIGFDN
msa45901.2{225_CJB110} -----WEHYQK EKKITIGFDN
msa45901.2{225_COH1} -----WEHYQK EKKITIGFDN
msa45901.2{225_H36B} -----WEHYQK EKKITIGFDN
msa45901.2{225_JM9130013} -----WEHYQK EKKITIGFDN
msa45901.2{225_M732} -----WEHYQK EKKITIGFDN
msa45901.2{225_M781} -----WEHYQK EKKITIGFDN
Consensus *****

51 100
msa45901.2{225_090} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_1169NT} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_18RS21} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_2603} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_A909} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_CJB110} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_COH1} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_H36B} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_JM9130013} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_M732} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
msa45901.2{225_M781} TFVPMGFESR SGDYTGFDID LANAVFKEYG ISVKWQPINW DMKETELNNG
Consensus *****

101 150
msa45901.2{225_090} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_1169NT} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_18RS21} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_2603} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_A909} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_CJB110} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_COH1} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_H36B} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_JM9130013} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_M732} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
msa45901.2{225_M781} NIDLIWNGYS KTAERAKKVA FTNPMNNHQ VIVTKTSSHI NSIKDMKGGK
Consensus *****

151 200
msa45901.2{225_090} LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDFTQALI DLKNNRIDGL
msa45901.2{225_1169NT} LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDFTQALI DLKNNRIDGL
msa45901.2{225_18RS21} LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDFTQALI DLKNNRIDGL
msa45901.2{225_2603} LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDFTQALI DLKNNRIDGL
msa45901.2{225_A909} LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDFTQALI DLKNNRIDGL
msa45901.2{225_CJB110} LGAQSGSSGF DAFNAKPDIL KKFVKGKEAV QYDFTQALI DLKNNRIDGL

Table 54: Comparative Sequences relating to SAG0949

msa45901.2{225_COH1}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_H36B}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_JM9130013}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M732}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M781}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
Consensus	*****	*****	*****	*****	*****
msa45901.2{225_090}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_1169NT}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_18RS21}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_2603}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_A909}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_CJB110}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_COH1}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_H36B}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_JM9130013}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M732}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M781}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
Consensus	*****	*****	*****	*****	*****
msa45901.2{225_090}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_1169NT}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_18RS21}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_2603}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_A909}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_CJB110}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_COH1}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_H36B}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_JM9130013}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_M732}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
msa45901.2{225_M781}	FKQLHNKGK	QKISYKWFGE	DVYSKE		
Consensus	*****	*****	*****		

Table 55: Comparative Sequences relating to SAG1592

SEQ ID NO. 5501
STRAIN 2603
ATGCTTAAATCTTTTGGATTTCCTTAGTTCGCTTTTACCAAAAAAATATTTCTCCAGCT
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA
AAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTAATTTGCGATGTCATCCCTTA
GCCACGGAGGAAATGATCCTGTCCCTGATCAITTTAGCTTAAGACGTAATAAAACGGAT
ATATCAGAT

SEQ ID NO. 5502
STRAIN 090
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTT

SEQ ID NO. 5503
STRAIN A909
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATA

SEQ ID NO. 5504
STRAIN H36B
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5505
STRAIN 18RS21
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5506
STRAIN M732
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5507
STRAIN COH1
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA
AAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTAATTTGCGATGTCATCCCTTA
GCCACGGAGGAAATGATCCTGTCCCTGATCAITTTAGCT

SEQ ID NO. 5508
STRAIN M781
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5509
STRAIN CJB110
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5510
STRAIN 1169NT
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
TATTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

SEQ ID NO. 5511
STRAIN JM9130013
TTCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAAACGGATATATCAGAT

PRETTY of: /biotmp/msa119306.2{*} April 29, 2003 06:23 ..

Table with 2 columns: sequence identifier and position. Row 1: msa119306.2{233_H36B} 1. Row 2: msa119306.2{233_JM9130013} 50.

Table 55: Comparative Sequences relating to SAG1592

msa119306.2{233_090}	-----	-----	-----	-----	-----	
msa119306.2{233_18RS21}	-----	-----	-----	-----	-----	
msa119306.2{233_2603}	atgcttaaat	cttttttgat	tttcttagtt	cgcttttacc	aaaaaaatat	
msa119306.2{233_A909}	-----	-----	-----	-----	-----	
msa119306.2{233_CJB110}	-----	-----	-----	-----	-----	
msa119306.2{233_COH1}	-----	-----	-----	-----	-----	
msa119306.2{233_M732}	-----	-----	-----	-----	-----	
msa119306.2{233_M781}	-----	-----	-----	-----	-----	
msa119306.2{233_1169NT}	-----	-----	-----	-----	-----	
Consensus	*****	*****	*****	*****	*****	
msa119306.2{233_H36B}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_JM9130013}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_090}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_18RS21}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_2603}	ttctccagct	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_A909}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_CJB110}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_COH1}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_M732}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_M781}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
msa119306.2{233_1169NT}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT	
Consensus	*****	*****	*****	*****	*****	
msa119306.2{233_H36B}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tcTGATGGGG
msa119306.2{233_JM9130013}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tcTGATGGGG
msa119306.2{233_090}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_18RS21}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_2603}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_A909}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_CJB110}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_COH1}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M732}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M781}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_1169NT}	-----	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	ggTGATGGGG
Consensus	*****	*****	*****	*****	*****	*****
msa119306.2{233_H36B}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_JM9130013}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_090}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_18RS21}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_2603}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_A909}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_CJB110}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_COH1}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M732}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M781}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_1169NT}	-----	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
Consensus	*****	*****	*****	*****	*****	*****
msa119306.2{233_H36B}	-----	TGTCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_JM9130013}	-----	TGTCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_090}	-----	TGTCCTGAT	cATTTTAGCT	t-----	-----	-----
msa119306.2{233_18RS21}	-----	TGTCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_2603}	-----	TGTCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_A909}	-----	TGTCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	ata-----
msa119306.2{233_CJB110}	-----	TGTCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_COH1}	-----	TGTCCTGAT	cATTTTAGCT	-----	-----	-----
msa119306.2{233_M732}	-----	TGTCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_M781}	-----	TGTCCTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_1169NT}	-----	TGTCCTGAT	tATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
Consensus	*****	*****	*****	*****	*****	*****
SEQ ID NO. 5512						
STRAIN 2603 frame: 1						
MLKSFLLFLVRFYQKNI SPAPFASCYRPTCSTYMI EAIQKHGLKGVLMGIARILRCHPL						
AHGGNDPVPDHFSLRRNKTDISD						
SEQ ID NO. 5513						
STRAIN 090 frame: 1						
FPASCYRPTCSTYMI EAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHF						
SEQ ID NO. 5514						
STRAIN A909 frame: 1						
FPASCYRPTCSTYMI EAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD						
I						
SEQ ID NO. 5515						
STRAIN H36B frame: 1						

Table 55: Comparative Sequences relating to SAG1592

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5516
STRAIN 18RS21 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5517
STRAIN M732 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5518
STRAIN COH1 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHF

SEQ ID NO. 5519
STRAIN M781 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5520
STRAIN CJB110 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5521
STRAIN 1169NT frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVVMGIARILRCHPLAHGGNDPVPDYFSLRRNKTD
ISD

SEQ ID NO. 5522
STRAIN JM9130013 frame: 1
FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

PRETTY of: /biotmp/msa119415.2(*) April 29, 2003 06:25 ..

	1			50
msa119415.2{233_090}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_18RS21}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_COH1}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_A909}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_2603}	mlksfliflv	rftyqknispa	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_CJB110}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_H36B}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_JM9130013}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_M732}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_M781}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_1169NT}	-----	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVVMG
Consensus	*****	*****	*****	*****
	51			83
msa119415.2{233_090}	IARILRCHPL	AHGGNDPVPD	hFS-----	---
msa119415.2{233_18RS21}	IARILRCHPL	AHGGNDPVPD	hFSLRRNKTD	ISD
msa119415.2{233_COH1}	IARILRCHPL	AHGGNDPVPD	hFS-----	---
msa119415.2{233_A909}	IARILRCHPL	AHGGNDPVPD	hFSLRRNKTD	I--
msa119415.2{233_2603}	IARILRCHPL	AHGGNDPVPD	hFSLRRNKTD	ISD
msa119415.2{233_CJB110}	IARILRCHPL	AHGGNDPVPD	hFSLRRNKTD	ISD
msa119415.2{233_H36B}	IARILRCHPL	AHGGNDPVPD	hFSLRRNKTD	ISD
msa119415.2{233_JM9130013}	IARILRCHPL	AHGGNDPVPD	hFSLRRNKTD	ISD
msa119415.2{233_M732}	IARILRCHPL	AHGGNDPVPD	hFSLRRNKTD	ISD
msa119415.2{233_M781}	IARILRCHPL	AHGGNDPVPD	hFSLRRNKTD	ISD
msa119415.2{233_1169NT}	IARILRCHPL	AHGGNDPVPD	yFSLRRNKTD	ISD
Consensus	*****	*****	-----	***

Table 56: Comparative Sequences relating to SAG0806

SEQ ID NO. 5601

STRAIN 2603

aagaagcttacttttatttgggatttagatgggacattaatagattcgta
tgtaccaatgatggaagctcttgaagaacctatcgtcatttttggtttaa
tatttgataaagaattaatccatgaatatattttacaggaatcagtgggg
aaattattggtaaacctttcagaggaagagcaaatcctcatgaaaaact
gaaagcatattttacaaaagaacaagaaagtcgagattctaaaaatcatt
taatgccatcagcaaaagagattttagaatggaccaagaacaagatc
cccaattttatgtatacacataaaggagcaagtacgcattcagtggtgga
aaccttgcagatctctcattatttggatgaaaatttaactgggtgtttcgg
gattcgagcgaaaaccacatccacaagggattaaattatttagttaaacga
tattctttagataaatcaatgacttattacataggagatcgtccactaga
tttggagggttgctcaaaatgctggtataaaatccataaacttaaggttag
agaattccaaagaaaactataatatttcaagctcacaagatataatatca
cttgatttcaactcgtttggat

SEQ ID NO. 5602

STRAIN COH1

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAA
TAGATTCGATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCAT
TTTGGCTTAATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGA
ATCAGTGGGGCAATTTATGGTAAACCTTTAGAGGAAGAGCAAAATACCTC
ATGAAAAAAGTGAAGCAATTTTACAAAAGAACAAGAAAGTCGAGATTTCT
AAAATACATTTAATGCCATATGCAAAAGAGATTTTGAATGGACCAAGA
ACAAGATATTCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT
CAGTGTGGAAACCTTGCAGATCTCTCATTATTTTATGAAATTTTAACT
GGTGTTCGGGATTCGAGCGAAAACCCATCCACAAGGGATTAATTAATTT
AGTTAAACGATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATC
GTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATAAATCCATAAAC
TTAAGGTTAGAGAATCCAAAGAAAACATAATATTTCAAGTCTCAAGA
TATAATATCACTTGATTTCACCTCGTTGGAT

SEQ ID NO. 5603

STRAIN A909

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAA
AGATTCGATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTGGT
TAAATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAAT
TATGGTAAACCTTTAGAGGAAGAGCAAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGA
ACAAGAAAGTCGAGATTTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTGAATG
GACCAAGAAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT
AGTGTGGAAACCTTGCAGATCTCTCATTATTTTATGAAATTTTAACTGGTGTTCGGG
ATTCGAGCGAAAACCCATCCACAAGGGATTAATTAATTTAGTTAAACGATATTCTTTAGA
TAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGC
TGGTATAAATCCATAAACCTTAAAGGTTAGAGAATCCAAAGAAAACATAATATTTCAAG
TCTCAAGATATAATATCACTTGATTTCACCTCGT

SEQ ID NO. 5604

STRAIN H36B

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAA
TAGATTCGATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTGGT
TAAATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAAT
TATGGTAAACCTTTAGAGGAAGAGCAAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGA
AGTTCGAGATTTCAAAATACATTTAATGCCATATGCAAAAGAGATTTTGAATGGACCAAA
GAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT
CAGTGTGGAAACCTTGCAGATCTCTCATTATTTTATGAAATTTTAACTGGTGTTCGGGATTCGAG
CGAAAACCCATCCACAAGGGATTAATTAATTTAGTTAAACGATATTCTTTAGATAAATCA
ATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATA
AAATCCATAAACCTTAAAGGTTAGAGAATCCAAAGAAAACATAATATTTCAAGTCTCAA
GATATAATATCACTTGATTTCACCTCGTTGGAT

SEQ ID NO. 5605

STRAIN 18RS21

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAA
CGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTGGT
TAAATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAAT
TATGGTAAACCTTTAGAGGAAGAGCAAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGA
AAAGTTCGAGATTTCAAAATACATTTAATGCCATATGCAAAAGAGATTTTGAATGGACCA
AAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT
CAGTGTGGAAACCTTGCAGATCTCTCATTATTTTATGAAATTTTAACTGGTGTTCGGGATTCG
AGCGAAAACCCATCCACAAGGGATTAATTAATTTAGTTAAACGATATTCTTTAGATAAAT
CAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAAATGCTGGTATA
TAAATCCATAAACCTTAAAGGTTAGAGAATCCAAAGAAAACATAATATTTCAAGTCTCAA
AAGATATAATATCACTTGATTTCACCTCGTTGGAT

SEQ ID NO. 5606

STRAIN M732

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAA
TCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTGGCTTAAAT
TATGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGCAAT
TATGGTAAACCTTTAGAGGAAGAGCAAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGA
CAAAGTTCGAGATTTCAAAATACATTTAATGCCATATGCAAAAGAGATTTTGAATGGACC
AAAGAACAAGATATTTCAAAATTTTATGTATACACATAAAGGAGCAAGTACGCATT
CAGTGTGGAAACCTTGCAGATCTCTCATTATTTTATGAAATTTTAACTGGTGTTCGGGATTCG

Table 56: Comparative Sequences relating to SAG0806

TTGGAAACCTTGCAGATCTCTCATTATTTTGATGAAATTTAACTGGTGTTCGGGATTCC
GAGCGAAAACCCACATCCACAAGGGATTAAATATTTAGTTAAACGATATTCCTTAGATAAA
TCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCTGGT
ATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTC
AAAGATATAATATCACTTGATTTCACTCGTTGGAT

SEQ ID NO. 5607

STRAIN CJB110

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATT
AATAGATTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTT
AATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGCAATTTAT
GGTAAACCTTTTCAGAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATAATTTTACAAA
AGAACAAAGAAAGTCGAGATTTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTGA
ATGGACCAAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCA
TTCAGTGTGGAAACCTTGCAGATCTCTCATTTATTTGATGAAATTTAACTGGTGTTC
TGGATTCGAGGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACGATATTTCTTT
AGATAAATCAATGACTTATTTACATAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAA
TGCTGTTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTT
AAGTCTCAAGGATATAATATCACTTGATTTCACTCGTT

SEQ ID NO. 5608

STRAIN 1169NT

aAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGTATGTACCAATTA
TAGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAAATATTTGATAAAGAATTAATCC
ATGAATATATTTTACAGGAATCAGTGGGGAAATTAATGGTAAACCTTTTCAGAGGAAGAGC
AAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGAACAGAAAGTCGAGATTTCTA
AAATACATTTAATGCCATACGCAAAAGAGATTTAGAATGGACCAAAGAACAGATATCC
CCAAATTTTATGTATACACATAAAGGAGCAAGTACGCAATTCAGTGTGGAAACCTTGCAGA
TCTCTCATTTTGTGATGAAATTTAACTGGTGTTCGGGATTCGAGCGAAAACCCACATC
CACAAAGGATTAATTTAGTTAAACGATATTCCTTAGATAAATCAATGACTTATTACA
TAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAATGCTGTTATAAAATCCATAAACT
TAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAGGATATAATATCAC
TTGATTTCACTCGTTGGAT

SEQ ID NO. 5609

STRAIN JM9130013

AGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGA
TTGATGTACCAATTTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTFATATTT
TGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTAATGGTAAA
CCTTTTCAGAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATAATTTTACAAAAGAAC
AGAAAGTCGAGATTTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTGAATGGAC
CAAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCAATTCAGT
GTTGGAAACCTTGCAGATCTCTCATTATTTGATGAAATTTAACTGGTGTTCGGGATTC
CGAGCGAAAACCATCCACAAGGGATTAATATTTAGTTAAACGATATTCCTTAGATAAA
ATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCTGG
TATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCT
CAAAGATATAATATCACTTGATTTCACTCGT

SEQ ID NO. 5610

STRAIN 090

AAGAAGCTTACTTTTATTTGG
GATTTAGATGGGACATTAATAGATTCGTATGTACCAATTATGGAAGCTCT
TGAAGAAACCTATCGTCATTTTGGCTTAAATATTTGATAAAGAATTAATCC
ATGAATATATTTTACAGGAATCAGTGGGGCAATTAATGGTAAACCTTTCA
GAGGAAGAGCAAATACCTCATGAAAAACTGAAAGCATATTTTACAAAAGA
ACAAAGAAAGTCGAGATTTCTAAAATACATTTAATGCCATATGCAAAAGAGA
TTTTAGAATGGACCAAAGAACAAGATATCCCAATTTTATGTATACACAT
AAAGGAGCAAGTACGCAATTCAGTGTGGAAACCTTGCAGATCTCTCATT
TTTTGATGAAATTTAACTGGTGTTCCTGATTCGAGCGAAAACCCACATC
CACAAAGGATTAATTTAGTTAAACGATATTCCTTAGATAAATCAATG
ACTTATTACATAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAATGCT
TGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATA
ATATTTCAAGTCTCAAGGATATAATATCACTTGATTTCACTCGT

SEQ ID NO. 5611

STRAIN M781

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGT
ATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA
ATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGG
GCAATTTATTTGGTAAACCTTTTCAGAGGAAGAGCAAATACCTCATGAAAA
TGAAAGCATATTTTACAAAAGAACAAAGTCGAGATTTTAAAATACAT
TTAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAAGAACAAGATAT
TCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCAATTCAGTGTGG
AAACCTTGCAGATCTCTCATTATTTGATGAAATTTAACTGGTGTTCG
GGATTCGAGCGAAAACCCACATCCACAAGGGATTAATTTAGTTAAACG
ATATTTCTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAG
ATTTGGAGGTTGCTCAAATGCTGGTATAAAATCCATAAACTTAAGGTTA
GAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAAGATATAATATC
ACTTGATTTCACTCGT

PRETTY of: /biotmp/msa45163.2[*] January 21, 2003 06:53 ..

Table 56: Comparative Sequences relating to SAG0806

	1				50
msa45163.2{240_18RS21}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_2603}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_A909}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_H36B}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_JM9130013}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_COH1}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M732}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M781}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_090}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_CJB110}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_1169NT}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
Consensus	*****	*****	*****	*****	*****
	51				100
msa45163.2{240_18RS21}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_2603}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_A909}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_H36B}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_JM9130013}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_COH1}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_M732}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_M781}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_090}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_CJB110}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_1169NT}	TGTACCAATT	ATgGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
Consensus	*****	*-*-*****	*****	*****	*****-*****
	101				150
msa45163.2{240_18RS21}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_2603}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_A909}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_H36B}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_JM9130013}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_COH1}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_M732}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_M781}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_090}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_CJB110}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
msa45163.2{240_1169NT}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTTACAGGA	ATCAGTGGGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa45163.2{240_18RS21}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_2603}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_A909}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_H36B}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_JM9130013}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_COH1}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M732}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M781}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_090}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_CJB110}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_1169NT}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
Consensus	-*****	*****	*****	*****	*****
	201				250
msa45163.2{240_18RS21}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_2603}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_A909}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_H36B}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_JM9130013}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_COH1}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M732}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M781}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTyT	AAAATACATT
msa45163.2{240_090}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_CJB110}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_1169NT}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
Consensus	*****	*****	*****	*****-*	*****
	251				300
msa45163.2{240_18RS21}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_2603}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_A909}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_H36B}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_JM9130013}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_COH1}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_M732}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_M781}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_090}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_CJB110}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_1169NT}	TAATGCCATA	cGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
Consensus	*****	-*****	*****	*****	*****-

Table 56: Comparative Sequences relating to SAG0806

	301			350
msa45163.2{240_18RS21}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_2603}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_A909}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_H36B}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_JM9130013}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_COH1}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_M732}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_M781}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_090}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_CJB110}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
msa45163.2{240_1169NT}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT
Consensus	*****	*****	*****	*****
	351			400
msa45163.2{240_18RS21}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_2603}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_A909}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_H36B}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_JM9130013}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_COH1}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_M732}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_M781}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_090}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_CJB110}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
msa45163.2{240_1169NT}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT
Consensus	*****	*****	*****	*****
	401			450
msa45163.2{240_18RS21}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_2603}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_A909}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_H36B}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_JM9130013}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_COH1}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_M732}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_M781}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_090}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_CJB110}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
msa45163.2{240_1169NT}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT
Consensus	*****	*****	*****	*****
	451			500
msa45163.2{240_18RS21}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_2603}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_A909}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_H36B}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_JM9130013}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_COH1}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_M732}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_M781}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_090}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_CJB110}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
msa45163.2{240_1169NT}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC
Consensus	*****	*****	*****	*****
	501			550
msa45163.2{240_18RS21}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_2603}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_A909}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_H36B}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_JM9130013}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_COH1}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_M732}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_M781}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_090}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_CJB110}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
msa45163.2{240_1169NT}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC
Consensus	*****	*****	*****	*****
	551			600
msa45163.2{240_18RS21}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_2603}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_A909}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_H36B}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_JM9130013}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_COH1}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_M732}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_M781}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_090}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_CJB110}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA
msa45163.2{240_1169NT}	AGAATTCCAA	AGAAAACAT	AATATTTCAA	GTCTCAAaGA

Table 56: Comparative Sequences relating to SAG0806

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Consensus ***** ***** ***** *****_** *****
msa45163.2{240_18RS21} 601          621
msa45163.2{240_2603} CTTGATTTCa CTCGTttgga t
msa45163.2{240_A909} CTTGATTTCa CTCGT-----
msa45163.2{240_H36B} CTTGATTTCa CTCGTttgga t
msa45163.2{240_JM9130013} CTTGATTTCa CTCGT-----
msa45163.2{240_COH1} CTTGATTTCa CTCGTttgga t
msa45163.2{240_M732} CTTGATTTCa CTCGTttgga t
msa45163.2{240_M781} CTTGATTTCa CTCGT-----
msa45163.2{240_090} CTTGATTTCa CTCGT-----
msa45163.2{240_CJB110} CTTGATTTCa CTCGTt-----
msa45163.2{240_1169NT} CTTGATTTCa CTCGTttgga t
Consensus ***** *****_-----

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SEQ ID NO. 5612
STRAIN 2603 frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GKL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5613
STRAIN A909 frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GKL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5614
STRAIN H36B frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GKL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5615
STRAIN 18RS21 frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GKL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5616
STRAIN M732 frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GQL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5617
STRAIN COH1 frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GQL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5618
STRAIN CJB110 frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GQL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5619
STRAIN 1169NT frame: 1
 KKLTFIWDL DGTLDISYVPIEAL EET YRHFG LI FDKELI HEYI LQESV GKL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTRLD

SEQ ID NO. 5620
STRAIN JM9130013 frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GKL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ
 ISHYFDEIL TGVS GFERKPH PQG INYL VKRYS LDKSM TYY I GDRPLD LEVAQNAGIKSIN
 LRLENSKENYNISSLKDIISLDFTR

SEQ ID NO. 5621
STRAIN 090 frame: 1
 KKLTFIWDL DGTLDISYVPIMEALEET YRHFG LI FDKELI HEYI LQESV GQL LVLN LSEEE
 QI PHEK LKAY FTKEQESRDSKIHLMPYAKE ILEWTKEQDI PNFMYTHKGASTHSVLETLQ

Table 56: Comparative Sequences relating to SAG0806

ISHYFDEILTVSGFERKPHPGQGINYLVKRYSLDKSMTTYIGDRPLDLEVAQNAGIKSIN
LRLNSKENYNISSLKDIISLDFTR

SEQ ID NO. 5622
STRAIN M781 frame: 1
KKLTFIWDLDGTLIDSYVPI MEALEETRYRHFGFLIFDKELIHEYILQESVGLLVNLSSEE
QIPHEKPKAYFTFKQESRDXKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHVSLETLO
ISHYFDEILTVSGFERKPHPGQGINYLVKRYSLDKSMTTYIGDRPLDLEVAQNAGIKSIN
LRLNSKENYNISSLKDIISLDFTR

PRETTY of: /biotmp/msa45645.2(*) January 21, 2003 06:57 ..

1 50
msa45645.2{240_18RS21} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_A909} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_JM9130013} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_2603} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_H36B} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_090} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_CJB110} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_M781} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_COH1} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_M732} KKLTFIWDLD GTLIDSYVPI mEALeETRYRH FGFLIFDKELI HEYILQESVG
msa45645.2{240_1169NT} KKLTFIWDLD GTLIDSYVPI iEALeETRYRH FGFLIFDKELI HEYILQESVG
Consensus ***** -***** *****

51 100
msa45645.2{240_18RS21} KLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_A909} KLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_JM9130013} KLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_2603} KLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_H36B} KLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_090} qLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_CJB110} qLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_M781} qLLVNLSEEE QIPHEKPKAY FTKEQESRDX KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_COH1} qLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_M732} qLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_1169NT} KLLVNLSEEE QIPHEKPKAY FTKEQESRDS KIHLMPLYAKE ILEWTKEQDI
Consensus -***** ***** *****

101 150
msa45645.2{240_18RS21} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_A909} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_JM9130013} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_2603} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_H36B} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_090} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_CJB110} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_M781} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_COH1} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_M732} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
msa45645.2{240_1169NT} PNFMYTHKGA STHSVLETLO ISHYFDEILT GVSFGERKPH PQGINYLVKR
Consensus ***** ***** *****

151 200
msa45645.2{240_18RS21} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_A909} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_JM9130013} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_2603} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_H36B} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_090} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_CJB110} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_M781} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_COH1} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_M732} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_1169NT} YSLDKSMTTY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
Consensus ***** ***** *****

201
msa45645.2{240_18RS21} LDFTRld
msa45645.2{240_A909} LDFTR--
msa45645.2{240_JM9130013} LDFTR--
msa45645.2{240_2603} LDFTRld
msa45645.2{240_H36B} LDFTRld
msa45645.2{240_090} LDFTR--
msa45645.2{240_CJB110} LDFTR--
msa45645.2{240_M781} LDFTR--
msa45645.2{240_COH1} LDFTRld
msa45645.2{240_M732} LDFTRld
msa45645.2{240_1169NT} LDFTRld
Consensus *****

Table 57: Comparative Sequences relating to SAG 1488

SEQ ID NO: 5701

STRAIN 2603

ATGCTTATGACAAAAATAATAGGACTGACAGGAGGGATAGCTTCT
 GGAAGTCAACGGTAACAAAAATAATACGAGAATCAGGTTTAAAGTCATAGATGCGGAT
 CAAGTGGTTCATAAAATGCAAGCTAAGGGTGGGAACTTTACCAAGCTTTATTAGAATGG
 TTGGGTCCTCCAGATACTTGATGCTGATGGTGGATGGATAGACCAAAGCTTTCTCAAATG
 ATTTTGTCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCTG
 CAAGAGTTAGCATGTGACGCGGACCAATTAACAACAAACAGAGAGATATTTTCATGGAT
 ATTCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTGATGAGATTTGGTTGGTATTT
 GTTGATAAAGAAAAACAATTACAACGATTAATGGCCGTAACAACTACAGTCGAGAAGAA
 GCAGAAATACGACTTTCACACCAAAATGCCTTTAACAGATAAAAAAGTTTCGCTAGTCTT
 ATTATTGACAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCAA
 CGTTTA

SEQ ID NO: 5702

STRAIN 090

AAGTCAACGGTAACAAAAATAATACGAGAATCAG
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAG
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCTCCGAGATACT
 TGATGCTGATGGTGGATGGATAGACCAAAGCTTTCTCAAATGATTTTGT
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 CGTCAAGAGTTAGCATGTGACGCGGACCAATTAACAACAAACAGAGAGAT
 ATTTTTCGTTGGATATTCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TTGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGA
 TTAATGGCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 ACACCAAATGCCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTA
 ATAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTT
 CAACGTTTA

SEQ ID NO: 5703

STRAIN A909

AAGTCAACGGTAACAAAAATAATACGAGAATCAG
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAG
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCTCCGAGATACT
 TGATGCTGATGGTGGATGGATAGACCAAAGCTTTCTCAAATGATTTTGT
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 CGTCAAGAGTTAGCATGTGACGCGGACCAATTAACAACAAACAGAGAGAT
 ATTTTTCATGGATATTCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TTGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGA
 TTAATGGCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 ACACCAAATGCCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTA
 ACAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTT
 CAACGTTTA

SEQ ID NO: 5704

STRAIN H36B

AAGTCAACGGTAACAAAAATAATACGAGAATCAG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCTCCGAGATACTT
 GATGCTGATGGTGGATGGATAGACCAAAGCTTTCTCAAATGATTTTGT
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 GTCAAGAGTTAGCATGTGACGCGGACCAATTAACAACAAACAGAGAGATA
 TTTTTCATGGATATTCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGA
 TTAATGGCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 CACCAAATACCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTA
 TAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTT
 AACGTTTA

SEQ ID NO: 5705

STRAIN 18RS21

AAGTCAACGGTAACAAAAATAATACGAGAATCAG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCTCCGAGATACTT
 GATGCTGATGGTGGATGGATAGACCAAAGCTTTCTCAAATGATTTTGT
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 GTCAAGAGTTAGCATGTGACGCGGACCAATTAACAACAAACAGAGAGATA
 TTTTTCATGGATATTCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TGATGAGATTTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAACGA
 TTAATGGCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 CACCAAATACCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTA
 CAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTT
 AACGTTTA

SEQ ID NO: 5706

STRAIN M732

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGTT
 TTAAGTTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAGGGT
 GGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCTCCGAGATACTTGA
 TGCTGATGGTGGATGGATAGACCAAAGCTTTCTCAAATGATTTTGTCTA
 ATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCTG
 CAAGAGTTAGCATGTGACGCGGACCAATTAACAACAAACAGAGAGATATT

Table 57: Comparative Sequences relating to SAG 1488

T TTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTG
 ATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGATTA
 ATGGCCCGTAACTACAGTTCGAGAAGAAGCAGAATTACGACTTTCCACA
 CCAAATGCCCTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGACA
 ATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCAA
 CGTTTTA

SEQ ID NO: 5707

STRAIN COH1

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAGGG
 TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGTCCCGAGATACTTG
 ATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGCT
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTCG
 TCAAGAGTTAGCATTGTAGCGCGACCAATTAACAACAAACAGAAGAGATAT
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT
 GATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGATT
 AATGGCCCGTAACTACAGTTCGAGAAGAAGCAGAATTACGACTTTCCAC
 ACCAAATGCCCTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGAC
 AATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCAA
 ACGTTTTA

SEQ ID NO: 5708

STRAIN M781

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTCG
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTC
 GTCAGAGTTAGCATGTAGCGCGACCAATTAACAACAAACAGAAGAGATA
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
 TGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGAT
 TAATGGCCCGTAACTACAGTTCGAGAAGAAGCAGAATTACGACTTTCCA
 ACCAAATGCCCTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGA
 CAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCA
 ACGTTTTA

SEQ ID NO: 5709

STRAIN CJB110

AAGTCAACGGTAACAAAAATAATACGAGAA
 TCAGGTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGC
 TAAGGGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGTCCCGAGA
 TACTTGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGAT
 TTTGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTAT
 CATTTCGTCAGAGTTAGCATGTAGCGCGACCAATTAACAACAAACAGAAG
 AGATATTTTTCGTTGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAA
 TGGTTTGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACA
 ACGATTAATGGCCCGTAACTACAGTTCGAGAAGAAGCAGAATTACGAC
 TTTTCAACCAAATGCCCTTAAACAGATAAAAAAGTTTCGCTAGTCTTATT
 ATTAATAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCT
 TCTTCAACGTTTTA

SEQ ID NO: 5710

STRAIN 1169NT

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTCG
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTC
 GTCAGAGTTAGCATGTAGCGCGACCAATTAACAACAAACAGAAGAGATA
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
 TGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGAT
 TAATGGCCCGTAACTACAGTTCGAGAAGAAGCAGAATTACGACTTTCCA
 ACCAAATACCTTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGA
 TAATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTCA
 AACGTTTTA

SEQ ID NO: 5711

STRAIN JM9130013

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATGCAAGCTAAGG
 TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGTCCCGAGATACTTG
 ATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTCGCT
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTTCG
 TCAAGAGTTAGCATGTAGCGCGACCAATTAACAACAAACAGAAGAGATA
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
 GATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATT
 AATGGCCCGTAACTACAGTTCGAGAAGAAGCAGAATTACGACTTTCCAC
 ACCAAATACCTTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGAT
 AATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTCAA
 ACGTTTTA

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221059.2{*} February 10, 2003 07:07 ..

	1				50
msa221059.2{245_H36B}	-----	-----	-----	-----	-----AA
msa221059.2{245_JM9130013}	-----	-----	-----	-----	-----AA
msa221059.2{245_1169NT}	-----	-----	-----	-----	-----AA
msa221059.2{245_090}	-----	-----	-----	-----	-----AA
msa221059.2{245_CJB110}	-----	-----	-----	-----	-----AA
msa221059.2{245_18RS21}	-----	-----	-----	-----	-----AA
msa221059.2{245_2603}	-----	-----	-----	-----	-----AA
msa221059.2{245_A909}	-----	-----	-----	-----	-----AA
msa221059.2{245_COH1}	-----	-----	-----	-----	-----AA
msa221059.2{245_M732}	-----	-----	-----	-----	-----AA
msa221059.2{245_M781}	-----	-----	-----	-----	-----AA
Consensus	*****	*****	*****	*****	*****
	51				100
msa221059.2{245_H36B}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_JM9130013}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_1169NT}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_090}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_CJB110}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_18RS21}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_2603}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_A909}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_COH1}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_M732}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
msa221059.2{245_M781}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTAAA	GTCATAGATG
Consensus	*****	*****	*****	*****	*****
	101				150
msa221059.2{245_H36B}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_JM9130013}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_1169NT}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_090}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_CJB110}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_18RS21}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_2603}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_A909}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_COH1}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_M732}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_M781}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
Consensus	*****	*****	*****	*****	*****
	151				200
msa221059.2{245_H36B}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_JM9130013}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_1169NT}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_090}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_CJB110}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_18RS21}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_2603}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_A909}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_COH1}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_M732}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_M781}	GCITTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
Consensus	*****	*****	*****	*****	*****
	201				250
msa221059.2{245_H36B}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_JM9130013}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_1169NT}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_090}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_CJB110}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_18RS21}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_2603}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_A909}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_COH1}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_M732}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_M781}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
Consensus	*****	*****	*****	*****	*****
	251				300
msa221059.2{245_H36B}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_JM9130013}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_1169NT}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_090}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_CJB110}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_18RS21}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_2603}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_A909}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_COH1}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_M732}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_M781}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT

Table 57: Comparative Sequences relating to SAG 1488

msa221059.2{245_M781}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
Consensus	*****	*****	*****	*****	*****
301					
msa221059.2{245_H36B}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_JM9130013}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_1169NT}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_090}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_CJB110}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_18RS21}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_2603}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_A909}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_COH1}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M732}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M781}	CAGCGCGACC	AATTA AAAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
Consensus	*****	*****	*****	*****	*****
351					
msa221059.2{245_H36B}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_JM9130013}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_1169NT}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_090}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_CJB110}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_18RS21}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_2603}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_A909}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_COH1}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_M732}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
msa221059.2{245_M781}	TTTATTGATT	GAAGAAAAGT	ATATAAAAATG	GTTTGATGAG	ATTGGTTGG
Consensus	*****	*****	*****	*****	*****
401					
msa221059.2{245_H36B}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_JM9130013}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_1169NT}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_090}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_CJB110}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_18RS21}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_2603}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_A909}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_COH1}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M732}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M781}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
Consensus	*****	*****	*****	*****	*****
451					
msa221059.2{245_H36B}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_JM9130013}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_1169NT}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_090}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_CJB110}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_18RS21}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_2603}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_A909}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_COH1}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M732}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M781}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
Consensus	*****	*****	*****	*****	*****
501					
msa221059.2{245_H36B}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_JM9130013}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_1169NT}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_090}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TaAtAATAAT	GGTGATTTAA
msa221059.2{245_CJB110}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TaAtAATAAT	GGTGATTTAA
msa221059.2{245_18RS21}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_2603}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_A909}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_COH1}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_M732}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_M781}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
Consensus	*****	*****	*****	*****	*****
551					
msa221059.2{245_H36B}	TAACTTTAAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_JM9130013}	TAACTTTAAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_1169NT}	TAACTTTAAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_090}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_CJB110}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_18RS21}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_2603}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_A909}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_COH1}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A

Table 57: Comparative Sequences relating to SAG 1488

```
msa221059.2{245_M732} TAACTTTAAA AGAGCAAATA TTGGATGCTC TTCAACGTTT A
msa221059.2{245_M781} TAACTTTAAA AGAGCAAATA TTGGATGCTC TTCAACGTTT A
Consensus      *****- ***** * ***** * ***** *
```

SEQ ID NO: 5712

STRAIN 2603 frame: 1
 MLMTKI IGLTGGIASGKSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI
 LDADGELDRPKLSQMI FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI
 EEKY I KWFDEI WL V FV DKEKQLQRLMARNNYSREAE LRLSHQMP L TDKKS FASLI IDNN
 GDLITLKEQILDALQRL

SEQ ID NO: 5713

STRAIN 090 frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFVDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQMP L TDKKS FASLI INNNGDLITLKEQILDALQR
 L

SEQ ID NO: 5714

STRAIN A909 frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQMP L TDKKS FASLI IDNNNGDLITLKEQILDALQR
 L

SEQ ID NO: 5715

STRAIN H36B frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQ I PLTDKKS FASLI IDNNNGDLITLKEQMLDALQR
 L

SEQ ID NO: 5716

STRAIN 18RS21 frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQMP L TDKKS FASLI IDNNNGDLITLKEQILDALQR
 L

SEQ ID NO: 5717

STRAIN M732 frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQMP L TDKKS FASLI IDNNNGDLITLKEQILDALQR
 L

SEQ ID NO: 5718

STRAIN COH1 frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQMP L TDKKS FASLI IDNNNGDLITLKEQILDALQR
 L

SEQ ID NO: 5719

STRAIN M781 frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQMP L TDKKS FASLI IDNNNGDLITLKEQILDALQR
 L

SEQ ID NO: 5720

STRAIN CJB110 frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFVDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQMP L TDKKS FASLI INNNGDLITLKEQILDALQR
 L

SEQ ID NO: 5721

STRAIN 1169NT frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQ I PLTDKKS FASLI IDNNNGDLITLKEQMLDALQR
 L

SEQ ID NO: 5722

STRAIN JM9130013 frame: 1
 KSTVTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPEI LDADGELDRPKLSQMI
 FANPDNMKTSARLQNSI I RQELACQRDQLKQTEE I FFMDI PLLI EEKY I KWFDEI WL V FV
 DKEKQLQRLMARNNYSREAE LRLSHQ I PLTDKKS FASLI IDNNNGDLITLKEQMLDALQR
 L

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221398.2(*) February 10, 2003 07:15 ..

1 50
msa221398.2{245_090} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_CJB110} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_1169NT} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_H36B} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_JM9130013} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_18RS21} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_2603} mlmtkiigt ggiasgKSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_A909} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_COH1} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_M732} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_M781} -----KSTV TKI IRESGFK VIDADQVVHK LQAKGGKLYQ
Consensus *****

51 100
msa221398.2{245_090} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_CJB110} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_1169NT} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_H36B} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_JM9130013} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_18RS21} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_2603} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_A909} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_COH1} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_M732} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
msa221398.2{245_M781} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSI IRQELAC
Consensus *****

101 150
msa221398.2{245_090} QRDQLKQTEE IFFvDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_CJB110} QRDQLKQTEE IFFvDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_1169NT} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_H36B} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_JM9130013} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_18RS21} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_2603} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_A909} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_COH1} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_M732} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_M781} QRDQLKQTEE IFFmDIPLLI EEKYIKWFE IWLVFVDKEK QLQRLMARNN
Consensus *****

151 197
msa221398.2{245_090} YSREEAELRL SHQmPLTDKK SFASLIInNN GDLITLKEQi LDALQRL
msa221398.2{245_CJB110} YSREEAELRL SHQmPLTDKK SFASLIInNN GDLITLKEQi LDALQRL
msa221398.2{245_1169NT} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_H36B} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_JM9130013} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_18RS21} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_2603} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_A909} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_COH1} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_M732} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_M781} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
Consensus *****

Table 58: Comparative Sequences relating to SAG0182

SEQ ID NO. 5801

STRAIN 2603

ATGTTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTATGATTTTAGCCCTTTTATTG
GTAATAATAGTTATTTTAGACAGTTAATTGAAGAGCGGTCTAAACGTGAAACGGTAGTC
CTTGTCATCATTTCGGCTGTTGTTTATTATATCTAATATAACAGGAATTGAAATAAAA
GGGGATCGAAGTTTGGTCGAGCGCCCTTTCTAACACAGATTCTCATTCTGACTCACTT
GCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTGGTTGGA
TCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTCAAGGAAGCTTTTCAGGTTCT
TTCATATTGTGTCAGTTCAAGTTCTAGTCGGCATTGTAGCGGAAAGATTGGTGATAAGCTT
AAGGAAAACCATCTCTACCCCTTCAACAAGCCAAGTTATTTAATTAGTATTAATGCCGAA
AGTATCCAGATGCTATTTGTTGGCAITTTTACAGGATGGGAACCTGFCAAAATGATTGTC
ATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATTGTTGAAAAC
TATTTTGTCAAATGAAAGTCAGTTACCGCGAGTTCAAACGAGAGATGTTCTGAAATGACT
CGACAGACTCTGCGCTACCTTAGACAAGTTTACACCGCAATCTGCTAGGAGCGTTTGC
GAAATATAAAGAGGCATACTAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTA
TTAGCTCATATTGGTGTGGCCATGATCACCATTGTCAGGACAACCGGTCAAACAGAC
TTATCTAAAAGTGTATTATTAAATAGTTTAGGTTCCACACTTTTCTTGGCATTGTTGAAA
TCTTGTCCAGATCAACACTGTGAGTTAAATCTGCTATTGTAGTTCCTCTAAAATAAAT
GATAAACTGTGGTGGCTTAAAATGTACTTTGTCAGGAGATAAGACAATGTCTGAGGTG
GAGGAAAACCTAGTCTTGGTTTAGCGCAATATTTTCCAGGACAACCTGGCAATGGGGATA
ACAGAGGAACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTTACAAGCAAAAATC
AACCTCATTTCTCTTTAAATGCAATTAACACAATTAAGTGCATTAATCCGTTATTGATTCT
GATAAAGCAGTTATGCTACTGATGTCAGTTAAGTACTTTTTTGAACAAGTTTGCAGGTT
GGTCAGGATCGTGGGTAACGCTTACGCAAGAAAATCACATGTGGATGCTTATATGAAT
GTTGAAAAATTCAGTTTCCCTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAA
AAAATGAAGTTACCACCTTTGGTTTACAGGTAAGTTAGGATGAGAGATGCAAGTTCGACATGCT
TTCAAAGAACGTAAGACGGACAACCATATATTTGGTTCAAATAAAGCCAGATGGTCATTAT
TATTGTTGTTCTGTAGTGAATGGACAAGGAATCTCAGATACTATCATTGATAAATTA
GGTCAAGAAACAGTTGCAGAGAGTAAGGGTACAGGTACTGCTCTAGTTAATCTAAATAAC
AGGCTGAATTTATTATATGGTAGTGTAAAGTTGCCCTTCAATTTTCGAGCGCAAGAATGGT
ACAAAAGTTTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTAAT
TCT

SEQ ID NO. 5802

STRAIN 090

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT
GATTTTAGCCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG
AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCTCATTTTTTCGGCTTG
TTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG
TTTGGTTCGAGCGCCCTTTCTAACACAGATTTCCTATTCTGACTCACTTG
CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
CTGGTTGGATCAATTTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCA
AGGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTCAAGTTCTAGTCCGCA
TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT
TCAACAAGCCAAGTTATTTAATTAGTATTATGCGGAAAGTATCCAGAT
GCTATTGTTGGTATTTTACAGGATGGGAACCTGFCAAAATGATTGTCA
TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATT
TTGAAAACCTTATTGTCAAATGAAAGTCAGTTACCGCGAGTTCAAACGAG
AGATGTTCTTGAATGACTCGACAGACTCTGCGCTTACCTCAGACAAGGTT
TGACACCGCAATCTGCTAGGAGCGTTTTCGCAAAATATAAAGAGGCATACT
AACTTTGATGCTGTAGGATTAACAGATCGGTCAAACGTTATTAGCTCATAT
TGGTGTGGCCATGATCACCATATTGCAGGACAACAGTCAAACAGACC
TATCTAAAAGTGTATTTTTTGATGGCGAACCAAGAATTGCGCAAGATAAA
GCGGCGATTTCTGTCCAGATCACAACTGTGAGTTAAATTTCTGCTATTGT
AGTTCCCTTAAAATAAATGATAAAAATCTGCGGTCCTTAAAATGTAAT
TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT
TTAGCGCAATATTTTCAGGACAACCTGGCAATGGGATAACAGAGGAACA
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTTACAAGCAAAATCA
ACCTCATTTCTTCTTAAATGCCATTAACACAATTAGTGCATTAATCCGT
ATTGATTTCTGATAAAGCAGTTATGCACTGATGTCAGTTAAGTACTTTTTT
TAGAACAGTTTTCAGGTTGGTTCAGGATCGTGAGGTAACGCTTGAGCAAG
AAAATCACATGTGGATGCTTATATGAATGTTGAAAATTACGTTTCCCT
GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAATGAAGTT
ACCGCTTTTGGTTTACAGGTAAGTTAGGATGAGGATGAGGATGAGCATGCTT
TCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT
GGTCAITATTATTGTTCTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
TACTATCATTGATAAATTAGGTCAGGAAACAGTTGCAGAGAGTAAGGGTA
CAGGTAAGTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
AGTGTAAAGTTGCCCTTCAITTTTCGAGCGCAAGAATGGTACAAAAGTTTG
GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTAAT
CT

SEQ ID NO. 5803

STRAIN A909

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT
GATTTTAGCCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG
AAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTCTCATTTTTTCGGCTTG
TTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG
TTTGGTTCGAGCGCCCTTTCTAACACAGATTTCCTATTCTGACTCACTTG
CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
CTGGTTGGATCAATTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCA
AGGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTCAAGTTCTAGTCGGCA
TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT

Table 58: Comparative Sequences relating to SAG0182

TCAACAAGCCAAGTTATTTAATTAGTATTATGCGGAAAGTATCCAGAT
 GCTATTTGTTGGCATTTTTACAGGATGGGAACCTTGTCAAATGATTGTCA
 TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATT
 TTGAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
 AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTT
 TGACACCGCAATCTGCTAGGAGCGTTTTCGAAATTTAAAGAGGCATACCT
 AACCTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATAT
 TGGTGTGGCCATGATCACCATATTTGCAGGACAACCGGTCAAAACAGACT
 TATCTAAAAGTGTATTTTGTATGGCGAACCAAGAATTTGCCAAGATAAA
 GCGCGGATTTCTGTCCAGATCACAACCTGTCACTTAATTTCTGCTATTGT
 AGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCTTAAAAATGACT
 TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAACCTAGTCTTGGT
 TTAGCGCAAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
 AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAATCA
 ACCCTCATTTCTTCTTAAATGCCATTAACACAATTAGTGCATTAATCCGT
 ATTTGATTCGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT
 TAGAACCAAGTTTGCAGGGTGGTCAAGGATCGTGAAGTAAACGCTTGGAGCAAG
 AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
 GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTT
 ACCACCTTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTGCACATGCTT
 TCAAAGAACGTAAGACGGACAACCATATTTGGTTCAAATAAAGCCAGAT
 GGTCAATPATTATTTGTGTTTCTGTTAGTGACAAATGGACAAGGAATCTCAGA
 TACTATCATTGATAAATAGGTCAGAAACAGTTGCAGAGAGTAAGGGTA
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
 AGTGTAAAGTTGCCTTCAATTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTAATT
 CT

SEQ ID NO. 5804

STRAIN H36B

TTGATGGTGTGTTTATTCCAAGGCTAGGAATTATTATG
 ATTTTAGCCTTTTATTTGGTAAATAATAGTTATTTAGACAGTTAATTGA
 AGAGCGGTCTAAACGTTGAAACGGTAGTCTTGTTCATCATTTTCGGCTTGT
 TTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGT
 TTGGTTCGAGCGCCCTTTCTAACAACGATTTCTCATTCTGACTCACTTGC
 TAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTC
 TGGTTGGATCAATTTGTTGGTTTATTTGGAGGAGTTCATCGCTTTTTTCAA
 GGAAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCACTTCTAGTCGGCAT
 TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTT
 CAACAAGCCAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGATG
 CTATTTGTTGGCATTTTTACAGGATGGGAACCTTGTCAAATGATTGTTCAT
 TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATT
 TGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA
 GATGTTCTTGAATGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT
 GACACCGCAATCTGCTAGGAGCGTTTGGCAAAATTAAGAGAGGCATACTA
 ACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGATTTAGCTCATATT
 GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGACTT
 ATCTAAAAGTGTATTTTGTATGGCGAACCAAGAATTGCCAAGATAAAG
 CGGCGATTTCTTGTCCAGATCACAACCTGTCACTTAAATTTCTGCTATTGTA
 GTTCTCTAAAATAAATGATAAACTGTGGGTGCCTTAAAATGTAAGTT
 TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGTT
 TAGCGCAAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAATCAA
 CCTCATTTCTTCTTAAATGCCATTAACACAATTAGTGCATTAATCCGTA
 TTGATTTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT
 AGAACCAAGTTTGCAGGGTGGTCAAGGATCGTGAAGTAAACGCTTGGAGCA
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG
 ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTTA
 CCACCTTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTTCGACATGCTTT
 CAAAGAACGTAAGACGGACAACCATATATTTGGTTCAAATAAAGCCAGATG
 GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT
 ACTATCATTGATAAATAGGTCAGAAACAGTTGCAGAGAGTAAGGGTAC
 AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA
 GTGTAAGTTGCCTTCAATTTTTCGAGCGACAAGAATGGTACAAAAGTTTG
 TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTAATTC
 T

SEQ ID NO. 5805

STRAIN 18RS21

TTGATGGTGTGTTTATTCCAAGGCTAGGAATTATTATG
 ATTTTAGCCTTTTATTTGGTAAATAATAGTTATTTAGACAGTTAATTGA
 AGAGCGGTCTAAACGTTGAAACGGTAGTCTTGTTCATCATTTTCGGCTTGT
 TTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGT
 TTGGTTCGAGCGCCCTTTCTAACAACGATTTCTCATTCTGACTCACTTGC
 TAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTC
 TGGTTGGATCAATTTGTTGGTTTATTTGGAGGAGTTCATCGCTTTTTTCAA
 GGAAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCACTTCTAGTCGGCAT
 TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTT
 CAACAAGCCAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGATG
 CTATTTGTTGGCATTTTTACAGGATGGGAACCTTGTCAAATGATTGTTCAT
 TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATT
 TGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA
 GATGTTCTTGAATGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT

Table 58: Comparative Sequences relating to SAG0182

GACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAGAGGCATACTA
 ACITTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATATT
 GGTGTTGGCCATGATCACCATATTGCAGGACAAACCGGTCAAAACAGACTT
 ATCTAAAAGTGTATTATTTTGGATGGCGAACCAAGaATTGCGCAAGATAAAG
 CGGCGATTTCTTGTCCAGATCAACAACGTGTCAGTTAAATTCTGCTATTGTA
 GTTCCTTAAAATAAATGATAAACTGTGGTGCCTTAAAATGTACTT
 TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCCTGGTT
 TAGCGCAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAA
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAATCAA
 CCCTCATTTCTTCTTAAATGCCATTAAACAATTAGTGCATTAAATCCGTA
 TTGATTCTGATAAAGCACGTTATGCACCTGATGCAGTTAAGTACTTTTTTT
 AGAACAAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGA
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATACGTTTCCCTG
 ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTA
 CCACCTTTTGGTTTACAGTACTGGTAGAGAATGCAGTTTCGACATGCTTT
 CAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG
 GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT
 ACTATCATTGATAAATTAGGTCAAGAACAGTTGCAGAGAGTAAGGGTAC
 AGGTACTGCTCAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA
 GTGTAAGTTGCTTCAITTTTCGAGCGACAAGATGGTACAAAAGTTTGG
 TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAATTC
 T

SEQ ID NO. 5806
 STRAIN M732

TTGATGGTGTGTTTATCCAAAGGCTAGGAATTTATTATGAT
 TTTAGCCTTTTATTTGGTAAATAATAGTTATTTTCAGACAGTTAATGAAG
 AGCGGTCTAAACGTTGAAACGGTAGTCCCTTGTTCATCATTTTTCGGCTTGT
 GTTATTATATCTAATAATAACAGGAATGAAATAAAGGGGATCGAAGTTT
 GGTTCGAGCGCCCTTTTCTAACACAGGATTTCCCATTCGACTCAGCTGCTA
 ATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTG
 GTTGGATCAATGTTGGTTTATTTGGAGGAGTTCATCGCTTTTTTCAAG
 AAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCAGTTCTAGTCCGCAITG
 TTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAAACCATCTCTACCCCTTCA
 ACAAGCCAAGTTATTTTAAATAGTATTATTGCGGAAAGTATCCAGATGCT
 ATTTGTTGGCATTTTTTACAGGATGGGAACCTTGTCAAATGATTGTCAITC
 CAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGATTTTG
 AAAAATTATTGTTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGA
 TGTTCCTGAATGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTTGA
 CACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAGAGGCATACTAAC
 TTTGATGCTGTGGGATTAACAGATCGGTCAAACGTTATTAGCTCATATTGG
 TATTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGACTTAT
 CTAAAAGTGTATTATTGATGGCGAACCAAGAATTGCGCAAGATAAAGCG
 GCGAATTCTGTCCAGATCAACAACGTGTCAGTTAAATCTGTCTATTGTAGT
 TCCCTTAAAATAAATGATAAACTGTGTGTGCCCTTAAAATGTACTTTG
 CAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCCTTGGTTTA
 GCGCAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAAA
 TAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAATCAACC
 CTCATTTCTTCTTAAATGCCATTAAACAATTAGTGCATTAAATCCGTATT
 GATTCTGATAAAGCACGTTATGCACCTGATGCAGTTAAGTACTTTTTTTAG
 AACAAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGAAA
 AATCACATGTGGATGCTTATATGAATGTTGAAAAATACGTTTCCCTGAT
 AAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTTACC
 GCCTTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTTCGACATGCTTTCA
 AAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGTT
 CATATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGATAC
 TATCATTGATAAATTAGGTCAAGAACAGTTGCAGAGAGTAAGGGGACAG
 GTACTGCTCAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTAGT
 GTAAGTTGCTTCAITTTTCGAGCGACAAGAAATGGTACAAAAGTTTGGTA
 TCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAATTC

SEQ ID NO. 5807
 STRAIN COHI

TTGATGGTGTGTTTATTTCCAAAGGCTAGGAATTTAT
 TATGATTTTTCAGCTTTTATTTGGTAAATAATAGTTATTTTCAGACAGTTAA
 TTGAAGAGCGGTCTAAACGTTGAAACGGTAGTCCCTTGTTCATCATTTTTCGGC
 TTGTTTGTATTATATCTAATAATAACAGGAATGAAATAAAGGGGATCG
 AAGTTTGGTTCGAGCGCCCTTTTCTAACACAGATTTCCCATTCGACTCAC
 TTGCTAAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGGA
 CCTCTGGTTGGATCAATGTTGGTFTTATTTGGAGGAGTTCATCGCTTTTT
 TCAAGGAAGCTTTTTCAGGTTCTTTCTATATTGTTCAGTTTCAGTTCTAGTCC
 GCAATGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAAACCATCTCTAC
 CCTTCAACAAGCCAAAGTTATTTTAAATAGTATTATTGCCGAAAGTATCCA
 GATGCTATTGTTGGCATTTTTACAGGATGGGAACCTTGTCAAATGATTG
 TCATTTCAAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGG
 ATTTTGAACACTTATTGTTCAAATGAAAGTCAGTTACGCGCAGTTCAAAC
 GAGAGATGTTCTGAAATGACTCGACAGACTCTGCCCTACCTTAGACAAG
 GTTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCAT
 ACTAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTTATTAGCTCA
 TATTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAG
 ACTTATCTAAAAGTGTATTATTGATGGCGAACCAAGAATGCGCAAGAT
 AAAGCGGATTTCTTGTCCAGATCAACAACGTGTCAGTTAAATCTGCTAT
 TGTAGTTCTCTAAAATAAATGATAAACTGTGTGTGCCCTTAAAATGT

Table 58: Comparative Sequences relating to SAG0182

ACTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTT
GGTTTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGA
ACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAA
TCAACCCTCATTTCTTCTTTAAAGCCATTAAACACAATTAGTGCATTAATC
CGTATTGATTTCTGATAAAGCACGTTATGCACCTGATGCAGTTAAGTACTTT
TTTTAGAACAAGTTTGCAGGTGGTCCAGGATCGTGAGGTAACGCTTGAGC
AAGAAAATCACATGTGGATGCTTATATGAATGTTGAAAATACGTTTC
CCTGATAAATATCAGTTATCTTATGATATTAGTGACCAGAAAATGAA
GTTACCGCTTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTGCACATG
CTTTCAAAGAACGTAAGACGGACAACCATATATTGGTCAAATAAAGCCA
GATGGTCATTATTATTTGTGTTCTGTTAGTGACAATGGACAAGGAATCTC
AGATACTATCATTGATAAATTAGGTCAGAAAACAGTTGCAGAGAGTAAGG
GGACAGGTACTGCTTAGTTAATCTAAATAACAGGCTGAATTTATTATAT
GGTAGTGAAGTTGCCTTCATTTTCGAGCGACAAGAATGGTACAAAAGT
TTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTA
ATTCT

SEQ ID NO. 5808

STRAIN M781

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTA
TGATTTAGCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATT
GAAGACGGTCTAAACGTTGAAACGGTAGTCCCTGTGTCATCATTTTCGGCTG
GTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAA
GTTTGGTCGAGCGCCCTTTCTAACACAGATTCCCATTTCTGACTCACTT
GCTAATAACAAGGACTTTAGTTATTACAAACGGCAAGTTTGGTTGGTGGACC
TCTGGTTGGATCAATTTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTTC
AAGGAAGCTTTTCAGGTTCTTTCTATATGTCAGTTTCAGTTCTAGTCGGC
ATTGTTAGCGGAAAGATTGGTGATAGCTTAAGGAAAACCATCTCTACCC
TTCAACAAGCCAAGTTAATTTAATTAGTATTATGCGGAAAGTATCCAGA
TGCATTTGTTGGCATTTTACAGGATGGGAACCTGTCAAATGATTGTC
ATTCCAATGATGATTTAATAAGTTTAGGTTCCACACTTTTCCTTGCGAT
TTTGAAAACCTTATTGTTCAAATGAAAGTCAGTTACGCGCAGTTCAAAACGA
GAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAGGTT
TTGACACCGCAATCTGCTAGGAGCGTTTGGCAAAATATAAAGAGGCATAC
TAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTTATGACTCATA
TTGGTGTGGCCATGATCACCATATTGCAAGGCAACCGGTCAAACAGAC
TTATCTAAAAGTGTATTTTTGTATGGCGAACCAAGAATTGCGCAAGATAA
AGCGGCGATTCTTGTGTCAGATCACAACTGTGAGTTAAATTTCTGCTAATTG
TAGTTCTCTAAAAATAAATGATAAACTGTGTGTGCTTAAAAATGTAC
TTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGG
TTTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAAC
AAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATC
AACCTCATTTCTTCTTAAATGCCATTAAACACAATTAGTGCATTAAATCCG
TATTGATTTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTT
TTAGAACAAGTTTTCAGGTTGGTCCAGGATCGTGAGGTAACGCTTGAGCAA
GAAAATCACATGTGGATGCTTATATGAATGTTGAAAATACGTTTCCC
TGATAAATATCAGTTATCTTATGATATTAGTGACCAGAAAATAAAGGAA
TACCGCCTTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTTCGACATGCT
TTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGA
TGGTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAG
ATACTATCATTGATAAATTAGGTCAGAAAACAGTTGCAGAGAGTAAGGGG
ACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGG
TAGTGTAAAGTTGCCTTCATTTTCGAGCGACAAGAATGGTACAAAAGTTT
GGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTAAT
TCT

SEQ ID NO. 5809

STRAIN CJB110

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTA
GATTTTAGCCTTTTATTTGGTAAATAATAGTTATTTTCAGACAGTTAATTG
AAGACGGTCTAAACGTTGAAACGGTAGTACTTGTGTCATCATTTTCGGCTG
TTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG
TTTGGTCGAGCGCCCTTTCTAACACAGATTTCCTCATTTCTGACTCACTTG
CTAATAACAAGGACTTTAGTTATTACAAACGGCAAGTTTGGTTGGTGGACCT
CTGGTTGGATCAATTTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTTCA
AGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAGTTCTAGTCGGCA
TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT
TCAACAAGCCAAGTTAATTTAATTAGTATTATTGCGGAAAGTATCCAGAT
GCTATTTGTTGGTATTTTTACAGGATGGGAACCTGTCAAATAAGATTGTC
TTCCAATGATGATTTAATAAGTTTAGGTTCCACACTTTCTCTTGGGATT
TTGAAAACCTTATTGTTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT
TGACACCGCAATCTGCTAGGAGCGTTTGGCAAAATATAAAGAGGCATACT
AACTTTGATGCTGTAGGATTAACAGATCGGTCAAACGTTATTAGCTCATAT
TGGTGTGGCCATGATCACCATATTGCAAGCAACCAAGTCAAACAGACC
TATCTAAAAGTGTATTTTTGTATGGCGAACCAAGAATTGCGCAAGATAAA
GCGGCGATTTCTGTCCAGATCACAACTGTCAAGTTAAATTTCTGCTATTGT
AGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACT
TTGCAAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTCTGGT
TTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA
ACCTCATTTTTCTTTAATGCCATTAAACACAATTAGTGCATTAATCCGT
ATTGATTTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT

Table 58: Comparative Sequences relating to SAG0182

TAGAACAAAGTTTGC AAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG
AAAAATCACATGTTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
GATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAGTT
ACCGCCTTTTGGTTTACAGGTAAGTGGTAGAATGCAGTTAGACATGCTT
TCAAAGAACGTAAGACGGACAACCATATATTTGGTTCAAATAAAGCCAGAT
GGTCATTATTTATGTTGTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
TACTATCATTGATAAATTAGGTCAGAAACAGTTGCAGAGAGTAAGGGTA
CAGGTAAGTCTAGTTAATCTAAATAACAGGCTGAATTTATATATGTT
AGTGTAAAGTTGCCCTTCAATTTTTCGAGCGACAAGATGTTACAAAAGTTTG
GTATCGAATACCTAATAGAAATAAGGGAGGATGAGCATGAAAATTTTAAAT
CT

SEQ ID NO. 5810

STRAIN I169NT

TTGATGGTGTGTTATTCCAAGGCTAGGAATTATT
ATGATTTTAGCCTTTTATTTGGTAATAATAGTTATTTTCAGACAGTTAAT
TGAAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTTCATCATTTTCGGCT
TGTTTGTATATATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA
AGTTTGGTCGAGCGCCCTTTTCTAACACAGATTTCTCATTCTGACTCACT
TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC
CTCTGGTTGGATCAATTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC
CAAGGAAGCTTTTCAGGTTCTTTCTATATTTGTCAGTTCAAGTTCTAGTCGG
CATTGTGAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC
CTTCAACAAGCCAAGTTATTTTAAATAGTATTTATGCGGAAAGTATCCAG
ATGCTATTTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTTGT
CATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCA
TTTTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACG
AGAGATGTTCTTGAATGACTCGACAGACTCTGCCCTACCTTAGACAAGG
TTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATATAAAGAGGCATA
CTAATTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCAT
ATTGGTGTGGCCATGATCACCATATTTGCAGGACAACCAAGTCAAACAGCA
CCTATCTAAAAGTGTATTTTGGATGGCGAACCAAGAATTGCGCAAGATA
AAGCGGCGATTTCTGTCCAGATCACAACTGTGAGTTAAATTTCTGCTATT
GTAGTTCTCTAAAATAAATGATAAACTGTGGTGCCTTAAAATGTA
CTTTGAGGAGATAAAGCAATGCTGAGGTGGAGGAAAACCTAGTCTCTTG
GTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA
CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAAT
CAACCTCATTTCTTCTTAAATGCCATTAAACAATTAGTGCATTAAATCC
GTATTGATTCGTAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT
TTTAGAACAAAGTTTGC AAGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCA
AGAAAAATCACATGTTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC
CTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAG
TTACCGCCTTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTTCGACATGC
TTTTAAAGAACGTAAGACGGACAACCATATATTTGGTTCAAATAAAGCCAG
ATGGTCATTATTTATGTTGTTCTGTTAGTGACAATGGACAAGGAATCTCA
GATACTATCATTGATAAATTAGGTCAGAAACAGTTGCAGAGAGTAAGGG
TACAGGTAAGTCTAGTTAATCTAAATAACAGGCTGAATTTTATATATG
GTAGTGTAAAGTTGCCCTTCAATTTTTCGAGCGACAAGAAATGTTACAAAAGTT
TGGTATCGAATACCTAATAGAAATAAGGGAGGATGAGCATGAAAATTTTAA
TTCT

SEQ ID NO. 5810

STRAIN JM9130013

TTGATGGTGTGTTATTCCAAGGCTAGGAATTATT
ATGATTTTAGCCTTTTATTTGGTAATAATAGTTATTTTCAGACAGTTAAT
TGAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTTCATCATTTTCGGCT
TGTTTGTATATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA
AGTTTGGTCGAGCGCCCTTTTCTAACACAGATTTCTCATTCTGACTCACT
TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC
CTCTGGTTGGATCAATTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC
CAAGGAAGCTTTTCAGGTTCTTTCTATATTTGTCAGTTCAAGTTCTAGTCGG
CATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC
CTTCAACAAGCCAAGTTATTTTAAATAGTATTTATGCGGAAAGTATCCAG
ATGCTATTTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTTGT
CATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCA
TTTTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACG
AGAGATGTTCTTGAATGACTCGACAGACTCTGCCCTACCTTAGACAAGG
TTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATATAAAGAGGCATA
CTAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCAT
ATTGGTGTGGCCATGATCACCATATTTGCAGGACAACCGGTCAAACAGCA
CTTATCTAAAAGTGTATTTTGGATGGCGAACCAAGAATTGCGCAAGATA
AAGCGGCGATTTCTTGTCCAGATCACAACTGTGAGTTAAATTTCTGCTATT
GTAGTTCTCTAAAATAAATGATAAACTGTGGTGCCTTAAAATGTA
CTTTGAGGAGATAAAGACAATGCTGAGGTGGAGGAAAACCTAGTCTCTTG
GTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA
CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAAT
CAACCTCATTTCTTCTTAAATGCCATTAAACAATTAGTGCATTAAATCC
GTATTGATTCGTAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT
TTTAGAACAAAGTTTGCAGGTTGGTCAGGATCGTGAGGTAACGCTTGAGCA
agAAAAATCACATGTTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC
CTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAG
TTACACCTTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTTCGACATGC
TTTCAAAGAACGTAAGACGGACAACCATATATTTGGTTCAAATAAAGCCAG

Table 58: Comparative Sequences relating to SAG0182

ATGGTCATTATTATTGTGTTTCTGTTAGTGACAAATGGACAAGGAATCTCA
GATACTATCATTGATAAATTAGGTCAGAAACAGTTGCAGAGAGTAAGGG
TACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG
GTAGTGTAGTTGCCCTTCATTTTTCGAGCGGACAAGAAATGGTACAAAAGTT
TGGTATCGAATACCTAATAGAATAAAGGGAGGATGAGCATGAAAATTTTAA
TTCT

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa442667.2{*} January 13, 2003 06:34 ..

1 50
msa442667.2{248_18RS21} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_2603} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_A909} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_H36B} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_JM9130013} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_COH1} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M781} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M732} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_090} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_CJB110} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_1169NT} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
Consensus *****

51 100
msa442667.2{248_18RS21} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_2603} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_A909} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_H36B} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_JM9130013} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_COH1} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M781} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M732} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_090} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_CJB110} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_1169NT} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
Consensus *****

101 150
msa442667.2{248_18RS21} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_2603} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_A909} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_H36B} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_JM9130013} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_COH1} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_M781} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_M732} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_090} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_CJB110} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
msa442667.2{248_1169NT} AACGTGAAAC GGTAGTcCTT GTCATCATT TCGGCTTGTT TGTTATTATA
Consensus *****

151 200
msa442667.2{248_18RS21} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_2603} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_A909} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_H36B} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_JM9130013} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_COH1} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M781} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M732} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_090} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_CJB110} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_1169NT} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
Consensus *****

201 250
msa442667.2{248_18RS21} CCCITTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_2603} CCCITTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_A909} CCCITTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_H36B} CCCITTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_JM9130013} CCCITTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_COH1} CCCITTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M781} CCCITTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M732} CCCITTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_090} CCCITTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_CJB110} CCCITTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_1169NT} CCCITTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
Consensus *****

251 300
msa442667.2{248_18RS21} CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTGGATCA
msa442667.2{248_2603} CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTGGATCA

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_A909}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_H36B}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_JM9130013}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_COH1}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M781}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M732}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_090}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_CJB110}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_1169NT}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
Consensus	*****	*****	*****	*****	*****

msa442667.2{248_18RS21}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_2603}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_A909}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_H36B}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_JM9130013}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_COH1}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_M781}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_M732}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_090}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_CJB110}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
msa442667.2{248_1169NT}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCITTTT
Consensus	*****	*****	*****	*****	*****

msa442667.2{248_18RS21}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_2603}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_A909}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_H36B}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_JM9130013}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_COH1}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_M781}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_M732}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_090}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_CJB110}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
msa442667.2{248_1169NT}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTLAGCGGAA
Consensus	*****	*****	*****	*****	*****

msa442667.2{248_18RS21}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_2603}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_A909}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_H36B}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_JM9130013}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_COH1}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_M781}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_M732}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_090}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_CJB110}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_1169NT}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
Consensus	*****	*****	*****	*****	*****

msa442667.2{248_18RS21}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_2603}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_A909}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_H36B}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_JM9130013}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_COH1}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M781}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M732}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_090}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_CJB110}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_1169NT}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
Consensus	*****	*****	*****	*****	*****

msa442667.2{248_18RS21}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_2603}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_A909}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_H36B}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_JM9130013}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_COH1}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_M781}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_M732}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_090}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_CJB110}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
msa442667.2{248_1169NT}	cATTTTAC	GGATGGGAAC	TTGTCAAAAT	GATTGTCATT	CCAATGATGA
Consensus	*****	*****	*****	*****	*****

msa442667.2{248_18RS21}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTAT
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Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_2603}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_A909}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_H36B}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_JM9130013}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_COH1}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_M781}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_M732}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_090}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_CJB110}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
msa442667.2{248_1169NT}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTTAT
Consensus	*****	*****	*****	*****	*****
601					
msa442667.2{248_18RS21}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_2603}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_A909}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_H36B}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_JM9130013}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_COH1}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M781}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M732}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_090}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_CJB110}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_1169NT}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
Consensus	*****	*****	*****	*****	*****
651					
msa442667.2{248_18RS21}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_2603}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_A909}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_H36B}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_JM9130013}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_COH1}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_M781}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_M732}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_090}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_CJB110}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
msa442667.2{248_1169NT}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCCGAAT
Consensus	*****	*****	*****	*****	*****
701					
msa442667.2{248_18RS21}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_2603}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_A909}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_H36B}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_JM9130013}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_COH1}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_M781}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_M732}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_090}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_CJB110}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
msa442667.2{248_1169NT}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	cTTTGATGCT
Consensus	*****	*****	*****	*****	*****
751					
msa442667.2{248_18RS21}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_2603}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_A909}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_H36B}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_JM9130013}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_COH1}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M781}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M732}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_090}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_CJB110}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_1169NT}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
Consensus	**..*****	*****	*****	*****	**..*****
801					
msa442667.2{248_18RS21}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_2603}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_A909}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_H36B}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_JM9130013}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_COH1}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_M781}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_M732}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_090}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_CJB110}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
msa442667.2{248_1169NT}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGACTTA	TCTAAAAGTG
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_2603}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_A909}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_H36B}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_JM9130013}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_COH1}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_M781}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_M732}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_090}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_CJB110}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_1169NT}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
Consensus	*****	*****	*****	*****	*****
	901				950
msa442667.2{248_18RS21}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_2603}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_A909}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_H36B}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_JM9130013}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_COH1}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M781}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M732}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_090}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_CJB110}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_1169NT}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
Consensus	*****	*****	*****	*****	*****
	951				1000
msa442667.2{248_18RS21}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_2603}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_A909}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_H36B}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_JM9130013}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_COH1}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M781}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M732}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_090}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_CJB110}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_1169NT}	AATAAATGAT	AAAACGTGCG	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa442667.2{248_18RS21}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_2603}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_A909}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_H36B}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_JM9130013}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_COH1}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M781}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M732}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_090}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_CJB110}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_1169NT}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa442667.2{248_18RS21}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_2603}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_A909}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_H36B}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_JM9130013}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_COH1}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M781}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M732}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_090}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_CJB110}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_1169NT}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa442667.2{248_18RS21}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_2603}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_A909}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_H36B}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_JM9130013}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_COH1}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M781}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M732}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_090}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_CJB110}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_1169NT}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

	1151			1200	
msa442667.2{248_18RS21}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_2603}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_A909}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_H36B}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_JM9130013}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_COH1}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_M781}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_M732}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_090}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_CJB110}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
msa442667.2{248_1169NT}	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	TGATTCTGAT
Consensus	*****	*****	*****	*****	*****
	1201			1250	
msa442667.2{248_18RS21}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_2603}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_A909}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_H36B}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_JM9130013}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_COH1}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_M781}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_M732}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_090}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_CJB110}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
msa442667.2{248_1169NT}	AAAGCACGTT	ATGCACCTGAT	GCAGTTAAGT	ACTTTTTTTTA	GAACAAGTTT
Consensus	*****	*****	*****	*****	*****
	1251			1300	
msa442667.2{248_18RS21}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_2603}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_A909}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_H36B}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_JM9130013}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_COH1}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_M781}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_M732}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_090}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_CJB110}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
msa442667.2{248_1169NT}	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	AAATCACATG
Consensus	***-*****	*****	*****	*****	*****
	1301			1350	
msa442667.2{248_18RS21}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_2603}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_A909}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_H36B}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_JM9130013}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_COH1}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_M781}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_M732}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_090}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_CJB110}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
msa442667.2{248_1169NT}	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	TAAATATCAG
Consensus	*****	*****	*****	*****	*****
	1351			1400	
msa442667.2{248_18RS21}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CaCCTTTTGG
msa442667.2{248_2603}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CaCCTTTTGG
msa442667.2{248_A909}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CaCCTTTTGG
msa442667.2{248_H36B}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CaCCTTTTGG
msa442667.2{248_JM9130013}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CaCCTTTTGG
msa442667.2{248_COH1}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CgCCTTTTGG
msa442667.2{248_M781}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CgCCTTTTGG
msa442667.2{248_M732}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CgCCTTTTGG
msa442667.2{248_090}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CgCCTTTTGG
msa442667.2{248_CJB110}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CgCCTTTTGG
msa442667.2{248_1169NT}	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	CgCCTTTTGG
Consensus	*****	*****	*****	*****	*-*****
	1401			1450	
msa442667.2{248_18RS21}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_2603}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_A909}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_H36B}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_JM9130013}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_COH1}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_M781}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_M732}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_090}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_CJB110}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
msa442667.2{248_1169NT}	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	AAAGAACGTA
Consensus	*****	*****	*****-*	*****	*****

Table 58: Comparative Sequences relating to SAG0182

	1451			1500	
msa442667.2{248_18RS21}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_2603}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_A909}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_H36B}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_JM9130013}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_COH1}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_M781}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_M732}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_090}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_CJB110}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
msa442667.2{248_1169NT}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT
Consensus	*****	*****	*****	*****	*****
	1501			1550	
msa442667.2{248_18RS21}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_2603}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_A909}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_H36B}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_JM9130013}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_COH1}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_M781}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_M732}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_090}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_CJB110}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
msa442667.2{248_1169NT}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA
Consensus	*****	*****	*****	*****	*****
	1551			1600	
msa442667.2{248_18RS21}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_2603}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_A909}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_H36B}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_JM9130013}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_COH1}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_M781}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_M732}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_090}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_CJB110}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
msa442667.2{248_1169NT}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGTACA	GGTACTGCTC
Consensus	*****	*****	*****	*****	*****
	1601			1650	
msa442667.2{248_18RS21}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_2603}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_A909}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_H36B}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_JM9130013}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_COH1}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_M781}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_M732}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_090}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_CJB110}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
msa442667.2{248_1169NT}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC
Consensus	*****	*****	*****	*****	*****
	1651			1700	
msa442667.2{248_18RS21}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_2603}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_A909}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_H36B}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_JM9130013}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_COH1}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_M781}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_M732}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_090}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_CJB110}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
msa442667.2{248_1169NT}	CTTCATTTT	CGAGCGACAA	GAATGGTACA	AAAGTTTGGT	ATCGAATACC
Consensus	*****	*****	*****	*****	*****
	1701			1740	
msa442667.2{248_18RS21}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_2603}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_A909}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_H36B}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_JM9130013}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_COH1}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_M781}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_M732}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_090}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_CJB110}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	
msa442667.2{248_1169NT}	TAATAGAATA	AGGGAGGATG	AGCATGAAAA	TTTTAATTCT	

Table 58: Comparative Sequences relating to SAG0182

Consensus *****

SEQ ID NO. 5811
STRAIN 2603 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVVLIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLGSSTLFLAIIKTYLSNESQLRAVQTRDVLELRTQTLPLYRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHIIVQIKPDGHYICVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRI REDEHENFNS

SEQ ID NO. 5812
STRAIN 090 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVVLIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLGSSTLFLAIIKTYLSNESQLRAVQTRDVLELRTQTLPLYRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHIIVQIKPDGHYICVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRI REDEHENFNS

SEQ ID NO. 5813
STRAIN A909 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVVLIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLGSSTLFLAIIKTYLSNESQLRAVQTRDVLELRTQTLPLYRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHIIVQIKPDGHYICVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRI REDEHENFNS

SEQ ID NO. 5814
STRAIN H36B frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVVLIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLGSSTLFLAIIKTYLSNESQLRAVQTRDVLELRTQTLPLYRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHIIVQIKPDGHYICVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRI REDEHENFNS

SEQ ID NO. 5815
STRAIN 18RS21 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVVLIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLGSSTLFLAIIKTYLSNESQLRAVQTRDVLELRTQTLPLYRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHIIVQIKPDGHYICVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRI REDEHENFNS

SEQ ID NO. 5816
STRAIN M732 frame: 1
LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVVLIIFGLFVIISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLGSSTLFLAIIKTYLSNESQLRAVQTRDVLELRTQTLPLYRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHIIVQIKPDGHYICVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRI REDEHENFNS

SEQ ID NO. 5817

Table 58: Comparative Sequences relating to SAG0182

STRAIN COH1 frame: 1
LMVLLFQRLGIIMILAFLLVNNNSYFRQLIEERSKRETVVLLVIFGLFVVISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTSASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLSTLFLAIIKTYLSNESQLRAVQTRDVLRLTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINNTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5818
STRAIN M781 frame: 1
LMVLLFQRLGIIMILAFLLVNNNSYFRQLIEERSKRETVVLLVIFGLFVVISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTSASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLSTLFLAIIKTYLSNESQLRAVQTRDVLRLTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINNTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5819
STRAIN CJB110 frame: 1
LMVLLFQRLGIIMILAFLLVNNNSYFRQLIEERSKRETVVLLVIFGLFVVISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTSASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLSTLFLAIIKTYLSNESQLRAVQTRDVLRLTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINNTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5820
STRAIN 1169NT frame: 1
LMVLLFQRLGIIMILAFLLVNNNSYFRQLIEERSKRETVVLLVIFGLFVVISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTSASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLSTLFLAIIKTYLSNESQLRAVQTRDVLRLTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINNTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5821
STRAIN JM9130013 frame: 1
LMVLLFQRLGIIMILAFLLVNNNSYFRQLIEERSKRETVVLLVIFGLFVVISNITGIEIKG
DRSLVERPFLTTISHSDSLANTRTLVITTSASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGI FTGWELVKMIVI
PMMILNSLSTLFLAIIKTYLSNESQLRAVQTRDVLRLTRQTLPYLRQGLTPQSARSVCE
IIKRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
CPDHNCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
EEQNKLASMAEIKALQAQINPHFFFNAINNTISALIRIDSDKARYALMQLSTFFRTSLQGG
QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNRR
LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

PRETTY of: /biotmp/msa442834.2{*} January 13, 2003 06:47 ..

Table with 5 columns: Accession/ID, Position, Consensus, and two sequence columns. Rows include msa442834.2{248_090}, msa442834.2{248_1169NT}, and Consensus. A second table below shows alignment between msa442834.2{248_090} and msa442834.2{248_1169NT} from position 51 to 100.

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_18RS21}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
msa442834.2{248_2603}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
msa442834.2{248_A909}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
msa442834.2{248_CJB110}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
msa442834.2{248_H36B}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
msa442834.2{248_JM9130013}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
msa442834.2{248_COH1}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
msa442834.2{248_M781}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
msa442834.2{248_M732}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTLVLVITTA	SLVGGPLVGS
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_1169NT}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_18RS21}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_2603}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_A909}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_CJB110}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_H36B}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_JM9130013}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_COH1}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M781}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M732}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_1169NT}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_18RS21}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_2603}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_A909}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_CJB110}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_H36B}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_JM9130013}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_COH1}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M781}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M732}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_1169NT}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_18RS21}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_2603}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_A909}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_CJB110}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_H36B}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_JM9130013}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_COH1}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M781}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M732}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_1169NT}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_18RS21}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_2603}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_A909}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_CJB110}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_H36B}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_JM9130013}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_COH1}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_M781}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
msa442834.2{248_M732}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEF	RIAQDKAAIS
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_1169NT}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_18RS21}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_2603}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_A909}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_CJB110}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_H36B}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_JM9130013}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_COH1}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M781}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M732}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINI	ISALIRIDSD

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_1169NT}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_18RS21}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_2603}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_A909}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_CJB110}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_H36B}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_JM9130013}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_COH1}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_M781}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
msa442834.2{248_M732}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAINT	ISALIRIDSD
Consensus	*****	*****	*****	*****	*****
	401				450
msa442834.2{248_090}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_1169NT}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_18RS21}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_2603}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_A909}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_CJB110}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_H36B}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_JM9130013}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_COH1}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_M781}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_M732}	KARYALMQLS	TFFRSLOGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
Consensus	*****	*****	*****	*****	*****
	451				500
msa442834.2{248_090}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_1169NT}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_18RS21}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_2603}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_A909}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_CJB110}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_H36B}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_JM9130013}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_COH1}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M781}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M732}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
Consensus	*****	*****	*****	*****	*****
	501				550
msa442834.2{248_090}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_1169NT}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_18RS21}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_2603}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_A909}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_CJB110}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_H36B}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_JM9130013}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_COH1}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M781}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M732}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
Consensus	*****	*****	*****	*****	*****
	551				580
msa442834.2{248_090}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_1169NT}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_18RS21}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_2603}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_A909}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_CJB110}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_H36B}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_JM9130013}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_COH1}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M781}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M732}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
Consensus	*****	*****	*****		

Table 59: Comparative Sequences relating to SAG2147

SEQ ID NO. 5901
 STRAIN 2603
 ATGAATAAAGAGAAAATTATCAAATTTGAATGTAAAAAACATCATTTAGCTTATGGA
 GCTATCACITTTAGTAGCCCTTTTTTCATGTATTTGGCTGTAAATGGTCATCTTTAAAAGT
 TCACAAGTTACTACTGAATCTTTGTCAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCA
 AAAATGACTAAGGCGACATCTAAATCAAAGTAGAAGATGTAAAAACAGGCTCCAAAACCT
 TCTCAGGCACTAATGAAGCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAG
 CAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAAACAGAAAACACC
 CCTGCTACCCAGTCAGGCACAACAAGCTTATGCTGTACTGAGACAACCTTATAGACCTGCT
 CAACACCAGACGAGTGGCCAAATATTGAGTAAATGGAATACTGCAGGGGCTATTGGCTCA
 GCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATT
 ATTGCCCGTGAATCAAATGGTAACTCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTT
 TTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTTCAGCT
 ATTAAGCTTATCGTGTCAAGGTTTATCAGCTTGGGGTTACTAG

SEQ ID NO. 5902
 STRAIN JM9130013
 AAAAGTTCAACAAGTTACTACTGAATCTTTGTCAA
 AGCAGATAAAGTTTCGCGTAGCCAAAAATCAAATGAATAAGGCAACAT
 CTAATCAAAGTAGAAGGTGTAAAAACAGGCTCCAAAACCAAGTTCTCAA
 TCTACAGAAGCTAATCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGC
 TGTAGAACAAAGCAGTTGTAAACAGAAAATACCCTGCTACCAGTCAAGCAC
 AACAGCTTATGCTGTACTGAGACAACCTTATAGACCTGCTCAACACCAG
 CCGAGTGGCCAAAGTATTGAGCAATGGAATACTGCAGGGTTATTGGCTC
 AGCAGCAGCAGCACAAAATGGCTGCTGCAACGGGAGTTCCTCAGTCTACTT
 GGGACATATTTATGCCCGTGAATCAAATGGTAACTCAACCTTGTCTAAT
 GCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAAC
 AGCTACAGTTCAGGATCAAGTTAATTCAGCTATTAAGCTTATCGTGTCT
 AAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5903
 STRAIN 1169NT reverse complement
 AAAAGTTCAACAAGTTACTACTGAATCTTTGTCAAAGCAGATAAAGTTTCGCGTAGCC
 AAAAAATCAAAGTACTAAGGCGACATCTAAATCAAAGTAGAAGATGTAAAAACAGGCT
 CCAAAAACCTTCTCAGGCACTAATGAAGTCCCAAATCAAGTTCTCAATCTACAGAAGCT
 AATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAA
 GAAAATACCCTGCTACCAGTCAGGCACAACAACCTTATGCTGTACTGAGACAACCTTAC
 AAACCTGCTCAACACCAGACAAGTGGCCAAAGTATTGAGCAATGGAATACTGCAGGGGCG
 GTCCGATCTGCTGCTGCGCAGCAAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGG
 GAACATATTATGCCCCTGAATCAAATGGTAACTCTAATGTTGCTAATGCCTCAGGAGCT
 TCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTT
 AATTCAGCTATTAAGCTTATCGTGTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5904
 STRAIN 18RS21 reverse complement
 AAAAGTTCAACAAGTTACTACTGAATCTTTGTCAAAGCAGATAAAGTTTC
 GCGTAGCCAAAAATCAAAGTACTAAGGCGACATCTAAATCAAAGTAGAAGATGTAA
 AACAGGCTCAAAAACCTTCTCAGGCATCTAATGAAGCCCAAATCAAGTTCTCAATCTA
 CAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGCTGTAGAACAAGCAG
 TTGTAAACAGAAAACACCCCTGCTACCAGTCCAGGCACAACAAGCTTATGCTGTACTGAGA
 CAATTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAAATGGAATACTG
 CAGGGGCTATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGT
 CTACTTGGGAACATATTTATGCCCGTGAATCAAATGGTAACTCTAATGTTGCTAATGCCT
 CAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGG
 ATCAAGTTAATTCAGCTATTAAGCTTATCGTGTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5905
 STRAIN 090 reverse complement
 TAGCCAAAAAATCAAAGTATTAAAGGCGACATCTAAATCAAAGTAGAAGATGTAAAAAC
 AGGCTCCAAAACCTTCTCAGGCACTAATGAAGCCCAAATCAAGTTCTCAATCTACAG
 AAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGCTGTAGAACAAGCAGTTG
 TAACAGAAAACACCCCTGCTACCAGTCCAGGCACAACAAGCTTATGCTGTACTGAGACAA
 CTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAAATGGAATACTGCAG
 GGGCTATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTA
 CTTGGGAACATATTTATGCCCGTGAATCAAATGGTAACTCTAATGTTGCTAATGCCTCAG
 GAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGA

SEQ ID NO. 5906
 STRAIN A909 reverse complement
 AAGGCGACATCTAAATCAAAGTAGAAGATGTAAAAACAGGCTCCAAAACCTTCTCAGGCA
 TCTAATGAAGCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTT
 ACTGCGAGTGAAGAGGCGAGCTGTAGAACAAGCAGTTGTAAACAGAAAACACCCCTGCTACC
 AGTCAGGCACAACAAGCTTATGCTGTACTGAGACAACCTTATAGACCTGCTCAACACCAG
 ACAAGTGGCCAAAGTATTGAGTAAATGGAATACTGCAGGGGCTATTGGCTCAGCAGCTGCA
 GCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTTATGCCCGT
 GAATCAAATGGTAACTCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACG
 ATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTCAGCTATTAAGCT
 TATCGTGTCAAGGTTTATCA

SEQ ID NO. 5907
 STRAIN CJB110 reverse complement
 AATCTTTGTCAAAGCAGATAAAGTTTCGCGTAGCCAAAAATCAAATGACTAAGGCGA

Table 59: Comparative Sequences relating to SAG2147

CATCTAAATCAAAAGTAGAAGATGTA AAAACAGGCTCCAAAACCTTCTCAGGCATCTAATG
AAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGA
GTGAAGAGGCAGCTGTAGAACCAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAGTCAGG
CACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAGACGAGTG
GCCAAGTATTGAGTAATGGAAATCTG CAGGGGCTATTGGCTCAGCAGCTGCAGCACAAA
TGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAA
ATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAAACGATGCCAG
GTTGGGGTTCAACAGCTACAGTT CAGGATCAAGTTAATTCAGCTATTAAGCTTATCGTG
CTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5908
STRAIN COH1 reverse complement
AAAAGTTCACAAGTTACTACTGAACTTTGTCAAAGCAGATAA
AGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGA
TGTA AAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCA
ATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACA
AGCAGTTGTTAACAGAAAATACCCCTGCTACCAGTCAGGCACAACAAACTTATGCTGTTAC
TGAGACAACCTTACAACCTGCTCAACACCAGACAAGTGGCCAAAGTATTGAGCAATGGAAA
TACTG CAGGGGCGGTCCGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCC
TCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAA
TGCTCAGGAGCTTCAGGACTTTTCCAAAACGATGCCAGGTTGGGGTTCAACAGCTACAGT
TCAGGATCAAGTTAATTCAGCTATTAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGG
TTAC

SEQ ID NO. 5909
STRAIN H36B reverse complement
AAAAGTTCACAAGTTACTACTGAACTTTGTCAAAGC
AGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGT
AGAAGATGTAAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAG
TTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGCTGT
AGAACAAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAGTCAGGCACAACAAGCTTATGC
TGTTACTGAGACAACCTTATAGACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGTAA
TGGAAAATCTG CAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGG
AGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGT
TGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAAACGATGCCAGGTTGGGGTTCAACAGC
TACAGTTCAGGATCAAGTTAATTCAGCTATTAAGCTT

SEQ ID NO. 5910
STRAIN M732 reverse complement
AAAAGTTCACAAGTTACTACTGAACTTTGTCAAAGCAGATAAAGTTCGCGTAGC
CAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAACAGGC
TCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGC
TAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAA
AGAAAATACCCCTGCTACCAGTCAGGCACAACAACCTTATGCTGTTACTGAGACAACCTTA
CAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAATCTGCAGGGGC
GGTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTG
GGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGC
TTCAGGACTTTTCCAAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGT
TAATTCAGCTATTAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA

SEQ ID NO. 5911
STRAIN M781 reverse complement
TCTTTGTCAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACA
TCTAAATCAAAAGTAGAAGATGTAAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAA
GCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGT
GAAGAGGCGGCTGTAGAACAAGCAGTTGTAAACAGAAAATACCCCTGCTACCAGTCAGGCA
CAACAAAACCTTATGCTGTTACTGAGACAACCTTACAACCTGCTCAACACCAGACAAGTGGC
CAAGTATTGAGCAATGGAAATCTG CAGGGGCGGTCCGATCTGCTGCTGCAGCACAAATG
GCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAAT
GGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAAACGATGCCAGGT
TGGGGTTCAACAGCTACAGTT CAGGATCAAGTTAATTCAGCTATTAAGCTTATCGTGCT
CAAGGTTTATCAGCTTGGGGTTAC

PRETTY of: /biotmp/msa519780.2{*} March 10, 2003 06:25 ..

Table with 5 columns: sequence identifier, position 1, position 50, position 51, position 100. Rows include msa519780.2{25_COH1}, msa519780.2{25_M781}, msa519780.2{25_M732}, msa519780.2{25_1169NT}, msa519780.2{25_18RS21}, msa519780.2{25_A909}, msa519780.2{25_090}, msa519780.2{25_CJB110}, msa519780.2{2603}, msa519780.2{25_H36B}, msa519780.2{25_JM9130013}, and Consensus. The Consensus row shows asterisks for all positions.

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	agcttatgga	gctatcactt	tagtagccct	ttttcatgt	attttggtg
msa519780.2{25_H36B}	-----	-----	-----	-----	-----
msa519780.2{25_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa519780.2{25_COH1}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_M781}	-----	-----	-----	-----	-----tc
msa519780.2{25_M732}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_1169NT}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_18RS21}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----aatc	tttgtcaaaa
msa519780.2{2603}	taatggatc	ctttaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_H36B}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_JM9130013}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
Consensus	*****	*****	*****	*****	*****
	151				200
msa519780.2{25_COH1}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_M781}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_M732}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_1169NT}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_18RS21}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----tagc	caaaaaatca	aaaatgattA	AGGCgACATC
msa519780.2{25_CJB110}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{2603}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_H36B}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_JM9130013}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
Consensus	-----	-----	-----	-----	****-*****
	201.				250
msa519780.2{25_COH1}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_M781}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_M732}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_1169NT}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_18RS21}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_A909}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_090}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_CJB110}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{2603}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_H36B}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_JM9130013}	TAAATCAAAA	GTAGAAGaTG	TAAAACAGGC	TCCAAAAC..
Consensus	*****	*****	*****	*****	-----
	251				300
msa519780.2{25_COH1}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_M781}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_M732}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_1169NT}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_18RS21}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_A909}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_090}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_CJB110}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{2603}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_H36B}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_JM9130013}CA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
Consensus	-----	-----	*****	*****	*****
	301				350
msa519780.2{25_COH1}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_M781}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_M732}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_1169NT}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_18RS21}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_A909}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_090}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_CJB110}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{2603}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_H36B}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_JM9130013}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa519780.2{25_COH1}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_M781}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAaCTTAT	GCTGTTACTG

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_M732}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_1169NT}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_18RS21}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_A909}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_090}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_CJB110}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{2603}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_H36B}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
msa519780.2{25_JM9130013}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAAGCTTAT	GCTGTTACTG
Consensus	*****-***	*****	***-*****	***-*****	*****
401					
msa519780.2{25_COH1}	AGACAACCTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_M781}	AGACAACCTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_M732}	AGACAACCTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_1169NT}	AGACAACCTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_18RS21}	AGACAACCTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_A909}	AGACAACCTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_090}	AGACAACCTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_CJB110}	AGACAACCTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{2603}	AGACAACCTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_H36B}	AGACAACCTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_JM9130013}	AGACAACCTTA	tAgACCTGCT	CAACACCAGc	CgAGTGGCCA	AGTATTGAGc
Consensus	*****	-*-*****	*****-	*-*****	*****-
451					
msa519780.2{25_COH1}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GctGctGCAG	CACAATGGC
msa519780.2{25_M781}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GctGctGCAG	CACAATGGC
msa519780.2{25_M732}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GctGctGCAG	CACAATGGC
msa519780.2{25_1169NT}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GctGctGCAG	CACAATGGC
msa519780.2{25_18RS21}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgctGCAG	CACAATGGC
msa519780.2{25_A909}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgctGCAG	CACAATGGC
msa519780.2{25_090}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgctGCAG	CACAATGGC
msa519780.2{25_CJB110}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgctGCAG	CACAATGGC
msa519780.2{2603}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgctGCAG	CACAATGGC
msa519780.2{25_H36B}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgctGCAG	CACAATGGC
msa519780.2{25_JM9130013}	AATGGAAATA	CTGCAGGGGt	taTtGGcTcA	GcAgcAgcAG	CACAATGGC
Consensus	*****	*****-	--*--*--*--	*--*--*--*	*****
501					
msa519780.2{25_COH1}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M781}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M732}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_1169NT}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_18RS21}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_A909}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_090}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_CJB110}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{2603}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_H36B}	TGCTGCAACa	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_JM9130013}	TGCTGCAACg	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
Consensus	*****-	*****-****	*****	*****	*****
551					
msa519780.2{25_COH1}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M781}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M732}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_1169NT}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_18RS21}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_A909}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_090}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_CJB110}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{2603}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_H36B}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_JM9130013}	AATCAAATGG	TAATCCTAAC	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
Consensus	*****	*****-	*****	*****	*****
601					
msa519780.2{25_COH1}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M781}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M732}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_1169NT}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_18RS21}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_A909}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_090}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgA-----
msa519780.2{25_CJB110}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{2603}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_H36B}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_JM9130013}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
Consensus	*****	*****	*****	*****	*--*-----
651					
msa519780.2{25_COH1}	taattcagct	attaagactt	atcgtgctca	aggtttatca	gcttgggggtt
700					

Table 59: Comparative Sequences relating to SAG2147

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msa519780.2{25_M781} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggt
msa519780.2{25_M732} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggt
msa519780.2{25_1169NT} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggt
msa519780.2{25_18RS21} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggt
msa519780.2{25_A909} taattcagct attaaagctt atcgtgctca aggtttatca -----
msa519780.2{25_090} -----
msa519780.2{25_CJB110} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggt
msa519780.2{2603} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggt
msa519780.2{25_H36B} taattcagct attaaagctt -----
msa519780.2{25_JM9130013} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggt
-----
Consensus -----

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701
msa519780.2{25_COH1} ac---
msa519780.2{25_M781} ac---
msa519780.2{25_M732} a----
msa519780.2{25_1169NT} ac---
msa519780.2{25_18RS21} ac---
msa519780.2{25_A909} -----
msa519780.2{25_090} -----
msa519780.2{25_CJB110} ac---
msa519780.2{2603} actag
msa519780.2{25_H36B} -----
msa519780.2{25_JM9130013} ac---
Consensus ----**

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SEQ ID NO. 5912

STRAIN 2603 frame: 1
MNKRRKLSKLVNKKHHLAYGAITLVALFSCILAVMVI FKSSQVTTESLSKADKVRVAKKS
KMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAEEAAVEQAVVTENT
PATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI
IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAI KAYRAQGLSAWGY

SEQ ID NO. 5913

STRAIN 1169NT frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEVPKSSSQSTEAN
SQQQVTAEEAAVEQAVVTENTPATSAQQQYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5914

STRAIN 18RS21 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTAEEAAVEQAVVTENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5915

STRAIN 2603 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTAEEAAVEQAVVTENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5916

STRAIN 090 frame: 3
AKKSKMIKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAEEAAVEQAVV
TENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQST
WEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQ

SEQ ID NO. 5917

STRAIN A909 frame: 1
KATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAEEAAVEQAVVTENTPAT
SAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI IAR
ESNNGNPNVANASGASGLFQTMPGWGSTATVQNVNSAI KAYRAQGLS

SEQ ID NO. 5918

STRAIN CJB110 frame: 3
SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTA
EEAAVEQAVVTENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQ
AAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAI KAYRA
QGLSAWGY

SEQ ID NO. 5919

STRAIN COH1 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTAEEAAVEQAVVTENTPATSAQQQYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5920

STRAIN H36B frame: 1

Table 59: Comparative Sequences relating to SAG2147

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSOAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKA

SEQ ID NO. 5921

STRAIN M732 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSOAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWG

SEQ ID NO. 5922

STRAIN M781 frame: 4

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
EEAAVEQAVVTENTPATSOAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAVGSAAAAQMA
AAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA
QGLSAWGY

SEQ ID NO. 5923

STRAIN JM9130013 frame: 1

KSSQVTTESLSKADKVRVAKKSKMKNKATSKSKVEGVKQAPKPSQSTEANSQQQVTASEE
AAVEQAVVTENTPATSOAQQAYAVTETTYRPAQHQPSSGQVLSNGNTAGVIGSAAAAQMAA
ATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQ
LSAWGY

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa519418.2(*) March 10, 2003 06:15 ..

1 50
msa519418.2{25_090}
msa519418.2{25_H36B}
msa519418.2{25_COH1}
msa519418.2{25_M781}
msa519418.2{25_1169NT}
msa519418.2{25_M732}
msa519418.2{25_18RS21}
msa519418.2{25_CJB110}
msa519418.2{25_2603}
msa519418.2{2603}
msa519418.2{25_A909}
msa519418.2{25_JM9130013}
Consensus

51 100
msa519418.2{25_090}
msa519418.2{25_H36B}
msa519418.2{25_COH1}
msa519418.2{25_M781}
msa519418.2{25_1169NT}
msa519418.2{25_M732}
msa519418.2{25_18RS21}
msa519418.2{25_CJB110}
msa519418.2{25_2603}
msa519418.2{25_A909}
msa519418.2{25_JM9130013}
Consensus

101 150
msa519418.2{25_090}
msa519418.2{25_H36B}
msa519418.2{25_COH1}
msa519418.2{25_M781}
msa519418.2{25_1169NT}
msa519418.2{25_M732}
msa519418.2{25_18RS21}
msa519418.2{25_CJB110}
msa519418.2{25_2603}
msa519418.2{25_A909}
msa519418.2{25_JM9130013}
Consensus

151 200
msa519418.2{25_090}
msa519418.2{25_H36B}
msa519418.2{25_COH1}
msa519418.2{25_M781}
msa519418.2{25_1169NT}
msa519418.2{25_M732}
msa519418.2{25_18RS21}
msa519418.2{25_CJB110}

Table 59: Comparative Sequences relating to SAG2147

msa519418.2{25_2603}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{2603}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_A909}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
msa519418.2{25_JM9130013}	NGNTAGviGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL
Consensus	*****--**	*****	*****	*****	*****
			201		234
msa519418.2{25_090}	FQTMPGWGST	ATVQ-----	-----		
msa519418.2{25_H36B}	FQTMPGWGST	ATVQDQVNSA	IKA-----	----	
msa519418.2{25_COH1}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M781}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_1169NT}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M732}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWG-	
msa519418.2{25_18RS21}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_CJB110}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_A909}	FQTMPGWGST	ATVQnQVNSA	IKAYRAQGLS	----	
msa519418.2{25_JM9130013}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
Consensus	*****	*****	*****	****	

Table 60: Comparative Sequences relating to SAG1945

SEQ ID NO. 6001
 STRAIN 2603
 ATGAAAGAAAAACAGTCGAAAAGGCTTATTTATATACTACTGGTTGTTCCATTATTTT
 ATAAGTGTTTTACATACAGTATAGCCAGCCTTCTAAACTACTTCCACCAAAGAATTA
 GTTATTCTAAGTCCAAATAGTCAAGCCATTTAACAGGAACGATCCAGCTTTGAGGAA
 AATACGGTATAAAGTAAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGATTA
 AGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATATACGCAATTT
 GAAAGTCATAAGGCATTGTTGAGTCTTACGTATCAAAGAATGTTCACTACTGTTATTCCA
 GACTATATCCATCCAAGTATACCGGCGACACCTTATACTATAAATGGGAGTGTCTTGATT
 GTAATTAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCT
 TCCTTAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCTCTAGTGTCTTCTCACA
 CTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAACTATGTT
 AAAAAAGCTACAACATAATTAATGCTATCAAATCTTCTAGCTCTCAGAAGTTTATCAA
 TCAGTTGCAGAGGAAAAATGATTGTGGGGCTGACTTACGAAAGCCCTAGTGTCAATTTG
 CAAAAAGTGGTGCATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCA
 TCTTCGGTTGCAATATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATTAAT
 TTTATGCTTTCTTAGATGTTCAAATGCCTTTGGGCGTCAACGAGTAACCGACCTATT
 CGTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAA
 GAAGATTATCGCTATGCTACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATT
 CGTAGAAATGCTGAT

SEQ ID NO. 6002
 STRAIN 090
 CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATTCTAAGT
 CCAAAATAGTCAAGCCATTTAACAGGAACGATTCAGCTTTTGGAGAAAA
 ATACGGTATAAAGTAAAGCTTATTCAAGGTGGGACAGGGCAACTAATAG
 ATAGATTAAAGTAAAGGGTAAAGCAGTTGAAGCGGATATTTCTTTGGA
 GAAAAATATACGCAATTTGAAAGTCATAAGGCATGTTGAGTCTTACGT
 ATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCATCCAAGTGATA
 CGCGCACCTTATACTATAAATGGGAGTGTCTTGATTGTAATAACGAA
 TTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCCTTC
 CTTAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTCTCTAGTGTCTT
 TCTCACAATCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCA
 AAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATAATGCTATCAA
 ATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGAAAGGAAAAATGA
 TTGTGGGGCTGACTTACGAAGACCTAGTGTCAATTTGCAAAAAAGTGGT
 GCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCATC
 TTCGGTTGCAATATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTAT
 TTAATAATTTTATGCTTCTTCTAGATGTTCAAATGCCTTTGGGCGTCA
 ACGAGTAACCGACCTATTGCTAAAGATGCCCAAACGAGTAATGGCATGAA
 AGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGCTACTA
 AGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTCTGTAGAAATGCT
 GAT

SEQ ID NO. 6003
 STRAIN A909
 CAGCCTTCTAAACTACTTCCACCAAAGAATTAG
 TTATTCTAAGTCCAAATAGTCAAGCCATTTAACAGGAACGATTCAGCT
 TTTGAGGAAAAATACGGTATAAAGTAAAGCTTATTCAAGGTGGGACAGG
 TCAACTAATAGATAGATTAAAGTAAAGGGGTAAGCAGTTGAAGGGCGGATA
 TTTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATGTTT
 GAGTCTTACGTATCAAAGAATATTCATCTGTTATTCCAGATTATATCCA
 TCCGAGTATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTG
 TAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTA
 TTACAGCCTTCTTAAAGGTAAAATTGCCTTTGCAGATCCGAATACTTC
 CTCTAGTGTCTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTT
 ACACCAATCCAAAGCGTGGAACTATGTTAAAAAGCTACAACATAATATT
 AATGCTATCAAATCTTCTAGCTCTTCAAGAAAGTTATCAATCAGTTGCAGA
 AGGAAAAATGATTGTGGGGTTGACTTACGAAGACCCCTAGTGTCAATTTGC
 AAAAAAGTGGTGGCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTT
 TTTGTCCCATCTTCGGTTGCAATATAAAGAATGCTCCTTCTATGAAGA
 AGCAAAGTTATTTATTAATTTTATGCTTCTTTAGATGTTCAAAATGCCT
 TTGGGCGTCAACGAGTAACCGACCTATTGTAAGATGCCCAAACGAGT
 AATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCG
 CTATGCTACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTCT
 GTAGAAATGCTGAT

SEQ ID NO. 6004
 STRAIN H36B
 TAAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAATAGTCAAG
 CCAATTTAACAGGAACGATTCAGCTTTTGGAGAAAAATACGGTATAAAGA
 GTTAAAGCTTATTCAAGGTGGGACAGGTCAACTAATAGATAGATTAAAGTAA
 GGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATATACGC
 AATTTGAAAGTCAATAAGGCATGTTGAGTCTTACGTATCAAAGAATATT
 CATACTGTTATTCCAGATTATATCCATCCGAGTGATACGGCGACACCTTA
 TACTATAAATGGGAGTGTCTTGATTGTAATAACGAATTAGTTAAAGGGAC
 TTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCTTAAAGGTAAA
 ATTGCTTTGCAGATCCGAATACTTCTCTAGTGTCTTCTCACAACCTCAC
 TAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAACT
 ATGTTAAAAAGCTACAACATAATTAATGCTATCAAATCTTCTAGCTCT
 TCAGAAGTTTATCAATCAGTTGCAGAAAGGAAAAATGATTGTGGGGTTGAC
 TTACGAAGACCCCTAGTGTCAATTTGCAAAAAAGTGGTGCATGTTTCTA
 TTGTATATCCGACAGAAGGGACAGTTTGTGCCATCTTCGGTTGCAATT

Table 60: Comparative Sequences relating to SAG1945

ATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATTAAATTTTAT
GCTTTCTTTAGATGTTCAAATGCCTTTGGGCGAGTCAACGAGTAACCGAC
CTATTTCGTAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGAT
ATTGCTACTCTTAAAGAAGATTATCGCTATGCTACTAAGCATAAGGGCCA
AATCCTTAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6005

STRAIN 18RS21

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAA
TAGTCAAGCCATTTAAACAGGAACGATTCAGCTTTTGAGGAAAAATACG
GTATAAAAGTTAAGCTTATTCAGGTTGGGACAGGGCACTAATAGATAGA
TTAAGTAAGGAGGGTAAGCAGTTGAAGGCCGATATTTCTTTGGAGGAAA
TTATACGCAATTTGAAAGTCATAAGGCATTTGTTGAGTCTTACGTATCAA
AGAATGTTTACTACTGTTATTCAGACTATATCCATCCAAGTGATACGGCG
ACACCTTATACTATAAATGGGAGTGTCTTGATTTAAATAACGAATTAGC
TAAGGGACTTACCATCAAGAGTTATGAAGATTTATACAGCCCTTCTTAA
AAGTAAAATTGCCTTTGCAGATCCGAATCTTCTCTAGTGTCTTCTCA
CAACTCATAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGC
GTGGAACTATGTTAAAAGCTACAAATAATTAATGCTATCAAATCTT
CTAGCTTTCAGAAATTTATCAATCAGTTGCAGAAAGGAAAAATGATTGTG
GGCTGACTTACGAAGACCTTAGTGTCAATTTGCAAAAAGTGGTGCCAA
TGTTTCTATTGTATATCCGACAGAAGGGACAGTTTTTGTCCCATCTTCGG
TTGCAATTAAGAAGATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATT
AATTTTATGCTTTCTTTAGATGTTCAAATGCCTTTGGGCGAGTCAACGAG
TAACCGACCTTATTCGTAAGATGCCCAAACGAGTAATGGCATGAAAGCTT
TAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGCTACTAAGCAT
AAGGGCAAATCCTTAAACCTATAATCGTATTCGTAGAAATGCTGAT

SEQ ID NO. 6006

STRAIN M732

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAGGTTGGGACAGGG
CACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATAT
TTCTTTGGAGGAAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTG
AGTCTTACGTATCAAAGAATGTTTACTGTTATTCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTTG
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTAT
TACAGCCTTCCTTAAAAGGTAATAATGCCTTTGCAGATCCGAATACTTCC
TCTAGTGTCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTA
CACC AATCCAAAAGCGTGAAGCTATGTTAAAAGCTACAAATAATATTA
ATGCTATCAAATCTTCTAGCTTTCAGAAAGTTTATCAATCAGTTGCAGAA
GGAAAATGATTGTGGGTTGACTTACGAAGACCTTAGTGTCAATTTGCA
AAAAAGTGGTGCCAAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTT
TTGTCCCATCTTCGGTTGCAATTTATAAAGAATGCTCCTTCTATGAAAGAA
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAATGCCTT
TGGGCGTCAACGAGTAACCGACCTATTCGTAAGATGCCAAACAAGTA
ATGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC
TATGCTACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCG
TAGAAATGCTGAT

SEQ ID NO. 6007

STRAIN COH1

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTT
ATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTT
TGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGTTGGGACAGGGC
AACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATT
TCTTTGGAGGAAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGA
GTCCTTACGTATCAAAGAATGTTTACTGTTATTCCAGACTATATCCATC
CGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTA
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTAT
ACAGCCTTCTTAAAAGGTAATAATGCCTTTGCAGATCCGAATACTTCTCT
CTAGTGTCTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTAC
ACCAATCCAAAAGCGTGAAGCTATGTTAAAAGCTACAAATAATATTTAA
TGCTATCAAATCTTCTAGCTCTTTCAGAAAGTTATCAATCAGTTGCAGAA
GAAAATGATTGTGGGTTGACTTACGAAGACCTTAGTGTCAATTTGCAA
AAAAGTGGTGCCAAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTT
TGTCCCATCTTCGGTTGCAATTTATAAAGAATGCTCCTTCTATGAAAGAAG
CAAAGTTATTTAATTAATTTTATGCTTTCTTTAGATGTTCAAATGCCTTT
GGGCGTCAACGAGTAACCGACCTATTCGTAAGATGCCCAAACAAGTAA
TGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCT
ATGCTACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCG
AGAAATGCTGAT

SEQ ID NO. 6008

STRAIN M781

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATT
CTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGA
GAAAAATACGGTATAAAGTTAAGCTTATTCAGGTTGGGACAGGGCAAC
TAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATTTCT
TTTGGAGGAAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTGAGTC
TTACTATCAAAGAATGTTTACTGTTATTCAGACTATATCCATCCGA
GTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAT

Table 60: Comparative Sequences relating to SAG1945

AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACA
GCCTTCCTTAAAAGGTAAAATTCCTTTGCAGATCCGAATCTTCTCTA
GTGCTTTCTCACAACTCACTAATATACTCTTGGCCAAGGGTGGTTACACC
AATCCAAAAGCGTGGAACTATGTTAAAAGCTACAACATAATATTAATGC
TATCAAATCTTCTAGCTCTTCCAGAAGTTTATCAATCAGTTGCAGAAAGGAA
AAATGATGTGGGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAA
AGTGGTGCCAAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTGTG
CCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAA
AGTTATTTATTAATTTTATGCTTCTTTAGATGTTCAAAATGCCTTTGGG
CAGTCAACGAGTAACCGACCTATTTCGTAAGATGCCCAAAACAAGTAATGG
CATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG
TCACTAAGCATAAGAGCCAATCCTTAAAACCTATAATCGCATTTCGTAGA
AATGCTGAT

SEQ ID NO. 6009

STRAIN CJB110

CAGCCTTTTAAACTACTTCCACCAAAAAGAATTAGTTATTCT
AAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGG
AAAAATACCGTATAAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA
ATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTTCTT
TGGAGGAAATATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTT
ACGTATCAAAGAATGTTCACTACTGTTATPCCAGACTATATCCATCCAAGT
GATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTTGTAATAA
CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGC
CTTCTTAAAAGGTAAAATTCCTTTGCAGATCCGAATACTTCTCTAGT
GCTTTCTCACACTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAA
TCCAAAAGCGTGGAACTATGTTAAAAGCTACAACATAATATTAATGCTA
TCAAATCTTCTAGCTCTTCAAGGTTTATCAATCAGTTGCAGAAAGGAAA
ATGATTTGTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAG
TGGTGCCAAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGTC
CATCTTCGGTTGCAATATAAAGAATGCTCCTTCTATGAAAGAAGCAAAG
TTATTTATTAATTTTATGCTTCTTTAGATGTTCAAATGCCTTTGGGCA
GTCAACGAGTAACCGACCTATTTCGTAAGATGCCCAAACGAGTAATGGCA
TGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTC
ACTAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTTCGTAGAAA
TGCTGAT

SEQ ID NO. 6010

STRAIN 1169NT

ATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAATAC
GGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG
ATTAAGTAAGGAGGGTAAGCATTGAAAGGCGGATATTTCTTGGAGGAA
ATTAACGCAATTTGAAAGTCATAAGGCATGTTTGAGTCTTACGTATCA
AAGAATGTTCACTACTGTTATPCCAGACTATATCCATCCAAGTGATACGGC
GACACCTTATACTATAAATGGGAGTGTCTTGATTTGTAATAACGAATTAG
CTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGCTTCTTAA
AAAGTAAAATTCCTTTGCAGATCCGAATACTTCTCTAGTGTCTTCTC
ACAACCTACCAATATACTCTTGGCAAAGGGTGGTTACACCAATCCAAAAG
CGTGGAACTATGTTAAAAGCTACAACATAATATTAATGCTATCAAATCT
TCTAGCTCTTCAAGGTTTATCAATCAGTTGCAGAAAGGAAAATGATTTG
GGGTTGACTTACGAAGACCCTAGTGTCAATTTGCAAAAAAGTGGTGCCA
ATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGTCCTATCTCG
GTTGCAATTTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTAT
TAATTTATGCTTCTTTAGATGTTCAAATGCCTTTGGGCAGTCAACGA
GTAAACCGACTATTTCGTAAGATGCCCAAACGAGTAATGGCATGAAAGCT
TTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCCTAAGCA
TAAGGGCCAAATCCTTAAAACCTATAATCGTATTTCGTAGAAATGCTGAT

SEQ ID NO. 6011

STRAIN JM91130013

CAGCCTTCTAAACTACTTCCACCAAAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT
TTGAGGAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT
TTTCTTTGGAGGAAATATACGCAATTTGAAAGTCATAAGGCATTGTTG
AGTCTTACGTATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTAT
TACAGCTTCTTAAAAGGTAAAATTCCTTTGCAGATCCGAATACTTCC
TCTAGTGTCTTCTCACAACTCACCATATACTCTTGGCAAAGGGTGGTTA
CACCAATCCAAAAGCGTGGAACTATGTTAAAAGCTACAACATAATATTA
ATGCTATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGAA
GGCAAATGATTTGGGGCTGACTTACGAAGACCCTAGTGTCAATTTGCA
AAAAAGTGGTGCCAAATGTTTCTATTGTGTATCCGACAGAAGGGACAGTTT
TGTGCCATCTTCGGTTGCAATATAAAGAATGCTCCTTCTATGAAAGAA
GCAAAGTATTTATTAATTTTATGCTTCTTTAGATGTTCAAATGCCTT
TGGGCAGTCAACGAGTAACCGACCTATTTCGTAAGATGCCCAAACGAGTA
ATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGC
TATGTCATAAGCATAAGGGCCAAATCCTTAAAACCTATAATCGTATTTCG
TAGAAATGCTGAT

PRETTY of: /biotmp/msa523010.2{*} April 28, 2003 08:55 ..

Table 60: Comparative Sequences relating to SAG1945

	1				50
msa523010.2{263_COH1}	-----	-----	-----	-----	-----
msa523010.2{263_M732}	-----	-----	-----	-----	-----
msa523010.2{263_M781}	-----	-----	-----	-----	-----
msa523010.2{263_A909}	-----	-----	-----	-----	-----
msa523010.2{263_H36B}	-----	-----	-----	-----	-----
msa523010.2{263_090}	-----	-----	-----	-----	-----
msa523010.2{263_18RS21}	-----	-----	-----	-----	-----
msa523010.2{263_2603}	atgaaagaaa	aacagtcgaa	aaggcttatt	tataactac	tggttggttc
msa523010.2{263_CJB110}	-----	-----	-----	-----	-----
msa523010.2{263_1169NT}	-----	-----	-----	-----	-----
msa523010.2{263_JM91130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa523010.2{263_COH1}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_M732}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_M781}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_A909}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_H36B}	-----	-----	-----	-----taaac	-----
msa523010.2{263_090}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_18RS21}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_2603}	cattatTTTT	ataagtgtt	ttacatacag	tattagccag	ccttctaaac
msa523010.2{263_CJB110}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_1169NT}	-----	-----	-----	-----	-----
msa523010.2{263_JM91130013}	-----	-----	-----	-----cag	ccttctaaac
Consensus	*****	*****	*****	*****	-----
	101				150
msa523010.2{263_COH1}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M732}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M781}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_A909}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_H36B}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_090}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_18RS21}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_2603}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_CJB110}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_1169NT}	-----	-----	-----	-----ATAG	TCAAGCCATT
msa523010.2{263_JM91130013}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
Consensus	-----	-----	-----	-----****	*****
	151				200
msa523010.2{263_COH1}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M732}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M781}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_A909}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_H36B}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_090}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_18RS21}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_2603}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_CJB110}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_1169NT}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_JM91130013}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa523010.2{263_COH1}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M732}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M781}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_A909}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_H36B}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_090}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_18RS21}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_2603}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_CJB110}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_1169NT}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_JM91130013}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
Consensus	*****	*****	*..*****	*****	*****
	251				300
msa523010.2{263_COH1}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M732}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M781}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_A909}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_H36B}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_090}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_18RS21}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_2603}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_CJB110}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_1169NT}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_JM91130013}	GTAAGCagTT	GAAGGCGGAT	gTTTTCTTTG	GAGGAAATTA	TACGCAATTT
Consensus	*****..*	*****	..*****	*****	*****

Table 60: Comparative Sequences relating to SAG1945

	301				350
msa523010.2{263_COH1}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M732}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M781}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_A909}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_H36B}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_090}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_18RS21}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_2603}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_CJB110}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_1169NT}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_JM91130013}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
Consensus	*****	*****	*****	*****	*_*_*_*_*_*_*_*
	351				400
msa523010.2{263_COH1}	TGTTATTCCA	GAcTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_M732}	TGTTATTCCA	GAcTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_M781}	TGTTATTCCA	GAcTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_A909}	TGTTATTCCA	GAcTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_H36B}	TGTTATTCCA	GAcTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_090}	TGTTATTCCA	GAcTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_18RS21}	TGTTATTCCA	GAcTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_2603}	TGTTATTCCA	GAcTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_CJB110}	TGTTATTCCA	GAcTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_1169NT}	TGTTATTCCA	GAcTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_JM91130013}	TGTTATTCCA	GAcTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
Consensus	*****	**_*_*_*_*_*_*_*	****_*_*_*_*_*	*****	*****
	401				450
msa523010.2{263_COH1}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M732}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M781}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_A909}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_H36B}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_090}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_18RS21}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_2603}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_CJB110}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_1169NT}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_JM91130013}	TAAATGGGAG	TGTCCTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
Consensus	*****	*****	*****	*****_*_*_*	*****
	451				500
msa523010.2{263_COH1}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_M732}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_M781}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_A909}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_H36B}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_090}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_18RS21}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_2603}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_CJB110}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_1169NT}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
msa523010.2{263_JM91130013}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTA AAAATTGC
Consensus	*****	*****	*****	*****	*****
	501				550
msa523010.2{263_COH1}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_M732}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_M781}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_A909}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_H36B}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_090}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_18RS21}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_2603}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_CJB110}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_1169NT}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_JM91130013}	CCTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
Consensus	*****	*****	*****	*****	*****_*_*_*_*
	551				600
msa523010.2{263_COH1}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_M732}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_M781}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_A909}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_H36B}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_090}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_18RS21}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_2603}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_CJB110}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_1169NT}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT
msa523010.2{263_JM91130013}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAActATGTT

Table 60: Comparative Sequences relating to SAG1945

Consensus	*****	*****	*****	*****	*****
	601				650
msa523010.2{263_COH1}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M732}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M781}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_A909}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_H36B}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_090}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_18RS21}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_2603}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_CJB110}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_1169NT}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_JM91130013}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa523010.2{263_COH1}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M732}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M781}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_A909}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_H36B}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_090}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_18RS21}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_2603}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_CJB110}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_1169NT}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_JM91130013}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAT	GATTGTGGGG	tTGACTTACG
Consensus	*****	*****	*****	*****	*****
	701				750
msa523010.2{263_COH1}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_M732}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_M781}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_A909}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_H36B}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_090}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_18RS21}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_2603}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_CJB110}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_1169NT}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTa
msa523010.2{263_JM91130013}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCATTGTg
Consensus	*****	*****	*****	*****	*****
	751				800
msa523010.2{263_COH1}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M732}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M781}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_A909}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_H36B}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_090}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_18RS21}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_2603}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_CJB110}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_1169NT}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_JM91130013}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
Consensus	**	*****	*****	*****	*****
	801				850
msa523010.2{263_COH1}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_M732}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_M781}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_A909}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_H36B}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_090}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_18RS21}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_2603}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_CJB110}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_1169NT}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
msa523010.2{263_JM91130013}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCCTT
Consensus	*****	*****	*****	*****	*****
	851				900
msa523010.2{263_COH1}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M732}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M781}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_A909}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_H36B}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_090}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_18RS21}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_2603}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_CJB110}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_1169NT}	CITTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT

Table 60: Comparative Sequences relating to SAG1945

msa523010.2{263_JM91130013}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
Consensus	*****	*****	*****	*****	*****
	901				950
msa523010.2{263_COH1}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M732}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M781}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_A909}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_H36B}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_090}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_18RS21}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_2603}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_CJB110}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_1169NT}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_JM91130013}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa523010.2{263_COH1}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_M732}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_M781}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_A909}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_H36B}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_090}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_18RS21}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_2603}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_CJB110}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_1169NT}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_JM91130013}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
Consensus	*****	*****	*****	*****	*****
	1001				1035
msa523010.2{263_COH1}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M732}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M781}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_A909}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_H36B}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_090}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_18RS21}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_2603}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_CJB110}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_1169NT}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_JM91130013}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
Consensus	*****	*****	*****	*****	

SEQ ID NO. 6012

STRAIN 2603 frame: 1

MKEKQSKRLIYILLVVSIIIFISVFTYSISQPSKLLPPKELVILSPNSQAILTGTIPAFEE KYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVPI PDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNL QKSGANVSI VYPTEGT VFPSSVAI IKNA PSMKEAKLF INFMLS LDVQNAFGQSTSNRPI RKDAQTSNGMKALKD IATLKEDYRYVTKHKGQILKTYNRI RRNAD

SEQ ID NO. 6013

STRAIN 090 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVPIPDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGT VFPSSVAI IKNA PSMKEAKLF INFMLS LDVQNAFGQSTSNRPI RKDAQTSNGMKALKD IATLKEDYRYVTKHKGQILKTYNRI RRNAD

SEQ ID NO. 6014

STRAIN A909 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNIHTVPIPDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGT VFPSSVAI IKNA PSMKEAKLF INFMLS LDVQNAFGQSTSNRPI RKDAQTSNGMKALKD IATLKEDYRYVTKHKGQILKTYNRI RRNAD

SEQ ID NO. 6015

STRAIN H36B frame: 2

KLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNIHTVPIPDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGT VFPSSVAI IKNA PSMKEAKLF INFMLS LDVQNAFGQSTSNRPI RKDAQTSNGMKALKD IATLKEDYRYVTKHKGQILKTYNRI RRNAD

SEQ ID NO. 6016

Table 60: Comparative Sequences relating to SAG1945

STRAIN 18RS21 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVI PDYIHPSTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSVAI IKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKD IATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6017
STRAIN M732 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVI PDYIHPSTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSVAI IKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKD IATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6018
STRAIN COH1 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVI PDYIHPSTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSVAI IKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKD IATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6019
STRAIN M781 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVI PDYIHPSTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSVAI IKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKD IATLKEDYRYVTKH
KSQILKTYNRIRRNAD

SEQ ID NO. 6020
STRAIN CJB110 frame: 1
QPFKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DIFFGGNYTQFESHKALFESYVSKNVHTVI PDYIHPSTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSVAI IKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKD IATLKEDYRYVTKH
KGQILKTYNRIRRNAD

SEQ ID NO. 6021
STRAIN 1169NT frame: 3
SQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKHLKADI FFGGNYTQFESHKAL
FESYVSKNVHTVI PDYIHPSTATPYTINGSVLIVNNELAKGLTI KSYEDLLQPSLKGKI
AFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA IKSSSSSEVYQSVAEQK
MIVGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSVAI IKNA PSMKEAKLFINFMLS LD
VQNAFGQSTSNRPIRKDAQTSNGMKALKD IATLKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6022
STRAIN JM91130013 frame: 1
QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
DVFFGGNYTQFESHKALFESYVSKNVHTVI PDYIHPSTATPYTINGSVLIVNNELAKGL
TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNI LLAKGGYTNPKAWNYVKKLQHNINA
IKSSSSSEVYQSVAEQKMI VGLTYEDPSVNLQKSGANVSI VYPTEGTVFVPSVAI IKNA
PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKD IATLKEDYRYVTKH
KGQILKTYNRIRRNAD

PRETTY of: /biotmp/msa523117.2{*} April 28, 2003 08:56 ..

Table with 5 columns: Sequence ID, Consensus, and alignment markers. It shows sequence alignments for various strains (COH1, M732, M781, 1169NT, CJB110, 18RS21, 2603, A909, JM91130013, H36B) against a consensus sequence. The table is split into two sections, one ending at position 50 and another starting at position 51.

Table 60: Comparative Sequences relating to SAG1945

msa523117.2{263_CJB110}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_090}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_18RS21}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_2603}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_A909}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_JM91130013}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	vFFGGNYTQF
msa523117.2{263_H36B}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M732}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M781}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_1169NT}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_CJB110}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_090}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_18RS21}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_2603}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_A909}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_JM91130013}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_H36B}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELvKGLT
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M732}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M781}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_1169NT}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_CJB110}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_090}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_18RS21}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_2603}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_A909}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_JM91130013}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_H36B}	IKSYEDLLQP	SLKGGIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_M732}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_M781}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_1169NT}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_CJB110}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_090}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_18RS21}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_2603}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_A909}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_JM91130013}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
msa523117.2{263_H36B}	KKLQHNINAI	KSSSSSEVYQ	SVAEgKMIVG	LTyEDPSVNL	QKSGANVSIV
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_M732}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_M781}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_1169NT}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_CJB110}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_090}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_18RS21}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_2603}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_A909}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_JM91130013}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
msa523117.2{263_H36B}	YPTEGTVFVP	SSVAI IKNAP	SMKEAKLFIN	FMLSldVQNA	FGQSTSNRPI
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_M732}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_M781}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_1169NT}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_CJB110}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_090}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_18RS21}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_2603}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_A909}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_JM91130013}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
msa523117.2{263_H36B}	RKDAQTSNGM	KALKDIATLK	EDYRYVTkHK	sQILKTYNRI	RRNAD
Consensus	*****	*****	*****	*****	*****

Table 61: Comparative Sequences relating to SAG1030

SEQ ID NO. 6101
STRAIN 2603
ATGGTAAAAGTTAGTGAAGTTCGTAGGAACTCAAGCATCAACAGTAGCTATTTCTATG
TTTAGTCGTATCGGCTTTAAATGATGCAATAACAAAACCTATCATCTTTTGACAGGGCT
GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTTAACT
CCGATGCTTCAAGGAATGATTCCTTTCTGAAACATTTGAGTGAGAAATGTACAGAATTA
CAAACCTTATATGTCTCAATTTGTGGTGTAGGATTTAGACTCTGTCGTTTGAATCA
AAATTAGCAAGTGTAGGGCATCATTAAGATTGCTGAAGCACITTTAGAGCATCTTAAC
GATGATCCAGAACCTTCCAATCTGCCATAAGTTCTACAAAAAGTAATATTAATAAATTA
AAAAACGTATAAAATCTAATCAAAGAAATAGACAACCTTAATGAATTTAACGCCAT
TCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAACTGTTAACCAAGCACTAGCG
GCTGTTTCAACAGGATTTTCTGGATATAATAGTAAACCGGAGCTTTTGGAAAACCAACA
TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAAGAAATGGAAAGAGCGAGAAAGCGCC
AAGCTGAAGAACTGAAAAGTAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAAATTGAA
AATACTACTAAAAAAGTAATGTTTCAAGTTGATAAAAAGAAATTAATAAAGCGGCTAAT
GAAGCGTATAAATAGGAGAAATAAAAAAGATACCTATGAATCAATTTATCAGTGGTTTA
AGTAATGCATCGGCTTACTTAAAGAGGTAGCTAAATCAAAATTGACTGACACAGCT
CGGTATTGATG

SEQ ID NO. 6102
STRAIN 090
TTAAATGATGCAATAACAAAACCTATCATCTTTTGACAGGGCT
GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG
AACGTTAACTCCGATGCTTCAAGGAATGATTCCTTTCTGAAACATTTGA
GTGAGAAATGTACAGAATTAACAACCTTATATGTCTCAATTTGTGGTGT
GAGGATTTAGACTCTGTCGTTTGAATCAAATTAGCAAGTGTAGGGC
ATCATTAAAGATTGCTGAAGCACTTTAGAGCATCTTAACGATGATCCAG
AACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAATAAATTA
AAAAACGTATAAAATCTAATCAAAGAAATAGACAACCTTAATGAATTT
TAACGCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA
CTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAAT
AGTAAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGAC
AAAGACAGTTAAGAAGAATTTGAAAGAGCGGAGAAAGCGCCAAAGCTGAAG
AAGTAAAAGTAAAAGGCTGAAGAAAGTAAAGAAAGCTTCAAAAATTGAA
AATACTACTAAAAAAGTAATGTTTCAAGTTGATAAAAAGAAATTAATAA
AGCGGCTAATGAAGCGTATAAATAGGAGAAATAAAAAAGATACCTATG
AATCAATTTATCAGTGGTTAAGTAATGCATCGGCTGCTTACTTAAAGAG
GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6103
STRAIN 18RS21
TTAAATGATGCAATAACAAAACCTATCATCTTTTGACAGGGC
TGCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTG
GAACGTTAACTCCGATGCTTCAAGGAATGATTCCTTTCTGAAACATTTG
AGTGAGAAATGTACAGAATTAACAACCTTATATGTCTCAATTTGTGGTGT
TGAGGATTTAGACTCTGTCGTTTGAATCAAATTAGCAAGTGTAGGGC
CATCATTAAAGATTGCTGAAGCACTTTAGAGCATCTTAACGATGATCCA
GAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAATAAAT
AAAAAAGCTATAAAATCTAATCAAAGAAATAGACAACCTTAATGAATTT
TAACGCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA
ACTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAA
TAGTAAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGA
CAAAGACAGTTAAGAAGAATTTGAAAGAGCGGAGAAAGCGCCAAAGCTGAA
GAAGTAAAAGTAAAAGGCTGAAGAAAGTAAAGAAAGCTTCAAAAATTGA
AATACTACTAAAAAAGTAATGTTTCAAGTTGATAAAAAGAAATTAATAA
AAGCGGCTAATGAAGCGTATAAATAGGAGAAATAAAAAAGATACCTATG
GAATCAATTTATCAGTGGTTAAGTAATGCATCGGCTGCTTACTTAAAGA
GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

PRETTY of: /biotmp/msa185066.2{*} May 13, 2003 07:01 ..

Table with 5 columns: sequence identifier, sequence, position 1, position 50, position 100, position 150, position 200. It shows multiple sequence alignments for strains msa185066.2{270_090}, msa185066.2{270_18RS21}, and msa185066.2{270_2603} with their respective consensus sequences.

Table 61: Comparative Sequences relating to SAG1030

Consensus	*****	*****	*****	*****	*****
	201				250
msa185066.2{270_090}	TCTTTTCTCT	GAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_18RS21}	TCTTTTCTCT	GAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_2603}	TCTTTTCTCT	GAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
Consensus	*****	*****	*****	*****	*****
	251				300
msa185066.2{270_090}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_18RS21}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_2603}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
Consensus	*****	*****	*****	*****	*****
	301				350
msa185066.2{270_090}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTTAGA
msa185066.2{270_18RS21}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTTAGA
msa185066.2{270_2603}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTTAGA
Consensus	*****	*****	*****	*****	*****
	351				400
msa185066.2{270_090}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_18RS21}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_2603}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
Consensus	*****	*****	*****	*****	*****
	401				450
msa185066.2{270_090}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAAATCTAA	TCAAAGAAAA
msa185066.2{270_18RS21}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAAATCTAA	TCAAAGAAAA
msa185066.2{270_2603}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAAATCTAA	TCAAAGAAAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa185066.2{270_090}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_18RS21}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_2603}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
Consensus	*****	*****	*****	*****	*****
	501				550
msa185066.2{270_090}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_18RS21}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_2603}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
Consensus	*****	*****	*****	*****	*****
	551				600
msa185066.2{270_090}	CAGGATTTTC	TGGATATAAT	AGTAAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_18RS21}	CAGGATTTTC	TGGATATAAT	AGTAAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_2603}	CAGGATTTTC	TGGATATAAT	AGTAAAACCG	GAGCTTTTGG	AAAACCAACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa185066.2{270_090}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_18RS21}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_2603}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
Consensus	*****	*****	*****	*****	*****
	651				700
msa185066.2{270_090}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAGGCT	GAAGAAAGTA
msa185066.2{270_18RS21}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAGGCT	GAAGAAAGTA
msa185066.2{270_2603}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAGGCT	GAAGAAAGTA
Consensus	*****	*****	*****	*****	*****
	701				750
msa185066.2{270_090}	AGAAAGCTTC	AAAAATGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_18RS21}	AGAAAGCTTC	AAAAATGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_2603}	AGAAAGCTTC	AAAAATGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
Consensus	*****	*****	*****	*****	*****
	751				800
msa185066.2{270_090}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_18RS21}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_2603}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
Consensus	*****	*****	*****	*****	*****
	801				850
msa185066.2{270_090}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_18RS21}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_2603}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
Consensus	*****	*****	*****	*****	*****
	851				900
msa185066.2{270_090}	CGGCTGCCTT	ACTTAAAGAG	GTAGCTAAAT	CAAAATTGAC	TGACACAGCT
msa185066.2{270_18RS21}	CGGCTGCCTT	ACTTAAAGAG	GTAGCTAAAT	CAAAATTGAC	TGACACAGCT

Table 61: Comparative Sequences relating to SAG1030

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msa185066.2{270_2603} CGGCTGCCTT ACTTAAAGAG GTAGCTAAAT CAAAATTGAC TGACACAGCT
Consensus *****
          901          912
msa185066.2{270_090} CGGCTATTGA TG
msa185066.2{270_18RS21} CGGCTATTGA TG
msa185066.2{270_2603} CGGCTATTGA TG
Consensus ***** **

SEQ ID NO. 6104
STRAIN 2603 frame: 1
MVKVSVSSVGTQASTVAISMFSRVSA LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLT
PMLQGMILFSETLSEKCTELQTLVYSICGDEDLDSVVLESKLASDRASLKIAEALLEHLN
DDPEPSKSAISSTKSNIKKLRKRIKSNQKKLDNLNEFNAHSATVFADISNAQSTVNQALA
AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDA KAEELKSKKAEESKASKIE
NTTKKSNVSVDKKKLIKAANEAYKLG EIKKDTYESIIISGLSNASAALLKEVAKSKLTDTA
RLLM

SEQ ID NO. 6105
STRAIN 090 frame: 1
LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLVVS
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLRKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDA KAEELKSKKAEESKASKIENITTKKSNVSVDKKKLIKAANEAYKLG
EIKKDTYESIIISGLSNASAALLKEVAKSKLTDARLLM

SEQ ID NO. 6106
STRAIN 18RS21 frame: 1
LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLVVS
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLRKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDA KAEELKSKKAEESKASKIENITTKKSNVSVDKKKLIKAANEAYKLG
EIKKDTYESIIISGLSNASAALLKEVAKSKLTDARLLM
PRETTY of: /biotmp/msa185181.2{*} May 13, 2003 07:03 ..

          1          50
msa185181.2{270_090} -----LND AITKLSSFAEA ATLQGTAYSN
msa185181.2{270_18RS21} -----LND AITKLSSFAEA ATLQGTAYSN
msa185181.2{270_2603} mvkvsvssvg tqastvaism fsvsaLNDA IITKLSSFAEA ATLQGTAYSN
Consensus *****

          51          100
msa185181.2{270_090} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVYSICGD EDLDSVVLES
msa185181.2{270_18RS21} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVYSICGD EDLDSVVLES
msa185181.2{270_2603} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVYSICGD EDLDSVVLES
Consensus *****

          101          150
msa185181.2{270_090} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKLRKRIKSNQKK
msa185181.2{270_18RS21} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKLRKRIKSNQKK
msa185181.2{270_2603} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKLRKRIKSNQKK
Consensus *****

          151          200
msa185181.2{270_090} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_18RS21} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_2603} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
Consensus *****

          201          250
msa185181.2{270_090} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKASKIE NTKKSNVSV
msa185181.2{270_18RS21} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKASKIE NTKKSNVSV
msa185181.2{270_2603} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKASKIE NTKKSNVSV
Consensus *****

          251          300
msa185181.2{270_090} DKKLIKAAN EAYKLGEIKK DTYESIIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_18RS21} DKKLIKAAN EAYKLGEIKK DTYESIIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_2603} DKKLIKAAN EAYKLGEIKK DTYESIIISGL SNASAALLKE VAKSKLTDTA
Consensus *****

          301
msa185181.2{270_090} RLLM
msa185181.2{270_18RS21} RLLM
msa185181.2{270_2603} RLLM
Consensus ****

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Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6201

STRAIN 2603

ATGATTTTAAAAAATTGTCGTGCAGCATATAGTTTACAATGGGGAGGTGTTTACCAATTA
GCTTTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATA
GCTTACGAGAAACAATATAAAAAGAAAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAATTGTTCAATTTTAAATACAATAGTTTACTTTTCCCTATATTTCCCAAATAT
AGAGAAGCGGCAGCTACTTTTAAATGAGGATGGTATTAGTTTAACTTCTGATTTTAAAGC
CATACATGTACGATTGAAACTGCAAACTAATTTTAAAGAAGGTAAAATCTTATCAGCA
GTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAAGATAAGAGGAATGCTGCTGGA
GACCCFAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATCTCGGTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTTAACAGTAGGT
TTAAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATCCTGATTCT
ATTTTGTGATGGTTATCATCCTGCTAAAATTAATAATCAGCTTCTTTAGCAGAACATTTA
GTTGATGTGTTATCCCAAAACATTAATCAAGAGATTATCAAGCCCTTGTGCCAATGAC
TTGAAACACAGGGTTTATTATTTAGATTACTGTAAACGAAACACTTTATGAGTGGAAATCAA
AAAGTTATGATTTTCTTTGTCAATTTGAAAATAAA

SEQ ID NO. 6202

STRAIN 090

TGGATTATCCTCTAATTAAGGCGTTTGAATTGGAAGGATAGGAGCTTTC
ATAGCTTACGAGAAACAATATAAAAAGAAAAATTGAGATACAATGTGACGA
TAAACATCTCCTCAAAAATTTGTTCAATTTTAAATACAATAGTTTATA
CTTTTCCCTATATTTCCCAAATATAGAGAAGCGGCAGCTACTTTTAAATGAG
GATGGTATTAGTTTAACTTCTGATTTTAAAGCCATAACATGTACGATTGA
AACTGCAAAATAAATTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAG
CCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCT
GGAGACCCFAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATAC
CAATCTGGTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCAT
CTGAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTCAGCTTTCATTTT
AATTAACAAGATATCATCAATCATCCTGATTTCTATTTTGTGATGGTTATCA
TCTGCTAAAATTAATAATCAACTTTCTTTAGCAGAACATTTAGTTGAT
GTGTTATCCCAAAACATTAATCAAGAAGATTATCAAGCCCTTGTGCCAAT
GACTTGAACACAGAGTTTATTATTTAGATTACTGTAAACGAAACACTTTA
TGAGTGGAAATCAAAAAGTTTATGATTTTCTTTGTCAATTTGAAAATAAA

SEQ ID NO. 6203

STRAIN A909

TTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAGGATA
GGAGCTTTCATAGCTTACGAGAAACAATATAAAAAGAAAAATTGAGATACA
ATGTGACGATAAACATCTCCTCAAAAATTTGTTCAATTTTAAATACA
ATAGTTTACTTTTCCCTATATTTCCCAAATATAGAGAAGCGGCAGCTACT
TTTAAATGAGGATGGTATAGTTTAACTTCTGATTTTAAAGCCATAACATG
TACGATTGAAACTGCAAAAATAAATTTTAAAGAAGGTAAAATCTTATCAG
CAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGG
AATGCTGCTGGAGACCCFAAGATTACTTTGACTATGTGATGTTGAACTG
GTCAAATACCAATCTCGTTTATCGTTTAGTAATGGAAAGATTGTTAGGCA
AAGCCATCTGAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTCAGC
TTTCAATTTAATTATCAAGATATCATCAATCATCCTGATTTCTATTTTGA
TGTTTATCATCTGCTAAAATTAATAATCAACTTTCTTTAGCAGAACATTT
TAGTTGCAATGTGTTATCCCAAAACATTAATCAAGAAGATTATCAAGCCCT
GTGCCTAATGACTTGAACACAGAGTTTATTATTTAGATTACTGTAAACGA
AACACTTTATGAGTGGAAATCAAAAAGTTTATGATTTTCTTTGTCAATTTG
AAAATAAA

SEQ ID NO. 6204

STRAIN H36B

TTAAGGCGTTTGAATTGGAAGGATAGGAGCTTTCATAGCTTACGAGAAA
CAATATAAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC
AAAAATTGTTCAATTTTAAATACAATAGTTTACTTTTCCCTATATTC
CCAAATATAGAGAAAGCGGCAGCTACTTTTAAATGAGGATGGTATTAGTTTA
ACTTCTGATTTTAAAGCCATAACATGTACGATTGAAACTGCAAAAATAA
TTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTG
CTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCFAAGAT
TACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATCTGGTTATCG
TTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTTAA
CAGTAGCTTTTAAAGCCAGGGGTCAGCTTTCATTTAATTATCAAGATATC
ATCAATCATCCTGATTTCTATTTTGTGATGTTATCATCCTGCTAAAATTA
AAATCAACTTTCTTTAGCAGAACATTTAGTTGATGTTATCCCAAAAC
ATTATCAAGAAGATTATCAAGCCCTTGTGCCAATGACTTGAACACAGA
GTTTATTATTTAGATTACTGTAAACGAAACACTTTATGAGTGGAAATCAAAA
AGTTTATGATTTTCTTTGTCAATTTGAAAATAAA

SEQ ID NO. 6205

STRAIN 18RS21

TTGCTGGATTATCCTCGAATTAAGGCGTT
TGAATTGGAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGAAAAATTGTT
CATTTTAAATACAATAGTTTACTTTTCCCTATATTTCCCAAATATAG
AGAAGCGGCAGCTACTTTTAAATGAGGATGGTATTAGTTTAACTTCTGATT
TTTTAAGCCATAACATGTACGATTGAAACTGCAAAAATAAATTTTAAAGAA
GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCFAAGATTACTTTGACT
ATGTGATGTTGAACTGGTCAAATACCAATCTCGTTATCTGTTTAGTAATG

Table 62: Comparative Sequences relating to SAG0690

GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
TAAGCCAGGGGTGAGTTTTCATTTTACTTATCAAGATATCATCAATCATC
CTGATTCATTTTTGATGGTTATCATCTCTGCTAAAATTAATAATCAGCTT
TCCTTAGCAGAACATTTAGTTGCATGTGTATCCCAAAACATTATCAAGA
AGATTATCAAAGCCTTGTGCCAATGACTTGAAACACAGGGTTTATTATT
TAGATTACTGTAACGAAACACTTTATGAGTGAATCAAAAAGTTTATGAT
TTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6206

STRAIN M732

TTGCTGGATTATCCTCGAATTAAGGCGTT
TGAAATGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAAACATATAAAA
GAAAAACTGAGATACAAATGTGACGATAAACATCTCCTCGCAAAAATGTT
CATTTTTTAAAATACAATAGTTTACITTTCCCTATATCCCAAATATAG
AGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
TTTTAAGCCATACATGTACGATGAAACTGCAAACTAATTTTTAAAGAA
GGTAAAATCTTATCAGCAGTTAAAGCCTTAAATAAGCCTGCTGAAGTACT
GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT
ATGTGATGTTGAACTGGTCAAAATACCAATCTGGTTATCGTTTAGTAATG
GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
TAAGCCAGGGGTGAGTTTTCATTTTACTTATCAAGATATCATCAATCATC
CTGATTCATTTTTGATGGTTATCATCTCTGCTAAAATTAATAATCAGCTT
TCCTTAGCAGAACATTTAGTTGCATGTGTATCCCAAAACATTATCAAGA
AGATTATCAAAGCCTTGTGCCAATGACTTGAAACACAGGGTTTATTATT
TAGATTACTGTAACGAAACACTTTATGAGTGAATCAAAAAGTTTATGAT
TTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6207

STRAIN COH1

TTGCTGGAT

TATCCTCGAATTAAGGCGTTTGAAATGGAAAGGATAGGAGCTTTCATAGC
TTACGAGAAAACATATAAAAGAAAACCTGAGATACAATGTGACGATAAAC
ATCTCCTCGCAAAAATGTTTCATTTTTTAAAATACAATAGTTTACTTTT
CCCTATATCCCAAATATAGAGAAGCGGCAGCTACTTTAATGAGGATGG
TATTAGTTTAACTTCTGATTTTTAAGCCATACATGTACGATTGAAACTG
CAAACTAATTTTTAAAGAAAGGTAATACTTATCAGCAGTTAAAGCCTTT
AATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAGA
CCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAAATACCAAT
CTGGTTATCGTTTAGTAAAGGAAAGATTGTTAGGCAAAGCACCATCTGAA
CAGGAGTTAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTTA
TCAAGATATCATCAATCATCTCTGATTTCTATTTTTGATGGTTATCATCCTG
CTAAAATTAATAATCAGCTTCTTTAGCAGAACATTTAGTTGCATGTGTT
ATCCAAAACATTTATCAAGAAGATTATCAAAGCCTTGTGCCAATGACTT
GAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGT
GGAATCAAAAAGTTTATGATTTTCTTTGGCAATTTGGAAAATAAA

SEQ ID NO. 6208

STRAIN M781

TTGCTGGA

TTATCCTCGAATTAAGGCGTTTGAAATGGAAAGGATAGGAGCTTTCATAG
CTTAGGAAACAATATAAAAGAAAACCTGAGATACAATGTGACGATAAAA
CATCTCCTCGCAAAAATGTTTCATTTTTTAAAATACAATAGTTTACTTTT
TCCTATATCCCAAATATAGAGAAGCGGCAGCTACTTTAATGAGGATG
GTATTAGTTTAACTTCTGATTTTTAAGCCATACATGTACGATTGAAACT
GCAAACTAATTTTTAAAGAAAGGTAATACTTATCAGCAGTTAAAGCCTTT
TAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAG
ACCCTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAAATACCAAT
TCTGGTTATCGTTTAGTAAAGGAAAGATTGTTAGGCAAAGCACCATCTGA
ACAGGAGTTAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTT
ATCAAGATATCATCAATCATCTCTGATTTCTATTTTTGATGGTTATCATCCT
GCTAAAATTAATAATCAGCTTCTTTAGCAGAACATTTAGTTGCATGTGT
TATCCAAAACATTTATCAAGAAGATTATCAAAGCCTTGTGCCAATGACTT
TGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGT
TGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6209

STRAIN CJB110

TTGCTGGATTATCCTCGAATTAAGGC

GTTTGAAATGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAAACATATA
AAAGAAAATTTAGATACAATGTGACGATAAACATCTCCTCACAATAAT
GTTTCAATTTTTTAAAATACAATAGTTTACTTTTCCCTATATCCCAAATA
TAGAGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTG
ATTTTTAAGCCATACATGTACGATTGAACTGCAAACTAATTTTTTAAA
GAAGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGT
ACTGTAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTG
ACTATGTGATGTTGAACTGGTCAAAATACCAATCTGGTTATCGTTTAGTA
ATGAAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGC
TTTTAAGCCAGGGGTGAGCTTTCAITTTAATTTATCAAGATATCATCAATC
ATCCTGATTCATTTTTGATGGTTATCATCTCTGCTAAAATTAATAATCAA
CTTTCTTTAGCAGAACATTTAGTTGCATGTGTATCCCAAACATTATCA
AGAAGATTATCAAAGCCTTGTGCCAATGACTTGAAACACAGAGTTTATT
ATTTAGATTACTGTAACGAAACACTTTATGAGTGAATCAAAAAGTTTAT
GATTTCTTTGTCATTTGGAAAATAAA

Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6210
 STRAIN 1169NT
 AATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGA
 AACAAATATAAAAGAAAACACTGAGATACAATGTGACGATAAACATCTCCTC
 GCAAAAATGTGTTTCAATTTTAAATACAATAGTTTACTTTTCCCTATAT
 TCCCAAATATAGAGAAGCGGCGAGCTACITTTAATGAGGATGTTATTAGTT
 TAACCTTCGATTTTTTAAAGCCATACATGTACGATTGAAAACGCAAACTA
 ATTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCC
 TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAG
 ATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCGTTTAT
 CGTTTAGTAATGGAAAGATTGTTAGGCCAAAGCACCATCTGAACAGGAGTT
 AACAGTAGGTTTAAAGCCAGGGGTCAGCTTTCATTTACTTATCAAGATA
 TCAATCAATCATCCTGATTCATTTTGGATGGTTATCATCCTGCTAAAAT
 AAAATCAGCTTCTTTAGCAGAACATTTAGTTGCGTGTGTTATCCCAA
 ACATTATCAAGAAGATTATCAAAATCTTGTGCCAATGACTTGAAACACA
 GAGTTTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAA
 AAGTTTATGATTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6211
 STRAIN JM9130013
 ATAGGAGCTTTCATAGCTTACGAGAAAACAATATAAAAGAAAATTGAGAT
 ACAATGTGACGATAAACATCTCCTCACAATAATGTTTCAATTTTTAAAT
 ACAATAGTTTTACTTTTCCCTATATTCCAAATATAGAGAAGCGGCGAGCT
 ACTTTAATGAGGATGGTATTAGTTTAACTTCGATTTTTTAAAGCCATAC
 ATGTACGATTGAAAACGCAAACTAAATTTTTAAAGAGGTAAAATCTTAT
 CAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAG
 AGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACTATGTGATGTTGAA
 CTGGTCAAATACCAATTCGGTTATCGTTTAGTAATGGAAAGATTGTTAG
 GCAAAGCACCATCTGAAACAGGAGTTAACAGTAGCTTTAAAGCCAGGGGTC
 AGCTTTCATTTAATTTATCAAGATATCATCAATCATCCTGATTTCTATTT
 TGATGTTATCATCCTGCTAAAATTAATAATCAACTTCTTTAGCAGAAC
 ATTTAGTTGCAATGTTTATCCCAAACATTATCAAGAAGATTATCAAAAGC
 CTTGTGCCAATGACTTGAAACACAGAGTTTATTTATTTAGATTACTGTAA
 CGAAACACTTTATGAGTGGAAATCAAAAAGTTTATGATTTTCTTTGTCAT
 TGAAAATAAA

PRETTY of: /biotmp/msa185284.2{*} May 13, 2003 07:08 ..

	1				50
msa185284.2{271_090}	-----	-----	-----	-----	-----
msa185284.2{271_H36B}	-----	-----	-----	-----	-----
msa185284.2{271_JM9130013}	-----	-----	-----	-----	-----
msa185284.2{271_A909}	-----	-----	-----	-----	-----
msa185284.2{271_CJB110}	-----	-----	-----	-----	-----
msa185284.2{271_18RS21}	-----	-----	-----	-----	-----
msa185284.2{271_2603}	atgat	tttaa	aaatt	tgctg	tcagcatat
msa185284.2{271_M732}	-----	-----	-----	-----	-----
msa185284.2{271_M781}	-----	-----	-----	-----	-----
msa185284.2{271_COH1}	-----	-----	-----	-----	-----
msa185284.2{271_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

	51				100
msa185284.2{271_090}	-----	-----	---tgg	attatcctct	aattaaggcg
msa185284.2{271_H36B}	-----	-----	-----	-----	---ttaaggcg
msa185284.2{271_JM9130013}	-----	-----	-----	-----	-----
msa185284.2{271_A909}	-----	---	TTGctgg	attatcctcg	aattaaggcg
msa185284.2{271_CJB110}	-----	---	TTGctgg	attatcctcg	aattaaggcg
msa185284.2{271_18RS21}	-----	---	TTGctgg	attatcctcg	aattaaggcg
msa185284.2{271_2603}	ttaccaatta	gct	TTGctgg	attatcctcg	aattaaggcg
msa185284.2{271_M732}	-----	---	TTGctgg	attatcctcg	aattaaggcg
msa185284.2{271_M781}	-----	---	TTGctgg	attatcctcg	aattaaggcg
msa185284.2{271_COH1}	-----	---	TTGctgg	attatcctcg	aattaaggcg
msa185284.2{271_1169NT}	-----	---	TTGctgg	attatcctcg	aattaaggcg
Consensus	*****	*****	-----	-----	-----

	101				150
msa185284.2{271_090}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_H36B}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_JM9130013}	-----	---ATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA
msa185284.2{271_A909}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_CJB110}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_18RS21}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_2603}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_M732}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_M781}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_COH1}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_1169NT}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
Consensus	-----	*****	*****	*****	*****

	151				200
msa185284.2{271_090}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT

Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_H36B}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_JM9130013}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_A909}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_CJB110}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_18RS21}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_2603}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M732}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M781}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_COH1}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_1169NT}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
Consensus	*****	*****	*****	-*****	*****

	201			250	
msa185284.2{271_090}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_H36B}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_JM9130013}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_A909}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_CJB110}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_18RS21}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_2603}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M732}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M781}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_COH1}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_1169NT}	AAAATACAAT	AGTTTTACTT	TTCCTATAT	TCCCAAATAT	AGAGAAGCGG
Consensus	*****	*****	*****	*****	*****

	251			300	
msa185284.2{271_090}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_H36B}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_JM9130013}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_A909}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_CJB110}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_18RS21}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_2603}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_M732}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_M781}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_COH1}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_1169NT}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
Consensus	*****	*****	*****	*****	*****

	301			350	
msa185284.2{271_090}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_H36B}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_JM9130013}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_A909}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_CJB110}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_18RS21}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_2603}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_M732}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_M781}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_COH1}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
msa185284.2{271_1169NT}	CATACATGTA	CGATTGAAAC	TGCAAAACTA	ATTTTTAAAG	AAGGTAAAAT
Consensus	*****	*****	*****	*****	*****

	351			400	
msa185284.2{271_090}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_H36B}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_JM9130013}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_A909}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_CJB110}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_18RS21}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_2603}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M732}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M781}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_COH1}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_1169NT}	CTTATCAGCA	GTTAAAGCCT	TTAATAAGCC	TGCTGAAGTA	CTGGTAAATG
Consensus	*****	*****	*****	*****	*****

	401			450	
msa185284.2{271_090}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_H36B}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_JM9130013}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_A909}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_CJB110}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_18RS21}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_2603}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M732}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M781}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_COH1}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_1169NT}	ATAAGAGGAA	TGCTGCTGGA	GACCCTAAAG	ATTACTTTGA	CTATGTGATG
Consensus	*****	*****	*****	*****	*****

Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_090}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_H36B}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_JM9130013}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_A909}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_CJB110}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_18RS21}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_2603}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_M732}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_M781}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_COH1}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_1169NT}	TTGAACTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_H36B}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_JM9130013}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_A909}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_CJB110}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_18RS21}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_2603}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M732}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M781}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_COH1}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_1169NT}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
Consensus	*****	*****	*****	*****-*	*****
msa185284.2{271_090}	GGGTCAGcTT	TCATTTTAAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_H36B}	GGGTCAGcTT	TCATTTTAAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_JM9130013}	GGGTCAGcTT	TCATTTTAAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_A909}	GGGTCAGcTT	TCATTTTAAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_CJB110}	GGGTCAGcTT	TCATTTTAAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_18RS21}	GGGTCAGcTT	TCATTTTAAcT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_2603}	GGGTCAGcTT	TCATTTTAAcT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M732}	GGGTCAGcTT	TCATTTTAAcT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M781}	GGGTCAGcTT	TCATTTTAAcT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_COH1}	GGGTCAGcTT	TCATTTTAAcT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_1169NT}	GGGTCAGcTT	TCATTTTAAcT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
Consensus	*****-*	*****-*	*****	*****	*****
msa185284.2{271_090}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_H36B}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_JM9130013}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_A909}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_CJB110}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_18RS21}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_2603}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M732}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M781}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_COH1}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_1169NT}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
Consensus	*****	*****	*****	*****-*	*****
msa185284.2{271_090}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_H36B}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_JM9130013}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_A909}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_CJB110}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_18RS21}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_2603}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M732}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M781}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_COH1}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_1169NT}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_H36B}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_JM9130013}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_A909}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_CJB110}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_18RS21}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_2603}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M732}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M781}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_COH1}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_1169NT}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
Consensus	***-*****	***-*****	*****	*-*****	*****

Table 62: Comparative Sequences relating to SAG0690

		751			800
msa185284.2{271_090}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_H36B}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_JM9130013}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_A909}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_CJB110}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_18RS21}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_2603}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_M732}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_M781}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_COH1}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
msa185284.2{271_1169NT}	TGTAACGAAA	CACITTTATGA	GTGGAATCAA	AAAGTTTATG	ATTTTCTTTG
Consensus	*****	*****	*****	*****	*****

		801	816
msa185284.2{271_090}	tCATTTGGAA	AATAAA	
msa185284.2{271_H36B}	tCATTTGGAA	AATAAA	
msa185284.2{271_JM9130013}	tCATTTGGAA	AATAAA	
msa185284.2{271_A909}	tCATTTGGAA	AATAAA	
msa185284.2{271_CJB110}	tCATTTGGAA	AATAAA	
msa185284.2{271_18RS21}	tCATTTGGAA	AATAAA	
msa185284.2{271_2603}	tCATTTGGAA	AATAAA	
msa185284.2{271_M732}	nCATTTGGAA	AATAAA	
msa185284.2{271_M781}	tCATTTGGAA	AATAAA	
msa185284.2{271_COH1}	gCATTTGGAA	AATAAA	
msa185284.2{271_1169NT}	tCATTTGGAA	AATAAA	
Consensus	*****	*****	

SEQ ID NO. 6212

STRAIN 2603 frame: 1

MILKICRAAYSLQWGGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIIVHFLKYNSTFFPYIPKYR

SEQ ID NO. 6213

STRAIN A909 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLTKIIVHFLKYNSTFFPYIPKYR

SEQ ID NO. 6214

STRAIN H36B frame: 3

KAFELERIGAFIAYEKQYKRKIEIQCDDKHLTKIIVHFLKYNSTFFPYIPKYR

SEQ ID NO. 6215

STRAIN 18RS21 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIIVHFLKYNSTFFPYIPKYR

SEQ ID NO. 6216

STRAIN M732 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIIVHFLKYNSTFFPYIPKYR

SEQ ID NO. 6217

STRAIN COH1 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIIVHFLKYNSTFFPYIPKYR

SEQ ID NO. 6218

STRAIN M781 frame: 1

Table 62: Comparative Sequences relating to SAG0690

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPABVLVNDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFHFTYQDIINHPSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6219

STRAIN CJB110 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPABVLVNDKRNAAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFHNYQDIINHPSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6220

STRAIN 1169NT frame: 2

IKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFFPYIPKYREAAATF
NEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPABVLVNDKRNAAGDPKDYFD
YVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFHFTYQDIINHPSIFDGYHP
AKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVYDFLC
HLENK

SEQ ID NO. 6221

STRAIN JM9130013 frame: 1

IGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFFPYIPKYREAAATFNEDGISLT
SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPABVLVNDKRNAAGDPKDYFDYVMLNWSN
TNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFHNYQDIINHPSIFDGYHPAKIKNQLS
LAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6222

STRAIN 090 frame: 3

DYPLIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFFPYIPKYREA
AATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPABVLVNDKRNAAGDPK
DYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFHNYQDIINHPSIFD
GYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVY
DFLCHLENK

PRETTY of: /biotmp/msa185358.2{*} May 13, 2003 07:11 ..

msa185358.2{271_090} 1 50
msa185358.2{271_JM9130013} -----IGAFI AYEKQYKRKi
msa185358.2{271_H36B} -----ka felerIGAFI AYEKQYKRKi
msa185358.2{271_A909} -----LLdyprika felerIGAFI AYEKQYKRKi
msa185358.2{271_CJB110} -----LLdyprika felerIGAFI AYEKQYKRKi
msa185358.2{271_1169NT} -----ika felerIGAFI AYEKQYKRKt
msa185358.2{271_18RS21} -----LLdyprika felerIGAFI AYEKQYKRKt
msa185358.2{271_2603} milkicraay slwgqgyvql aLLdyprika felerIGAFI AYEKQYKRKt
msa185358.2{271_M732} -----LLdyprika felerIGAFI AYEKQYKRKt
msa185358.2{271_M781} -----LLdyprika felerIGAFI AYEKQYKRKt
msa185358.2{271_COH1} -----LLdyprika felerIGAFI AYEKQYKRKt
Consensus ***** ***** **-----***** *****

msa185358.2{271_090} 51 100
msa185358.2{271_JM9130013} EIQCDDKHLL tKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_H36B} EIQCDDKHLL tKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_A909} EIQCDDKHLL tKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_CJB110} EIQCDDKHLL tKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_1169NT} EIQCDDKHLL aKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_18RS21} EIQCDDKHLL aKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_2603} EIQCDDKHLL aKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_M732} EIQCDDKHLL aKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_M781} EIQCDDKHLL aKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_COH1} EIQCDDKHLL aKIVHFLKYN SFTFFPYIPKY REAAATFNED GISLTSDFLS
Consensus ***** -***** ***** ***** *****

msa185358.2{271_090} 101 150
msa185358.2{271_JM9130013} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_H36B} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_A909} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_CJB110} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_1169NT} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_18RS21} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVkDKRNAAG DPKDYFDYVM
msa185358.2{271_2603} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVkDKRNAAG DPKDYFDYVM
msa185358.2{271_M732} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVkDKRNAAG DPKDYFDYVM
msa185358.2{271_M781} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVkDKRNAAG DPKDYFDYVM
msa185358.2{271_COH1} HTCTIETAKL IFKEGKILSA VKAFNKPABV LVkDKRNAAG DPKDYFDYVM

Table 62: Comparative Sequences relating to SAG0690

Consensus	*****	*****	*****	**_*****	*****
	151				200
msa185358.2{271_090}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINH _{PDS}
msa185358.2{271_JM9130013}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINH _{PDS}
msa185358.2{271_H36B}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINH _{PDS}
msa185358.2{271_A909}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINH _{PDS}
msa185358.2{271_CJB110}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINH _{PDS}
msa185358.2{271_1169NT}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINH _{PDS}
msa185358.2{271_18RS21}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINH _{PDS}
msa185358.2{271_2603}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINH _{PDS}
msa185358.2{271_M732}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINH _{PDS}
msa185358.2{271_M781}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINH _{PDS}
msa185358.2{271_COH1}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINH _{PDS}
Consensus	*****	*****	*****_	*****_	*****
	201				250
msa185358.2{271_090}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_JM9130013}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_H36B}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_A909}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_CJB110}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_1169NT}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQnLVPND	LKHRVYYLDY
msa185358.2{271_18RS21}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_2603}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M732}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M781}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_COH1}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
Consensus	*****	*****	*****	*****_*****	*****
	251				272
msa185358.2{271_090}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_JM9130013}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_H36B}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_A909}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_CJB110}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_1169NT}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_18RS21}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_2603}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_M732}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_M781}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_COH1}	CNETLYEWNQ	KVYDFLCHLE	NK		
Consensus	*****	*****_***	**		

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6301
 STRAIN 2603
 ATGAAAAGTCGAAAAAAGATAAATGGTATTGAGGTTAACAACAACACTATTGGTTTTT
 GGTTTGGGTGGGGTTTGGTTTTATAAATTATAAAAATGATAATGTCGAACCGACAGTCACT
 AGTGCATCGGATCAAACGACGACTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATT
 TCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCC
 AGTGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
 TATAAAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGAAAGGCAATATGACT
 CAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTAATCTGCTTCACTATATGATTATGCT
 GAGTTAGTATCTAGTCAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAG
 GATGCTACTGACGCTCTAACAGGCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
 AACCAAATTAATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6302
 STRAIN 090
 GGGGTTTGGTTTTTATAATTATAA
 AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
 CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
 GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG
 TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
 AAGGAGAATATAAAGGTAATCTGTCCAATGCCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
 TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
 ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGCTTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
 CCAAATTAATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6303
 STRAIN A909
 GGGGTTTGGTTTTTATAATTATAA
 AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
 CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
 GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG
 TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
 AAGGAGAATATAAAGGTAATCTGTCCAATGCCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
 TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
 ATGCATCTGCTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGCTTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
 CCAAATTAATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6304
 STRAIN H36B
 GGGGTTTGGTTTTTATAATTATAAAAATGATA
 ATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATT
 CAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTA
 TGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAAT
 CAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
 TATAAAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGG
 CAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTAATCTG
 CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCATCT
 GCTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGACGCTCTAAC
 AGGCTTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATTA
 TTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6305
 STRAIN I8RS21
 GGGGTTTGGTTTTTATAATTATAAAAATGATAATG
 TCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
 ACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGC
 GTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAG
 ATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATAT
 AAAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAA
 TATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTAATCTGCTT
 CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCATCTGTT
 TGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGACGCTCTAACAGG
 TCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATTAATTG
 AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6306
 STRAIN M732
 GGGGTTTGGTTTTTATAATTATAA
 AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
 CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
 GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG
 TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
 AAGGAGAATATAAAGGTAATCTGTCCAATGCCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
 TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
 ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGCTTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
 CCAAATTAATTGAAACCTACAGTCTAGATGCTTATGATAAA

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6307
 STRAIN COH1
 GGGGTTTGGTTTTATAATTATAA
 AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
 CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
 GATTTGTATGCCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG
 TGGCAATCAGATTTGTCTAAGGCTCCTAATTTATAACCTCTTTGGCATCA
 AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
 TTATCTGCTTCACTATATGATTTATGCTGAGTTAGTATCTAGTCAAAGT
 ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGCTTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
 CCAAATTTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6308
 STRAIN M781
 GGGGTTTGGTTTTATAATTATAAAAAATGA
 TAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTT
 TTCAAACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTG
 TATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACA
 ATCAGATTTGTCTAAGGCTCCTAATTTATAACCTCTTTGGCATCAAAGGAG
 AATAATAAAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAA
 GGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTTCT
 TGCTTCACTATATGATTTATGCTGAGTTAGTATCTAGTCAAAGTATGAT
 CTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTA
 ACAGGCTTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAT
 TATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6309
 STRAIN CJB110
 GGGGTTTGGTTTTATAATTATAAAAAATGATAATGT
 CGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
 CGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
 TCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAGA
 TTTGTCTAAGGCTCCTAATTTATAACCTCTTTGGCATCAAAGGAGAATATA
 AAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
 ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTTCTGCTTC
 ACTATATGATTTATGCTGAGTTAGTATCTAGTCAAAGTATGATCTGTTT
 GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
 CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATTTATGTA
 AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6310
 STRAIN I169NT
 GGGGTTTGGTTTTATAATTATAAAAAATGATAATGT
 CGAACAGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
 CGATTTCCCCAACAGCTATTGAAATTTCTAAGACCTATGATTTGTATGCG
 TCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAGA
 TTTGTCTAAGGCTCCTAATTTATAACCTCTTTGGCATCAAAGGAGAATATA
 AAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
 ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTTCTGCTTC
 ACTATATGATTTATGCTGAGTTAGTATCTAGTCAAAGTATGATCTGTTT
 GGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
 CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATTTATGTA
 AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6311
 STRAIN JM9130013
 TTTGGTTTTATAATTATAAAAAATGATAATGTCGAACCGACAGTCACTAGT
 GCATCGGATCAAACGACGACTTTTATTCAAACGATTTCCCCAACAGCTAT
 TGAATTTCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAAG
 CTATTTTGGAAATCATCCAGTGGACAATCAGATTTGTCTAAGGCTCCTAAT
 TATAACCTCTTTGGCATCAAAGGAGAATATAAAGGTAATCTGTTCAAAT
 GCCTACTTTAGAAGATGATGGGAAAGGTAATATGACCCAAATCCAAGCTC
 CTTTTCGCGCCTATCCAAATTTCTGCTTCACTATATGATTTATGCTGAG
 TTAGTATCTAGTCAAAGTATGATCTGTTTGGAAATCAAATACTTCTTCT
 TTATAAGGATGCTACTGCAGCTCTAACAGGCTTTTATGCGACAGATACTG
 CTTATGCTAGTAAATTAACCAAATTTATTGAAAACCTACAGTCTAGATGCT
 TATGATAAA

PRETTY of: /biotmp/msa243324.2{*} February 11, 2003 05:11 ..

	1				50
msa243324.2{275_A909}	-----	-----	-----	-----	-----
msa243324.2{275_H36B}	-----	-----	-----	-----	-----
msa243324.2{275_090}	-----	-----	-----	-----	-----
msa243324.2{275_18RS21}	-----	-----	-----	-----	-----
msa243324.2{275_2603}	atgaaaagtc	gaaaaaaaga	taaatgggta	ttgagggttaa	caacaacact
msa243324.2{275_CJB110}	-----	-----	-----	-----	-----
msa243324.2{275_COH1}	-----	-----	-----	-----	-----
msa243324.2{275_M732}	-----	-----	-----	-----	-----

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M781}	-----	-----	-----	-----	-----
msa243324.2{275_1169NT}	-----	-----	-----	-----	-----
msa243324.2{275_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
51					
msa243324.2{275_A909}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_H36B}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_090}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_18RS21}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_2603}	attggttttt	ggtttgggtg	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_CJB110}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_COH1}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_M732}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_M781}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_1169NT}	-----g	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_JM9130013}	-----	-----	---TTTGGTT	TTATAATTAT	AAAAATGATA
Consensus	*****	*****	---*****	*****	*****
101					
msa243324.2{275_A909}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_H36B}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_090}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_18RS21}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_2603}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_CJB110}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_COH1}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M732}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M781}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_1169NT}	ATGTCGAACA	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_JM9130013}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
Consensus	*****	*****	*****	*****	*****
151					
msa243324.2{275_A909}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_H36B}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_090}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_18RS21}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_2603}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_CJB110}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_COH1}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M732}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M781}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_1169NT}	CAAACGATTT	CcCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_JM9130013}	CAAACGATTT	CcCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
Consensus	*****	*-*****	*****	*****	*****
201					
msa243324.2{275_A909}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_H36B}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_090}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_18RS21}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_2603}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_CJB110}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_COH1}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_M732}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_M781}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_1169NT}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
msa243324.2{275_JM9130013}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAAATCATCC	AGTGGACAAAT
Consensus	*****	*****	*****	*****	*****
251					
msa243324.2{275_A909}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_H36B}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_090}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_18RS21}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_2603}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_CJB110}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_COH1}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_M732}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_M781}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_1169NT}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
msa243324.2{275_JM9130013}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCFTTGGCAT	CAAAGGAGAA
Consensus	*****	*****	*****	*****	*****
301					
msa243324.2{275_A909}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_H36B}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_090}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_18RS21}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_2603}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_CJB110}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_COH1}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M732}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_M781}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_1169NT}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_JM9130013}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
Consensus	*****	*****_**	*****	*****	*****
351					
msa243324.2{275_A909}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_H36B}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_090}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_18RS21}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_2603}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_CJB110}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_COH1}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M732}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M781}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_1169NT}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_JM9130013}	CAATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
Consensus	*****	*****	*****	*****	*****
401					
msa243324.2{275_A909}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_H36B}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_090}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_18RS21}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_2603}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_CJB110}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_COH1}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_M732}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_M781}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_1169NT}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_JM9130013}	CTTCACATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
Consensus	*****	*****	*****	*****	*****
451					
msa243324.2{275_A909}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_H36B}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_090}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_18RS21}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_2603}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_CJB110}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_COH1}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_M732}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_M781}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_1169NT}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_JM9130013}	GcTTGGAAAT	CAAATAcTC	TTCCTATAAG	GATGCTACTG	CAGCTCTAAC
Consensus	*******	*****_**	*****	*****	*****
501					
msa243324.2{275_A909}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_H36B}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_090}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_18RS21}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_2603}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_CJB110}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_COH1}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_M732}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_M781}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_1169NT}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_JM9130013}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
Consensus	*****	*****	*****	*****	*****
551					
msa243324.2{275_A909}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_H36B}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_090}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_18RS21}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_2603}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_CJB110}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_COH1}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_M732}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_M781}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_1169NT}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_JM9130013}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
Consensus	*****_***	*****	*****	*****	**

SEQ ID NO. 6312
 STRAIN 2603 frame: 1
 MKSRKDKLVRLRITTTLLVFLGGVWFYNYKNDNVEPTVTSASDQTTTFIQFISPTALEI
 SKTYDLYASVLLAQAILLESSGQSDLKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMT
 QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALFGLYATDTAYASKL
 NQIETYSLDAAYDK

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6313
STRAIN 090 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6314
STRAIN A909 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6315
STRAIN H36B frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6316
STRAIN 18RS21 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6317
STRAIN M732 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6318
STRAIN M781 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6319
STRAIN CJB110 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6320
STRAIN 1169NT frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6321
STRAIN JM9130013 frame: 3
WFFYNYKNDNVEPTVTSASDQTTTFFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQSD
LSKAPNYNLFGIKGEYKGSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSS
QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSLDAYDK

PRETTY of: /biotmp/msa243476.2{*} February 11, 2003 05:17 ..

msa243476.2{275_090} 1
msa243476.2{275_18RS21}
msa243476.2{275_2603}
msa243476.2{275_CJB110}
msa243476.2{275_M732}
msa243476.2{275_M781}
msa243476.2{275_A909}
msa243476.2{275_H36B}
msa243476.2{275_JM9130013}
msa243476.2{275_1169NT}
Consensus *****

msa243476.2{275_090} 51
msa243476.2{275_18RS21}
msa243476.2{275_2603}
msa243476.2{275_CJB110}
msa243476.2{275_M732}
msa243476.2{275_M781}
msa243476.2{275_A909}
msa243476.2{275_H36B}
msa243476.2{275_JM9130013}
msa243476.2{275_1169NT}
Consensus *****

Table 63: Comparative Sequences relating to SAG1912

	101				150
msa243476.2{275_090}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_18RS21}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_2603}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_CJB110}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M732}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M781}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_A909}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_H36B}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_JM9130013}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_1169NT}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
Consensus	*****	*****	*****	*****	*****
	151				194
msa243476.2{275_090}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_18RS21}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_2603}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_CJB110}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M732}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M781}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_A909}	aWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_H36B}	aWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_JM9130013}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_1169NT}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
Consensus	-*****	*****	*****	*****	*****

Table 64: Comparative Sequences relating to SAG 0827

SEQ ID NO. 6401
 STRAIN 2603
 ATGAACAAGTCTAAGAAAATCGAAAATTATCAATTATTACTACAAGCGCAAGCTCTA
 TTCTCAGATGAAACAAATGCTCTTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT
 ATGCTTCCAAATCTGTATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAAATCTT
 GGCCCTTTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGGT
 GAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGCTAACTAT
 ATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTATGTTTAAAAATGGCAA
 CTCTAGGAGTTCTAGATTTAGATTTCTCTTTAGTAGCAGATTATGATGAGATTTGATCAA
 GAATACTTAGAAAATTTGTAGGTATTCTAGTAGAACATACGATTGGAAATTTGGATATG
 TTTGGAGTTGAAAAG

SEQ ID NO. 6402
 STRAIN 090
 CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
 TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTAC
 AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTTCTGGCCCTTTCCAGG
 GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGGTGTAA
 TCTGCACAACTGCTAAGACGCTGATTTGATGATGTTACAAAGCATGC
 TAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
 TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTCTTTA
 GTAGCAGATTATGATGAGATTTGATCAAGAATACTTAGAAAATTTGTAGG
 TATTCTAGTAGAACATACGATTGGAAATTTGGATA

SEQ ID NO. 6403
 STRAIN A909
 CTCTATTCTCAGATGAAACAAATGCTCTTGCCAA
 CTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTAT
 TTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTTCTGGCCCTTTCC
 CAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGGTGG
 TGAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC
 ATGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTA
 CCTATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTCT
 TTTAGTAGCAGATTATGATGAGATTTGATCAAGAATACTTAGAAAATTTG
 TAGGTATTCTAGTAGAACATACGATTGGAAATTTGGATATGTTGGAGTT
 GAAAAG

SEQ ID NO. 6404
 STRAIN H36B
 CTCTATTCTCAGATGAAACAAATGCTCTTGCC
 CAACTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTG
 TATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTTCTGGCCCT
 TTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGG
 TGGTGAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAA
 AGCATGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTA
 GTACCTATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCT
 TTCTTTAGTAGCAGATTATGATGAGATTTGATCAAGAATACTTAGAAAAT
 TTGTAGGTATTCTAGTAGAACATACGATTGGAAATTTGGATATGTTTGGAA
 GTTGAAGAAG

SEQ ID NO. 6405
 STRAIN 18RS21
 CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
 ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA
 CAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTTCTGGCCCTTTCCAG
 GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGGTGTGA
 ATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG
 CTAATATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCT
 ATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTCTTT
 AGTAGCAGATTATGATGAGATTTGATCAAGAATACTTAGAAAATTTGTAG
 GTATTCTAGTAGAACATACGATTGGAAATTTGGATATGTTTGGAGTTGAA
 AAG

SEQ ID NO. 6406
 STRAIN M732
 CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
 ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA
 CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTTCTGGCCCTTTTCAG
 GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGGTGTGA
 ATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG
 CTAATATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCT
 ATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTCTTT
 AGTAGCAGATTATGATGAGATTTGATCAAGAATACTTAGAAAATTTGTAG
 GTATTCTAGTAGAACATACGATTGGAAATTTGGATATGTTTGGAGTTGAA
 AAG

SEQ ID NO. 6407
 STRAIN COH1
 CTCTATTCTCAGATGAAACAAATGCTCTTGCCAAC
 TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTT
 TACAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTTCTGGCCCTTTTC
 AGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGGTGGT

Table 64: Comparative Sequences relating to SAG 0827

GAATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCA
TGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAATCGTAGTAC
CCATGTTTAAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTTCT
TTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGT
AGGTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTGGAGTTG
AAAAAG

SEQ ID NO. 6408

STRAIN M781
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAATCGTAGTACCC
ATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTTCTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTGGAGTTGAA
AAG

SEQ ID NO. 6409

STRAIN CJB110
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCCTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTGGAGTTGAAA
AG

SEQ ID NO. 6410

STRAIN 1169NT
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCCTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAATCGTAGTACCCA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTGGAGTTGAAA
AG

SEQ ID NO. 6411

STRAIN JM9130013
CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTAC
AGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCCTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTTGGAATTTGGATATGTTGGAGTTGAAA
AG

PRETTY of: /biotmp/msa236796.2{*} February 11, 2003 02:42 ..

Table with sequence alignment columns (1, 50, 51, 100) and rows for various strains (msa236796.2{282_COH1}, msa236796.2{282_M732}, msa236796.2{282_M781}, msa236796.2{282_090}, msa236796.2{282_CJB110}, msa236796.2{282_18RS21}, msa236796.2{282_2603}, msa236796.2{282_A909}, msa236796.2{282_H36B}, msa236796.2{282_JM9130013}, msa236796.2{282_1169NT}, Consensus) and a final row for msa236796.2{282_2603} with a gcaagCTCTA mutation.

Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_A909}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_H36B}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_JM9130013}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_1169NT}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	101	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT	150
msa236796.2{282_M732}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_M781}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_090}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_CJB110}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_18RS21}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_2603}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_A909}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_H36B}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_JM9130013}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_1169NT}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
Consensus	*****	*****	*****	*****	*****	*****	
msa236796.2{282_COH1}	151	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT	200
msa236796.2{282_M732}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_M781}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_090}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_CJB110}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_18RS21}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_2603}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_A909}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_H36B}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_JM9130013}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
msa236796.2{282_1169NT}	TATTTATTTG	ATGGAgAgGA	GTTAATTCCT	GGCCCTTTc	AGGGTGGTGT		
Consensus	*****	*****	*****	*****	*****	*****	
msa236796.2{282_COH1}	201	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC	250
msa236796.2{282_M732}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_M781}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_090}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_CJB110}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_18RS21}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_2603}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_A909}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_H36B}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_JM9130013}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_1169NT}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
Consensus	*****	*****	*****	*****	*****	*****	
msa236796.2{282_COH1}	251	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT	300
msa236796.2{282_M732}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_M781}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_090}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_CJB110}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_18RS21}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_2603}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_A909}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_H36B}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_JM9130013}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_1169NT}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
Consensus	*****	*****	*****	*****	*****	*****	
msa236796.2{282_COH1}	301	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA	350
msa236796.2{282_M732}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_M781}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_090}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_CJB110}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_18RS21}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_2603}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_A909}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_H36B}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_JM9130013}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_1169NT}	ATCTCCTGTG	ATTCAAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
Consensus	*****	*****	*****	*****	*****	*****	
msa236796.2{282_COH1}	351	AAATGGCAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTCT	TTAGTAGCAG	400
msa236796.2{282_M732}	AAATGGCAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTCT	TTAGTAGCAG		
msa236796.2{282_M781}	AAATGGCAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTCT	TTAGTAGCAG		
msa236796.2{282_090}	AAATGGCAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTCT	TTAGTAGCAG		
msa236796.2{282_CJB110}	AAATGGCAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTCT	TTAGTAGCAG		
msa236796.2{282_18RS21}	AAATGGCAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTCT	TTAGTAGCAG		

Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_2603}	AAATGGCAAA	CCTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_A909}	AAATGGCAAA	CCTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_H36B}	AAATGGCAAA	CCTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_JM9130013}	AAATGGCAAA	CCTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_1169NT}	AAATGGCAAA	CCTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
Consensus	*****	*****	*****	*****	*****
401					
msa236796.2{282_COH1}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_M732}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_M781}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_090}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_CJB110}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_18RS21}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_2603}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_A909}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_H36B}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_JM9130013}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_1169NT}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
Consensus	*****	*****	*****	*****	*****
450					
495					
msa236796.2{282_COH1}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_M732}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_M781}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_090}	GTAGAACATA	CGATTGGAA	TTGGGATA--	-----	-----
msa236796.2{282_CJB110}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_18RS21}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_2603}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_A909}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_H36B}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_JM9130013}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
msa236796.2{282_1169NT}	GTAGAACATA	CGATTGGAA	TTGGGATAtg	tttggagttg	aaaag
Consensus	*****	*****	*****	-----	-----

SEQ ID NO. 6412

STRAIN 2603 frame: 1
MNKSKKIENYQLLLLQAQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIIL
GPFQGGVSCVHIITLKGKVCGESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGK
LLGVLDLSSSLVADYDEIDQEYLEKFGVILVEHTIWNLDMPGVEK

SEQ ID NO. 6413

STRAIN 090 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIILGPFQGGVSCVHIITLKGKVC
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFGVILVEHTIWNLD

SEQ ID NO. 6414

STRAIN A909 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIILGPFQGGVSCVHIITLKGKVC
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFGVILVEHTIWNLDMPGVEK

SEQ ID NO. 6415

STRAIN H36B frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIILGPFQGGVSCVHIITLKGKVC
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFGVILVEHTIWNLDMPGVEK

SEQ ID NO. 6416

STRAIN 18RS21 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIILGPFQGGVSCVHIITLKGKVC
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFGVILVEHTIWNLDMPGVEK

SEQ ID NO. 6417

STRAIN M732 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIILGPFQGGVSCVHIITLKGKVC
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFGVILVEHTIWNLDMPGVEK

SEQ ID NO. 6418

STRAIN COH1 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIILGPFQGGVSCVHIITLKGKVC
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID
QEYLEKFGVILVEHTIWNLDMPGVEK

SEQ ID NO. 6419

STRAIN M781 frame: 3
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIILGPFQGGVSCVHIITLKGKVC
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID

Table 64: Comparative Sequences relating to SAG 0827

QEYLEKFGVILVEHTIWNLDMFGVEK

SEQ ID NO. 6420

STRAIN M781 frame: 3

LFSDETALANLSNASAMLNAMLNPNVFTGFYLFDFGEEILIGPPFQGGVSCVHITLGKGVCGESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEIDQEYLEKFGVILVEHTIWNLDMFGVEK

SEQ ID NO. 6421

STRAIN CJB110 frame: 3

LFSDETALANLSNASAMLNAMLNPNVFTGFYLFDFGKELIIGPPFQGGVSCVHITLGKGVCGESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEIDQEYLEKFGVILVEHTIWNLDMFGVEK

SEQ ID NO. 6422

STRAIN 1169NT frame: 3

LFSDETALANLSNASAMLNAMLNPNVFTGFYLFDFGEEILIGPPFQGGVSCVHITLGKGVCGESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEIDQEYLEKFGVILVEHTIWNLDMFGVEK

SEQ ID NO. 6423

STRAIN JM9130013 frame: 3

LFSDETALANLSNASAMLNAMLNPNVFTGFYLFDFGEEILIGPPFQGGVSCVHITLGKGVCGESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEIDQEYLEKFGVILVEHTIWNLDMFGVEK

PRETTY of: /biotmp/msa237960.2{*} February 11, 2003 02:46 ..

1 50
msa237960.2{282_1169NT} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_18RS21} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_2603} mnkskkieny qllllqaqaL FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_A909} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_COH1} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_H36B} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_JM9130013} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_M732} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_M781} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_090} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
msa237960.2{282_CJB110} -----L FSDETNALAN LSNASAMLNA MLPNSVFTGF
Consensus *****

51 100
msa237960.2{282_1169NT} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_18RS21} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_2603} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_A909} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_COH1} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_H36B} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_JM9130013} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_M732} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_M781} YLFDGeELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_090} YLFDGkELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
msa237960.2{282_CJB110} YLFDGkELIL GPFQGGVSCV HITLGKGVCG ESAQTAKTLI VDDVTKHANY
Consensus *****

101 150
msa237960.2{282_1169NT} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_18RS21} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_2603} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_A909} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_COH1} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_H36B} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_JM9130013} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_M732} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_M781} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_090} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
msa237960.2{282_CJB110} ISCDKAMSE IVVPMFKNGK LLGVLDLSS LVADYDEIDQ EYLEKFGVIL
Consensus *****

151 165
msa237960.2{282_1169NT} VEHTIWNLDm fgvek
msa237960.2{282_18RS21} VEHTIWNLDm fgvek
msa237960.2{282_2603} VEHTIWNLDm fgvek
msa237960.2{282_A909} VEHTIWNLDm fgvek
msa237960.2{282_COH1} VEHTIWNLDm fgvek
msa237960.2{282_H36B} VEHTIWNLDm fgvek
msa237960.2{282_JM9130013} VEHTIWNLDm fgvek
msa237960.2{282_M732} VEHTIWNLDm fgvek
msa237960.2{282_M781} VEHTIWNLDm fgvek
msa237960.2{282_090} VEHTIWNLDm -----
msa237960.2{282_CJB110} VEHTIWNLDm fgvek
Consensus *****

Table 65: Comparative Sequences relating to SAG0231

SEQ ID NO. 6501
STRAIN 2603
 ATGAAAAGAGTACCCAAATAACTACTAATAAGTTGCA
 TTATTACATCTGTTTTAGCGGAGGATTTATATGAAAGAACCAACAAAGAAAAGAGAA
 CTAAAACGGAATCGAGAAATGAAAGTTAGTCTAGTCAAAGCATTGAAAAATCCTATGAG
 AATATAGAAAGAAATAAAATCACACATCCTGTTTCAACTGAAATTCCTGGAGATTGGCAT
 TGTACTGTAAAGATTTCAATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAAT
 TTGGAAATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTGAT
 TCAAGAAATGGTAAAACAAAAAACTATAAAAAATATTTTTTTCAGATGGTCAGGAGAAG
 ATACAA

SEQ ID NO. 6502
STRAIN 090
 GGAGGATTTTATATGAAAGAACA
 ACAAAGAAAAGAAAGAACTAAAACGGAATCGAGAAATGAAAGTTAGTCTAG
 TCAAAGCATTGAAAAATCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTAAGTAAAGAT
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
 AATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTT
 TTTGATTTCAAGAAATGGTAAAACAAAAAACTATAAAAAATATTTTTTTC
 AGATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6503
STRAIN A909
 GGAGGATTTTATATGAAAGAACAACA
 AGAAAAGAAAGAACTAAAACGGAATCGAGAAATGAAAGTTAGTCTAGTCAA
 AGCATTGAAAAATCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTAAGTAAAGATTTCA
 TTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAAATC
 GAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTTG
 ATTTCAAGAAATGGTAAAACAAAAAACTATAAAAAATATTTTTTTCAGAT
 GGTCAGGAGAAGATaCAA

SEQ ID NO. 6504
STRAIN H36B
 GGAGGATTTTATATGAAAGAACAACA
 ACAAAGAAAAGAAAGAACTAAAACGGAATCGAGAAATGAAAGTTAGTCTAG
 TCAAAGCATTGAAAAATCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTAAGTAAAGAT
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
 AATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTT
 TTTGATTTCAAGAAATGGTAAAACAAAAAACTATAAAAAATATTTTTTTC
 AGATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6505
STRAIN 18RS21
 GGAGGATTTTATATGAAAGAACAACA
 AAAGAAAAGAAAGAACTAAAACGGAATCGAGAAATGAAAGTTAGTCTAGTCT
 AAAGCATTGAAAAATCCTATGAGAATATAGAAGAAATAAAATCACACATC
 TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTAAGTAAAGATTT
 CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
 TCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTT
 TGATTTCAAGAAATGGTAAAACAAAAAACTATAAAAAATATTTTTTTCAG
 ATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6506
STRAIN M781
 GGAGGATTTTATATGAAAGAACAACAAGAAAA
 GAAGAACTAAAACGGAATCGAGAAATGAAAGTTAGTCTAGTCAAAGCATT
 GAAAAATCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTT
 CAACTGAAATTCCTGGAGATTGGCATTGTAAGTAAAGATTTCAATTTAAT
 GATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAAATCGAAAA
 AAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTTGATTTCAA
 GAATGGTAAAACAAAAAACTATAAAAAATATTTTTTTCAGATGGTCAG
 GAGAAGATaCAA

SEQ ID NO. 6507
STRAIN CJB110
 GGAGGATTTTATATGAAAGAACAACAAGAAAAGAA
 CTAAAACGGAATCGAGAAATGAAAGTTAGTCTAGTCAAAGCATTGAAAA
 TTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTTCAACTG
 AAAATCCTGGAGATTGGCATTGTAAGTAAAGATTTCAATTTAATGATAAA
 AATCTATTGTTTATAATATTACACATAATTTGGAAATCGAAAAAAATTA
 TAGCGAAATTTAATGAAAAAAATATGAATTTTTTTGATTTCAAGAAATG
 GAAAAACAAAAAACTATAAAAAATATTTTTTTCAGATGGTCAGGAGAAG
 ATaCAA

SEQ ID NO. 6508
STRAIN 1169NT
 GGAGGATTTTATATGAAAGAACAACAAG
 AAAAGAAAGAACTAAAACGGAATCGAGAAATGAAAGTTAGTCTAGTCAAAG
 CATTGAAAAATCCTATGAGAATATAGAAGAAATAAAATCACACATCCT

Table 65: Comparative Sequences relating to SAG0231

GTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTTCATT
TAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGA
AAAAAAATTTAGTGGAAAATTTAATGAAAAAAATATGAATTTTTTTGAT
TCAAGAAATGGTAAAACAAAAAAACTATAAAAAATTTATTTTTTCAGATGG
TCAGGAGAAGATACAA

SEQ ID NO. 6509

STRAIN JM9130013

GGAGGATTTTATATGAAAGAACAAC
AAAGAAAAGAACTAAAACGGAAATCGAGAATATGAAGTTAGTCTAGTC
AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACA
TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT
CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
TCGAAAAAAATTTAGCGGAAAATTTAATGAAAAAAATATGAATTTTTTT
TGATTCAAGAAATGGTAAAACAAAAAAACTATAAAAAATTTATTTTTTCAG
AtGGtCAGGAGAAGATACAA

PRETTY of: /biotmp/msa75400.2{*} March 10, 2003 09:56 ..

1 50
msa75400.2{286_090}
msa75400.2{286_CJB110}
msa75400.2{286_18RS21}
msa75400.2{286_2603} atgaaaaaga gtacccaaat aataactacta atagtgtgcat tattcatact
msa75400.2{286_A909}
msa75400.2{286_H36B}
msa75400.2{286_JM9130013}
msa75400.2{286_M781}
msa75400.2{286_1169NT}
Consensus *****

51 100
msa75400.2{286_090} GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_CJB110} GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_18RS21} GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_2603} tgttttttagc GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_A909} GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_H36B} GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_JM9130013} GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_M781} GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
msa75400.2{286_1169NT} GGAGGATTTT ATATGAAAGA ACAACAAAGA AAAGAAGAAC
Consensus *****

101 150
msa75400.2{286_090} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
msa75400.2{286_CJB110} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
msa75400.2{286_18RS21} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
msa75400.2{286_2603} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
msa75400.2{286_A909} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
msa75400.2{286_H36B} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
msa75400.2{286_JM9130013} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
msa75400.2{286_M781} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
msa75400.2{286_1169NT} TAAAACGGAA TCGAGAATAT GAAGTTAGTC TAGTCAAAGC AITGAAAAAT
Consensus *****

151 200
msa75400.2{286_090} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_CJB110} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_18RS21} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_2603} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_A909} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_H36B} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_JM9130013} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_M781} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
msa75400.2{286_1169NT} TCCTATGAGA ATATAGAAGA AATAAAAATC ACACATCCTG TTTCAACTGA
Consensus *****

201 250
msa75400.2{286_090} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
msa75400.2{286_CJB110} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
msa75400.2{286_18RS21} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
msa75400.2{286_2603} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
msa75400.2{286_A909} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
msa75400.2{286_H36B} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
msa75400.2{286_JM9130013} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
msa75400.2{286_M781} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
msa75400.2{286_1169NT} AATTCCTGGA GATTGGCATT GTACTGTAAA GATTTCAATT AATGATAAAA
Consensus *****

251 300
msa75400.2{286_090} AATCTATTGT TTATAATATT ACACATAATT TGGAAATCGAA AAAAAATTAT
msa75400.2{286_CJB110} AATCTATTGT TTATAATATT ACACATAATT TGGAAATCGAA AAAAAATTAT
msa75400.2{286_18RS21} AATCTATTGT TTATAATATT ACACATAATT TGGAAATCGAA AAAAAATTAT

Table 65: Comparative Sequences relating to SAG0231

msa75400.2{286_2603}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_A909}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_H36B}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_JM9130013}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_M781}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_1169NT}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
Consensus	*****	*****	*****	*****	*****

msa75400.2{286_090}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_CJB110}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_18RS21}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_2603}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_A909}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_H36B}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_JM9130013}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_M781}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_1169NT}	AGcGGAAaT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
Consensus	**-----*	*****	*****	*****	*****

msa75400.2{286_090}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_CJB110}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_18RS21}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_2603}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_A909}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_H36B}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_JM9130013}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_M781}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_1169NT}	TAAAACAAAA	AAAACATAAA	AAATATTTT	TTCAGATGGT	CAGGAGAAGA
Consensus	*****	*****	*****	*****	*****

msa75400.2{286_090}	TACAA
msa75400.2{286_CJB110}	TACAA
msa75400.2{286_18RS21}	TACAA
msa75400.2{286_2603}	TACAA
msa75400.2{286_A909}	TACAA
msa75400.2{286_H36B}	TACAA
msa75400.2{286_JM9130013}	TACAA
msa75400.2{286_M781}	TACAA
msa75400.2{286_1169NT}	TACAA
Consensus	****

SEQ ID NO. 6510
 STRAIN 2603 frame: 1
 MKKSTQIILLIVALFIIIVFSGGYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
 THPVSTEIPGDWHCTVKISFNDDKKSIVYNI THNLESKKNYSKGFNEKNMNFDSRIGKTK
 KTIKIFSDGQEKIQ

SEQ ID NO. 6511
 STRAIN 090
 GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
 WHCTVKISFNDDKKSIVYNI THNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIFSDGQ
 EKIQ

SEQ ID NO. 6512
 STRAIN A909
 GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH
 CTVKISFNDDKKSIVYNI THNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIFSDGQEK
 IQ

SEQ ID NO. 6513
 STRAIN H36B
 GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
 WHCTVKISFNDDKKSIVYNI THNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIFSDGQ
 EKIQ

SEQ ID NO. 6514
 STRAIN 18RS21
 GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW
 HCTVKISFNDDKKSIVYNI THNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIFSDGQEK
 KIQ

SEQ ID NO. 6515
 STRAIN CJB110
 GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK
 ISFNDDKKSIVYNI THNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIFSDGQEKIQ

SEQ ID NO. 6516
 STRAIN JM9130013
 GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW

Table 65: Comparative Sequences relating to SAG0231

HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQE
KIQ

SEQ ID NO. 6517

STRAIN 1169NT frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQEKIQ

SEQ ID NO. 6518

STRAIN M781 frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQEKIQ

PRETTY of: /biotmp/msa75376.2{*} March 10, 2003 10:01 ..

	1			50
msa75376.2{286_090}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_1169NT}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_18RS21}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_2603}	mkkstqiill	ivalfilvfs	GGFYMKEQQR	KEELKRNREY
msa75376.2{286_A909}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_CJB110}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_H36B}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_JM9130013}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_M781}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
Consensus	*****	*****	*****	*****

	51			100
msa75376.2{286_090}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
msa75376.2{286_1169NT}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
msa75376.2{286_18RS21}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
msa75376.2{286_2603}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
msa75376.2{286_A909}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
msa75376.2{286_CJB110}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
msa75376.2{286_H36B}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
msa75376.2{286_JM9130013}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
msa75376.2{286_M781}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI
Consensus	*****	*****	*****	*****

	101			135
msa75376.2{286_090}	SGnFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
msa75376.2{286_1169NT}	SGkFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
msa75376.2{286_18RS21}	SGkFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
msa75376.2{286_2603}	SGkFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
msa75376.2{286_A909}	SGkFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
msa75376.2{286_CJB110}	SGnFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
msa75376.2{286_H36B}	SGkFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
msa75376.2{286_JM9130013}	SGkFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
msa75376.2{286_M781}	SGkFNEKNMN	FFDSRIGGTK	KTIKIIFSDG	QEKI Q
Consensus	**~*****	*****	*****	*****

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6601
 STRAIN 2603
 TTGACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATG
 GAAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAGCAGCGCTT
 ACAAAGGGGCATAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTAAG
 GATCCTAGATTAACTACATTAGGGGAGATATTAACAAGCTGATAAGATTCAATTTAGAA
 GACAGAACTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAATCAACTAGAT
 GAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGTCAAAAATCAAATACCA
 AAGTTAGTTTATATTTACGCCAACAGCGGCTATTAGCTTACATTAAAAGTAAAAGGAAG
 GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATG
 TATGGTGAAGAGCGACCTCTCTCGATTTCGAAGCCAAGTGTATAAAGTTATTTAGTCAT
 TTGCCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTAGTAGGGCA
 GAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAATCCTTTCTATTGAAGAA
 TTAATAATAATAA

SEQ ID NO. 6602
 STRAIN 090
 ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAAT
 GAAGGAGAGGGAACTATGGAATACTGATTGCAGGTGGTAGTGGTTTTTT
 AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
 ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
 ACCTACATTAGGGGAGATATTAACAAGCTGATAAGATTCAATTTAGAAGA
 CAGAACCTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAATC
 AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGT
 CACAAAATCAAATACCAAGTTAGTTTATATTTACGCCAACAGCGGCTA
 TTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
 GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG
 CGACCTCTCTCGATTTCGAAGCCAAGTGTATAAAGTTATTTAGTCATTT
 GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGA
 TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
 ATCCTTTCTATTGAAGAATTAATAATAATAA

SEQ ID NO. 6603
 STRAIN A909
 ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAATG
 AAGGAGAGGGAACTATGGAATACTGATTGCAGGTGGTAGTGGTTTTTTA
 GGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
 CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
 CCTACATTAGGGGAGATATTAACAAGCTGATAAGATTCAATTTAGAAGAC
 AGAACCTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAATCA
 ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGT
 CACAAAATCAAATACCAAGTTAGTTTATATTTACGCCAACAGCGGCTAT
 TCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
 CCGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAGC
 GACCTCTCTCGATTTCGAAGCCAAGTGTATAAAGTTATTTAGTCATTTG
 CCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGAT
 AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
 TCCTTTCTATTGAAGAATTAATAATAATAA

SEQ ID NO. 6604
 STRAIN H36B
 TATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAACTATGG
 AAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAA
 GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG
 TAAAGGTGATATATTTAAGGATCCTAGATTAACTTACATTAGGGGAGATA
 TTACAAGACTGATAAGATTCAATTTAGAAGCAGAACTTTGATATATTA
 ATTGACTGTATTGGAGCGATTAAAGCCAATCAACTAGATGAGCTTAACGT
 TAAAGCAACCCAAAAGCAGTAGCACTCTGTCAAAAATCAAATACCAA
 AGTTAGTTTATATTTACGCCAACAGCGGCTATTAGCTTACATTAAAAGT
 AAAAGGAAGGCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTT
 TGTAAAGACCAGGTTGATGTATGGTGAAGAGCGACCTCTCTCGATTTTCC
 AAGCCAAGTGTATAAAGTTATTTAGTCATTTGCCCTTTCTTAGGTATTGTT
 GTACAAAAGGTCTTTCCAACTAAGGTTGTAGTAGTGGCAGAAGCAATCGT
 TACTACGCTTAGGAAAAAACCAACCCAAAAAATCCTTTCTATTGAAGAAT
 TAAATAATAATAA

SEQ ID NO. 6605
 STRAIN 18RS21
 ACAAGGCATATAAAAATTTCTATACTAAATTTACAAAAT
 GAAGGAGAGGGAACTATGGAATACTGATTGCAGGTGGTAGTGGTTTTTT
 AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
 ACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTA
 ACCTACATTAGGGGAGATATTAACAAGCTGATAAGATTCAATTTAGAAGA
 CAGAACCTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAATC
 AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGT
 CACAAAATCAAATACCAAGTTAGTTTATATTTACGCCAACAGCGGCTA
 TTCAGCTTACATTAAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGCAA
 GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG
 CGACCTCTCTCGATTTCGAAGCCAAGTGTATAAAGTTATTTAGTCATTT
 GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGTGA
 TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
 ATCCTTTCTATTGAAGAATTAATAATAATAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6606

STRAIN M732

CAAAATGAAGGAGAGGGAACTATGgAAATACTGATTGCAGGTGGTAGTGG
TTTTCTAGGGAAGCAGATAATAAAAAGCAGCGCTTACAAAAGGGCATAAGG
TGGCTTACTTATCAAGGCATGAAGGTAAGGTGATATATTTAAGGATCcT
AGATTAACCTTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCAATTT
AgAcATAGAAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGC
CCAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCA
CTCTGTCAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAG
CGGCTATTAGCTTACATTAAGGTAAGGGAAGGCAGAGCAGATAATCA
AAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGTATGATGGT
GAAGAGCGACCTCTCTCGATTTTCCAAGCCAAAGTGTATAAAAATTTATTAG
TCATTTGCCCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGG
TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACT
CAAAAATCCTTTCTATTGAAGAATTAATAATAAA

SEQ ID NO. 6607

STRAIN COH1

ACAAGGCATATAAAAATTTCTATACTAAATTTAC
AAAAATGAAGGAGAGGGAACTATGGAATACTGATTGCAGGTGGTAGTGGT
TTTTCTAGGGAAGCAGATAATAAAAAGCAGCGCTTACAAAAGGGCATAAGGT
GGCTTACTTATCAAGGCATGAAGGTAAGGTGATATATTTAAGGATCCTA
GATTAACCTTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCAATTTA
GAACATAGAAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCC
CAATCAACTAGATGAGCTTAAACGTTAAAGCAACCCAAAAGCAGTAGCAC
TCTGTCAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAGC
GGCTATTAGCTTACATTAAGGTAAGGGAAGGCAGAGCAGATAATCAA
AGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGTATGATGGTG
AAGAGCGACCTCTCTCGATTTTCCAAGCCAAAGTGTATAAAAATTTATTAGT
CAATTTGCCCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGGT
TGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACTC
AAAAATCCTTTCTATTGAAGAATTAATAATAAA

SEQ ID NO. 6608

STRAIN M781

ACAAGGCATATAAAAATTTCTATACTAAATTTaCA
AAATGAAGGAGAGGGAACTATGGAATACTGATTGCAGGTGGTAGTGGTT
TTCTAGGGAAGCAGATAATAAAAAGCAGCGCTTACAAAAGGGCATAAGGTG
GCTTACTTATCAAGGCATGAAGGTAAGGTGATATATTTAAGGATCCTAG
ATTAACCTTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCAATTTAG
AACATAGAAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCC
AATCAACTAGATGAGCTTAAACGTTAAAGCAACCCAAAAGCAGTAGCACT
CTGTCAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAGCG
GCTATTAGCTTACATTAAGGTAAGGGAAGGCAGAGCAGATAATCAA
GCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGTATGATGGTGA
AGAGCGACCTCTCTCGATTTTCCAAGCCAAAGTGTATAAAAATTTATTAGT
ATTTGCCCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGGTT
GTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAAACCAACTCA
AAAAATCCTTTCTATTGAAGAATTAATAATAAA

SEQ ID NO. 6609

STRAIN 1169NT

ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAACTATGGAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC
TTACTTATCAAGCATGAAGGTAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAA
TCAACTAGATGAGCTTAAACGTTAAAGCAACCCAAAAGCAGTAGCACTCT
GTCACAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAACAGCGGC
TATTAGCTTACATTAAGGTAAGGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGTATGATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAAGTGTATAAAAATTTATTAGTCAT
TTGCCCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGGTTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACTCAA
AAATCCTTTCTATTGAAGAATTAATAATAAA

SEQ ID NO. 6610

STRAIN CJB110

ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA
ATGAAGGAGAGGGAACTATGGAATACTGATTGCAGGTGGTAGTGGTTTT
TTAGGAAAGCAGATAATAAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC
TTACTTATCAAGCATGAAGGTAAGGTGATATATTTAAGGATCCTAGAT
TAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAA
TCAACTAGATGAGCTTAAACGTTAAAGCAACCCAAAAGCAGTAGCACTCT
GTCACAAAATCAAATACCAAAGTTAGTTTATATTTAGCCCAACAGCGGC
TATTAGCTTACATTAAGGTAAGGGAAGGCAGAGCAGATAATCAAAGC
AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGTATGATGGTGAAG
AGCGACCTCTCTCGATTTTCCAAGCCAAAGTGTATAAAAATTTATTAGTCAT
TTGCCCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACCTAAGGTTGT
GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAA
AAATCCTTTCTATTGAAGAATTAATAATAAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6611

STRAIN JM9130013

ACAAGGCATATAAAAATTCTATACTAAATTTACAAAATG
AAGGAGGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA
GGAAAGCAGATAATAAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
CcTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAITTAGAAGAC
AGAACITTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA
ACTAGATGAGCTTAAAGCTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTC
ACAAAATCAAATACCAAAGTTAGTTTATATTTTCAGCCAACACGGCTAT
TCAGCTTACATTAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
CGGCTCGGATTTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAGC
GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAITTTG
CCTTTCTTAGGTATTTGTGTACAAAAGGCTTTCCAACCTAAGGTTGTGAT
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAA
TCCTTTCTATTGAAGAATTAATAATAAA

PRETTY of: /biotmp/msa137119.2{*} April 10, 2003 03:30 ..

msa137119.2{303_COH1} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_M732} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_m781} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_090} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_18RS21} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_2603} ttgacaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_A909} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_CJB110} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_H36B} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_JM9130013} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
msa137119.2{303_1169NT} ---acaagggc atataaaaaat ttctatacta aatttaCAAA ATGAAGGAGA
Consensus ***-----*****

msa137119.2{303_COH1} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
msa137119.2{303_M732} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
msa137119.2{303_m781} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT cTAGGgAAGC
msa137119.2{303_090} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaaAGC
msa137119.2{303_18RS21} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaaAGC
msa137119.2{303_2603} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaaAGC
msa137119.2{303_A909} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaaAGC
msa137119.2{303_CJB110} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaaAGC
msa137119.2{303_H36B} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaaAGC
msa137119.2{303_JM9130013} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaaAGC
msa137119.2{303_1169NT} GGGAACTATG GAAATACTGA TTGCAGGTGG TAGTGGTTTT tTAGGaaAGC
Consensus *****-*****

msa137119.2{303_COH1} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAggTGGC TTACTTATCA
msa137119.2{303_M732} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAggTGGC TTACTTATCA
msa137119.2{303_m781} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAggTGGC TTACTTATCA
msa137119.2{303_090} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAagTGGC TTACTTATCA
msa137119.2{303_18RS21} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAagTGGC TTACTTATCA
msa137119.2{303_2603} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAagTGGC TTACTTATCA
msa137119.2{303_A909} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAagTGGC TTACTTATCA
msa137119.2{303_CJB110} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAagTGGC TTACTTATCA
msa137119.2{303_H36B} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAagTGGC TTACTTATCA
msa137119.2{303_JM9130013} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAagTGGC TTACTTATCA
msa137119.2{303_1169NT} AGATAATAAA AGCAGCGCTT ACAAAGGGC ATAAagTGGC TTACTTATCA
Consensus *****-*****

msa137119.2{303_COH1} AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_M732} AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_m781} AGgCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_090} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_18RS21} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_2603} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_A909} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_CJB110} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_H36B} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_JM9130013} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
msa137119.2{303_1169NT} AGaCATGAAG GTAAAGGTGA TATATTTAAG GATCCTAGAT TAACCTACAT
Consensus *****-*****

msa137119.2{303_COH1} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
msa137119.2{303_M732} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
msa137119.2{303_m781} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA cAtAGAAaTT
msa137119.2{303_090} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
msa137119.2{303_18RS21} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT
msa137119.2{303_2603} TAaGGGAGAT ATTACAGAAG CTGATAAGAT TCATTTAGAA gAcAGAAcTT

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_A909}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_CJB110}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_H36B}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_JM9130013}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_1169NT}	TAAGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
Consensus	**_*****	*****	*****	*****	_*_*_*_*_*_**
	251				300
msa137119.2{303_COH1}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_M732}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_m781}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_090}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_18RS21}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_2603}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_A909}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_CJB110}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_H36B}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_JM9130013}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_1169NT}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
Consensus	*****	*****	*****	*****	*****
	301				350
msa137119.2{303_COH1}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_M732}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_m781}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_090}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_18RS21}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_2603}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_A909}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_CJB110}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_H36B}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_JM9130013}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_1169NT}	GAGCTTAACG	TTAAAGCAAC	CCAAAAGCA	GTAGCACTCT	GTCACAAAAA
Consensus	*****	*****	*****	*****	*****
	351				400
msa137119.2{303_COH1}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_M732}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_m781}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAtAGCGGC	TATTcAGCTT
msa137119.2{303_090}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTcAGCTT
msa137119.2{303_18RS21}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTcAGCTT
msa137119.2{303_2603}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTcAGCTT
msa137119.2{303_A909}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTcAGCTT
msa137119.2{303_CJB110}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTcAGCTT
msa137119.2{303_H36B}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTcAGCTT
msa137119.2{303_JM9130013}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTcAGCTT
msa137119.2{303_1169NT}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAcAGCGGC	TATTcAGCTT
Consensus	*****	*****	*_*****	***_*****	*****
	401				450
msa137119.2{303_COH1}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_M732}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_m781}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_090}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_18RS21}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_2603}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_A909}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_CJB110}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_H36B}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_JM9130013}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_1169NT}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
Consensus	*****_***	*****	*****	*****	*****
	451				500
msa137119.2{303_COH1}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_M732}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_m781}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_090}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_18RS21}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_2603}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_A909}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_CJB110}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_H36B}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_JM9130013}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_1169NT}	GATTATCITT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
Consensus	*****	*****	*****	*****	*****
	501				550
msa137119.2{303_COH1}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_M732}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_m781}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_090}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT
msa137119.2{303_18RS21}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TTGCCTTTCT

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_2603}	CTCGATTTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_A909}	CTCGATTTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_CJB110}	CTCGATTTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_H36B}	CTCGATTTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_JM9130013}	CTCGATTTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_1169NT}	CTCGATTTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
Consensus	*****	*****	*****_**	*****	*****
551					
msa137119.2{303_COH1}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_M732}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_m781}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_090}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_18RS21}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_2603}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_A909}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_CJB110}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_H36B}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_JM9130013}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_1169NT}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
Consensus	*****	*****_*	*****	*****	*****
601					
msa137119.2{303_COH1}	GAAGCAATCG	TACTTcCGCT	TAGGaaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_M732}	GAAGCAATCG	TACTTcCGCT	TAGGaaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_m781}	GAAGCAATCG	TACTTcCGCT	TAGGaaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_090}	GAAGCAATCG	TACTTaCGCT	TAGGaaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_18RS21}	GAAGCAATCG	TACTTaCGCT	TAGGaaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_2603}	GAAGCAATCG	TACTTaCGCT	TAGGaaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_A909}	GAAGCAATCG	TACTTaCGCT	TAGGaaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_CJB110}	GAAGCAATCG	TACTTaCGCT	TAGGaaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_H36B}	GAAGCAATCG	TACTTaCGCT	TAGGaaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_JM9130013}	GAAGCAATCG	TACTTaCGCT	TAGGaaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_1169NT}	GAAGCAATCG	TACTTaCGCT	TAGGaaAAAA	CCAActCAAA	AAATCCTTTC
Consensus	*****	*****_****	*****_****	*****_****	*****
651					
msa137119.2{303_COH1}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_M732}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_m781}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_090}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_18RS21}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_2603}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_A909}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_CJB110}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_H36B}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_JM9130013}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_1169NT}	TATTGAAGAA	TAAATAATA	AA		
Consensus	*****	*****	**		

SEQ ID NO. 6612

STRAIN 2603 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNIQPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPKVVIVABAI VITLTKKPTQKILSIEELNNK

SEQ ID NO. 6613

STRAIN 090 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNIQPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPKVVIVABAI VITLTKKPTQKILSIEELNNK

SEQ ID NO. 6614

STRAIN A909 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNIQPK
LVYISANSGYSAYIKSKRKAEQIIKASGLDYLFVVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPKVVIVABAI VITLTKKPTQKILSIEELNNK

SEQ ID NO. 6615

STRAIN H36B frame: 2

IKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRL
TYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNIQPKLVY
ISANSGYSAYIKSKRKAEQIIKASGLDYLFVVRPGLMYGEERPLSIFQAKCIKLFSHLPFL
GIVVQKVFPKVVIVABAI VITLTKKPTQKILSIEELNNK

SEQ ID NO. 6616

Table 66: Comparative Sequences relating to SAG 0754

STRAIN 18RS21 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVVAYLSRHEGKGDIFKD
PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSYSAYIKSKRKAQEQIKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPPTKVVI VAEAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6617

STRAIN M732 frame: 1

QNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVVAYLSRHEGKGDIFKDPRLTYIKGDIT
EADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPKLVYISANSYS
AYIKSKRKAQEQIKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHLPFLGIVVQKV
FTKVVIVAEAVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6618

STRAIN COH1 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVVAYLSRHEGKGDIFKD
PRLTYIKGDIT TEADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSYSAYIKSKRKAQEQIKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPPTKVVI VAEAVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6619

STRAIN M781 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVVAYLSRHEGKGDIFKD
PRLTYIKGDIT TEADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSYSAYIKSKRKAQEQIKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPPTKVVI VAEAVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6620

STRAIN 1169NT frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKLAYLSRHEGKGDIFKD
PRLTYIKGDIT TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSYSAYIKSKRKAQEQIKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPPTKVVI VAEAVTTLRKTPTQKILSIEELNNK

SEQ ID NO. 6621

STRAIN CJB110 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVVAYLSRHEGKGDIFKD
PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSYSAYIKSKRKAQEQIKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPPTKVVI VAEAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6622

STRAIN JM9130013 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVVAYLSRHEGKGDIFKD
PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
LVYISANSYSAYIKSKRKAQEQIKASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSHL
PFLGIVVQKVFPPTKVVI VAEAVTTLRKKPTQKILSIEELNNK

PRETTY of: /biotmp/msa137299.2{*} April 10, 2003 03:37 ..

Table with 6 columns: Accession, Consensus, and sequence alignment. It compares the reference sequence (msa137299.2) with several other sequences (COH1, M732, M781, 090, 18RS21, 2603, A909, CJB110, JM9130013, H36B, 1169NT) and a consensus sequence. The alignment shows high similarity across all sequences, with some gaps indicated by dashes.

Table 66: Comparative Sequences relating to SAG 0754

	101			150
msa137299.2{303_COH1}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_M732}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_M781}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_090}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_18RS21}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_2603}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_A909}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_CJB110}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_JM9130013}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_H36B}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
msa137299.2{303_1169NT}	LNVKATQKAV	ALCHKNQIPK	LVYISANSYG	SAYIkSKRKA EQI IKASGLD
Consensus	*****	*****	*****	****_*****
	151			200
msa137299.2{303_COH1}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_M732}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_M781}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_090}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_18RS21}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_2603}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_A909}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_CJB110}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_JM9130013}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_H36B}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_1169NT}	YLFVVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV FPTKVVIVAE
Consensus	*****	*****	*****	*****
	201			223
msa137299.2{303_COH1}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_M732}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_M781}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_090}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_18RS21}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_2603}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_A909}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_CJB110}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_JM9130013}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_H36B}	AIVTtLRkKP	TQKILSIEEL	NNK	
msa137299.2{303_1169NT}	AIVTtLRkKP	TQKILSIEEL	NNK	
Consensus	****-***	*****	***	

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6701

STRAIN 090

CAATAACAACATTTGAAAATAAAAAAGTTT...
TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGT...
AGTTAATGATGGCAAACCATTTGATGAAAA...
TGGAAAGAGGGTATTAAAGTGGTTGTGGTAGT...

SEQ ID NO. 6702

STRAIN A909

CAATAACAACATTTGAAAATAAAAAAGTTT...
TCTGGAGAAGCTGCTGCACGTTTGTAGCTAAGT...
AGTTAATGATGGCAAACCATTTGATGAAAA...
TGGAAAGAGGGTATTAAAGTGGTTGTGGTAGT...

SEQ ID NO. 6703

STRAIN H36B

GGACGAGTAATGAAAACAATAACAACATTTG...
AAAAAAGTTT...
TGTAGCTAAGTTAGGAGCAATAGTGACAGT...
TTGATGAAAATCCAACAGCAAGTCTTTGTGGA...

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6704

STRAIN 18RS21

GGACGAGTAATGAAAAACAATAACAACATTTG
AAAATAAAAAAGTTT TAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCT
GCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA
ACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTA
AAGTGGTTTGGTGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT
TACATGATTAATAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA
AGCATTAGAAAAACAATCCCTGTTTGAAGTGAAGTTAGCATACT
TAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACG
ACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGG
TTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTG
CGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATG
GGAGTTAAGGAATTTGCTCCTCATATTGCAGTAATTAATAATTTAATGCC
AACTCATTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAAAT
GGAATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAATTTT
AATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGT
TCCTTTCTCTACTACGGAAAAAGTTGATGGTGTCTACGTACAAGACAAGC
AACTTTTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTTGGTGT
CCAGGAAGCCATAACGCTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAA
ACTGGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTG
GAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGTTATAGT
TTCTATAACGACAGCAAGTCAACTAATAATATTGGCAACTCAAAAAGCAAT
ATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGCTTGATC
GCGGTAATGAGTTTGTAGTAATTGATACAGATATCACTGGACTTAAACAT
ATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGCTGCTGCACAAAA
AGCAGGAGTAACCTTAGCGATGCTTTAGATGTTAGAGATGCGGTACATA
AAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCTGCA
AATGCATCATGGGACATGTATAAGAATTTTCAAGTCCGTGGTGATGAATT
CATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6705

STRAIN M732

GGACGAGTAATGAAAAACAATAACAACATTTGAAA
ATAAAAAAGTTT TAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTGCA
CGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACC
ATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAG
TGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGTAC
ATGATTAATAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGC
ATTAGAAAAACAATCCCTGTTTGAAGTGAAGTTAGCATACTTAG
TTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGACA
ACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGTTT
GTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGCGG
aTGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGA
GTTAAGGAATTTGCTCCTCATATTGCAGTAATTACTAATTTAATGCCAAC
TCAETTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAAATGGA
ATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAAATTTAAT
CAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAaTCGTTCC
TTTCTCTACTACGGAAAAAGTTGATGGTGTCTACGTACAAGACAAGCAAC
TTTTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTTGGTGTCCA
GGAAGCCATAACGCTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACT
AGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTGGAG
GTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGTTATGATTTT
TATAACGACAGCAAGTCAACTAATATAATTGGCAACTCAAAAAGCAATATC
TGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGCTTTGATCGCG
GTAATGAGTTTGTAGTAATTGATACAGATATCACTGGACTTAAACATATG
GTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGCTGCTGCACAAAAAGC
AGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAAAG
CTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCTGCAAAAT
GCATCATGGGACATGTATAAGAATTTTCAAGTCCGTGGTGATGAATTCAT
TGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6706

STRAIN COH1

GGACGAGTAATGAAAAACAATAACAACATTTGA
AAAATAAAAAAGTTT TAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTG
CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAAC
CCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTA
AGTGGTTTGGTGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT
ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA
GCATTAGAAAAACAATCCCTGTTTGAAGTGAAGTTAGCATACTT
AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA
CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGG
TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGC
GGAATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGG
GAGTTAAGGAATTTGCTCCTCATATTGCAGTAATTAATAATTTAATGCCA
ACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAAATG
GAATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAATTTTA
ATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTT
CCTTTCTCTACTACGGAAAAAGTTGATGGTGTCTACGTAACAAGACAAGCA
ACTTTTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTTGGTGTCC
CAGGAAGCCATAACGCTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA

Table 67: Comparative Sequences relating to SAG0475

CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGG
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAAGTTTCATGGTATTAGTT
TCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTAA
TCTGGCTTTGATAATACTAAAGTTATCCTAATTCAGGAGGCTTTGATCG
CGGTAATGAGTTTGTGTAATTGATACCAGATATCACTGGACTTAAACATA
TGGTTCTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAA
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA
AGCTTATAGGTGGCACAAACAGGGCGATGTTATCTTGCTAAGTCTTGCAA
ATGCATCATGGACATGTATAAGAATTTTCAAGTCCGTGGTGTGAATTC
ATTGATACTTTGAAA

SEQ ID NO. 6707

STRAIN M781

GGACGAGTAATGAAAACAATAACAACATT
TGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGCATCTGGAGAAGCCG
CTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGC
AAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTAT
TAAAGTGGTTTGTGGTAGTCACTCTTTAGAAATGTTAGATGAGGATTTTT
GTTACATGATTAATAAATCCAGGAATACCTTATAACAATCCTATGGTCAAA
AAAGCATTAGAAAAACAATCCCTGTTTGGACTGAAGTGGAAATAGCATA
CTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGAAAA
CGACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGA
GGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCCAGC
TGCGGATGATAAAGATATCTAGTTATGGAATATCAAGTTTTCAGCTAA
TGGGAGTTAAGGAATTTCTGCTCATATTGCAGTAATTAATAATTTAATG
CCAATCATTAGATTATCATGGGTCTTTGAAGATTATGTTGCTGCAAA
ATGGAAATATCCAAAATCAAATGCTTTCATCTGATTTTGGTACTTAAT
TTAATCAAGTATTTCTAAAGAGTTAGCTAAAACACTAAAGCAaCAATC
GTTCTTTCTCTACTACGGAAAAGTTGATGGTGTACGTACAAGACAA
GCAACTTTTCTATAAAGGGAGAAATATATGTCACTAGATGACATTGCTG
TCCCAGGAAGCCATAACGTAGAGAATGCTTAGCAACTATGCGGTTGCT
AAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTAAAGCAATTT
TGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGGTATTA
GTTTCTATAACGACAGCAAGTCAACTAATAATATTGGCAACTCAAAAAGCA
TTATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGA
TCGCGGTAATGAGTTTGTAGTAATTGATACCAGATATCACTGGACTTAAAC
ATATGGTTGTTTAgGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAA
AAAGCAGGAGTACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACA
TAAAGCTTATGAGGTGGCACAAACAGGGCGATGTTATCTTGCTAAGTCTG
CAAAATGCATCATGGACATGTATAAGAATTTTCAAGTCCGTGGTGTGAAT
TTCATGATACTTTGAAAAGTCTTAGAGGAGAG

SEQ ID NO. 6708

STRAIN CJB110

GGACGAGTAATGAAAACAATAACAACATTTGA
AAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGCATCTGGAGAAGCCGCTG
CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAA
CCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA
AGTGGTTTGTGGTAGTCACTCTTTAGAAATGTTAGATGAGGATTTTTGTT
ACATGATTAATAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA
GCATTAGAAAACAATCCCTGTTTGGACTGAAGTGGAAATAGCATACTT
AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA
CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGT
TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCCAGGCTGC
GGATGATAAAGATATTTCTAGTTATGGAATTTCAAGTTTTCAGCTAATGG
GAGTTAAGGAATTTCTGCTCATATTGCAGTAATTAATAATTTAATGCCA
ACTCATTAGATTATCATGGGTCTTTGAGAATATGTTGCTGCAAAATG
GAATATCCAAAATCAAATGCTTTCATCTGATTTTTTGGTACTTAATTTIA
ATCAAGGTATTTCTAAAGAGTTAGCTAAAACACTAAAGCAACAAATCGTT
CCTTTCTCTACTACGGAAAAGTTGATGGTGTACGTACAAGACAAGCA
ACTTTTCTATAAAGGGGAGAAATATGTTAGTAGATGACATTGGTGTCC
CAGGAAGCCATAACGTAGAGAATGCTTAGCAACTATGCGGTTGCTAAA
CTAGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTTGG
AGGTGTTAAACACCGCTTGAATCACTCGGTAAGGTTTATGGTATTAGTT
TCTATAATGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTAA
TCTGGCTTTGATAATACTAAAGTTATCCTAATTCAGGAGGTCTTGATCG
CGGTAATGAGTTTGTGTAATTGATACCAGATATCACTGGACTTAAACATA
TGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAA
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA
AGCTTATAGGTGGCACAAACAGGGCGATGTTATCTTGCTAAGTCTTGCAA
ATGCATCATGGACATGTATAAGAATTTTCAAGTCCGTGGTGTGAATTC
ATTGATACTTTGAAAAGTCTTAGAGGAGAG

SEQ ID NO. 6709

STRAIN 1169NT

CAATAACAACATTTGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGCA
TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAAACATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAAAGGGTATTAAAGTGGTTTGTGGTAGTCACTCTTTAGAAATTTGTTA
GATGAGGATTTTTGTACATGATTAATAAATCCAGGAATACCTTATAACAA
TCCATATGGTCAAAAAGCATTAGAAAACAATCCCTGTTTGGACTGAAG
TGGAAATAGCATACTTAGTTTCAGAAATCTCAGCTAATAGGTAATTACAGGC
TCTAACGGGAAAACGACAACGACAACGATGATTGCAGAAGTCTTGAATGC

Table 67: Comparative Sequences relating to SAG0475

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa30176.2{*} April 29, 2002 02:09 ..

	1				50
msa30176.2{305_18RS21}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_2603}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_A909}	-----	-----CAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_H36B}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_JM9130013}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_COH1}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_M781}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305e_M732}	-----	-----CAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_090}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_CJB110}	-----	-----CAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
msa30176.2{305_1169NT}	-----	-----CAAT	AACAACATTT	GAAAATAAAA	AAGTTTTAGT
Consensus	-----	-----****	*****	*****	*****
	51				100
msa30176.2{305_18RS21}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_2603}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_A909}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_H36B}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_JM9130013}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_COH1}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_M781}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305e_M732}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_090}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_CJB110}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_1169NT}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
Consensus	*****	*****	*****	*****	*****
	101				150
msa30176.2{305_18RS21}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_2603}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_A909}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_H36B}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_JM9130013}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_COH1}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_M781}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305e_M732}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_090}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_CJB110}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_1169NT}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
Consensus	*****	*****	*****	*****	*****
	151				200
msa30176.2{305_18RS21}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_2603}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_A909}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_H36B}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_JM9130013}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_COH1}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_M781}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305e_M732}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_090}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_CJB110}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_1169NT}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa30176.2{305_18RS21}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_2603}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_A909}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_H36B}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_JM9130013}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_COH1}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_M781}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305e_M732}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_090}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_CJB110}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_1169NT}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
Consensus	*****	*****	*****	*****	*****
	251				300
msa30176.2{305_18RS21}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_2603}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_A909}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_H36B}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_JM9130013}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_COH1}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_M781}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305e_M732}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_090}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_CJB110}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCAITAGA	AAAACAAATC
msa30176.2{305_1169NT}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCAITAGA	AAAACAAATC
Consensus	*****	*****	*****	*****	*****
301					
msa30176.2{305_18RS21}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_2603}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_A909}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_H36B}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_JM9130013}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_COH1}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_M781}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305e_M732}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_090}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_CJB110}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_1169NT}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
Consensus	*****	*****	*****	*****	*****
351					
msa30176.2{305_18RS21}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_2603}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_A909}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_H36B}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_JM9130013}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_COH1}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_M781}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305e_M732}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_090}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_CJB110}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_1169NT}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
Consensus	*****	*****	*****	*****	*****
401					
msa30176.2{305_18RS21}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_2603}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_A909}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_H36B}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_JM9130013}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_COH1}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_M781}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305e_M732}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_090}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_CJB110}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_1169NT}	CAGAAGTCTT	gAATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
Consensus	*****	-*****	*****	*****	*****
450					
msa30176.2{305_18RS21}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_2603}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_A909}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_H36B}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_JM9130013}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_COH1}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_M781}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305e_M732}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_090}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_CJB110}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_1169NT}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
Consensus	*****	*****	*****	***-*****	*****-***
501					
msa30176.2{305_18RS21}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_2603}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_A909}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_H36B}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_JM9130013}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_COH1}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_M781}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305e_M732}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_090}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_CJB110}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_1169NT}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
Consensus	*****	*****	*****	*****	*****
550					
msa30176.2{305_18RS21}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_2603}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_A909}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_H36B}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_JM9130013}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_COH1}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_M781}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305e_M732}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_090}	CFCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
msa30176.2{305_CJB110}	CFCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
msa30176.2{305_1169NT}	CFCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_2603}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_A909}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_H36B}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_JM9130013}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_COH1}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_M781}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305e_M732}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_090}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_CJB110}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_1169NT}	GGGTCITTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
Consensus	*****	****-*****	*****	*****	*****
msa30176.2{305_18RS21}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_2603}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_A909}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_H36B}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_JM9130013}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_COH1}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_M781}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305e_M732}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_090}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_CJB110}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_1169NT}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_2603}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_A909}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_H36B}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_JM9130013}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_COH1}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_M781}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305e_M732}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_090}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_CJB110}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
msa30176.2{305_1169NT}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCITTTCTC	TACTACGGAA
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_2603}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_A909}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_H36B}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_JM9130013}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_COH1}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_M781}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305e_M732}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_090}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_CJB110}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_1169NT}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_2603}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_A909}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_H36B}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_JM9130013}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_COH1}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_M781}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305e_M732}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_090}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_CJB110}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_1169NT}	GAATATTATG	TcAGTAGATg	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
Consensus	*****	*-*****-*	*****	*****	*****
msa30176.2{305_18RS21}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_2603}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_A909}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_H36B}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_JM9130013}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_COH1}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_M781}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305e_M732}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_090}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_CJB110}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_1169NT}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
Consensus	*****	*****	*****	****_****	*****
	901				950
msa30176.2{305_18RS21}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_2603}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_A909}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_H36B}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_JM9130013}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_COH1}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_M781}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305e_M732}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_090}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_CJB110}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_1169NT}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
Consensus	*****	*****	*****	*****	*****
	951				1000
msa30176.2{305_18RS21}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_2603}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_A909}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_H36B}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_JM9130013}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_COH1}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_M781}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305e_M732}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_090}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_CJB110}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
msa30176.2{305_1169NT}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAC	GACAGcAAGt
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa30176.2{305_18RS21}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_2603}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_A909}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_H36B}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_JM9130013}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_COH1}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_M781}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305e_M732}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_090}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_CJB110}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
msa30176.2{305_1169NT}	caactaatat	attggcaact	caaaaagcat	tatctggcct	tgataaact
Consensus	-----	-----	-----	-----	-----
	1051				1100
msa30176.2{305_18RS21}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_2603}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_A909}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_H36B}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_JM9130013}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_COH1}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_M781}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305e_M732}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_090}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_CJB110}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
msa30176.2{305_1169NT}	aaagttatcc	taattgcagg	aggtcttgat	cgcggtaatg	agtttgatga
Consensus	-----	-----	-----	-----	-----
	1101				1150
msa30176.2{305_18RS21}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_2603}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_A909}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_H36B}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_JM9130013}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_COH1}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_M781}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305e_M732}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_090}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_CJB110}	attgatacca	gatatactg	gacttaaaca	tatggttggt	ttaggggaat
msa30176.2{305_1169NT}	attgatacca	gatatactg	gacttaagca	tatggttggt	ttaggggaat
Consensus	-----	-----	-----	-----	-----
	1151				1200
msa30176.2{305_18RS21}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_2603}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_A909}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_H36B}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_JM9130013}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_COH1}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_M781}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305e_M732}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_090}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_CJB110}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_1169NT}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
Consensus	-----	-----	-----	-----	-----
1201					
msa30176.2{305_18RS21}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_2603}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_A909}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_COH1}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_M781}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305e_M732}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_090}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_CJB110}	gatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_1169NT}	aatgctttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
Consensus	-----	-----	-----	-----	-----
1251					
msa30176.2{305_18RS21}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305_2603}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305_A909}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305_COH1}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305_M781}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305e_M732}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305_090}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305_CJB110}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
msa30176.2{305_1169NT}	acagggcgat	gttatcttgc	taagtctctgc	aaatgcatca	tgggacatgt
Consensus	-----	-----	-----	-----	-----
1301					
msa30176.2{305_18RS21}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_2603}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_A909}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_COH1}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_M781}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305e_M732}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_090}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_CJB110}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_1169NT}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
Consensus	-----	-----	-----	-----	-----
1351					
msa30176.2{305_18RS21}	cttagaggag	ag			
msa30176.2{305_2603}	cttagaggag	ag			
msa30176.2{305_A909}	cttagaggag	ag			
msa30176.2{305_H36B}	-----	---			
msa30176.2{305_JM9130013}	cttagaggag	ag			
msa30176.2{305_COH1}	-----	---			
msa30176.2{305_M781}	cttagaggag	ag			
msa30176.2{305e_M732}	cttagaggag	ag			
msa30176.2{305_090}	cttagaggag	ag			
msa30176.2{305_CJB110}	cttagaggag	ag			
msa30176.2{305_1169NT}	-----	---			
Consensus	-----	---			

SEQ ID NO. 6711

STRAIN 090 frame: 3

ITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI KVVCGS
HPLELLEDDEFYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITGSNGK
TTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVAADDKDI LVMELSSFQLMGVKFEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSDDFLVLFNFQGISKELAKTTKATI VPF
STTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATI IAVAKLAGISNQVIRET
LSNFGGVKHRQLSLGKVGHSIFYNDSKSTNII LQKALSGFDNTKVI LIIAGGLDRGNEFD
ELIPDITGLKHMVVLGESSASRVKRAAQKAGVVTYSDALDVRDAVHKAYEVAQQGDVILLSP
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6712

STRAIN A909 frame: 3

ITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI KVVCGS
HPLELLEDDEFYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITGSNGK
TTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVAANDKDTLVMELSSFQLMGVKFEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSDDFLVLFNFQGISKELAKTTKATI VPF
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVXNALATI IAVAKLAGISNQVIRET
LSNFGGVKHRQLSLGKVGHSIFYNDSKSTNII LQKALSGFDNTKVI LIIAGGLDRGNEFD

Table 67: Comparative Sequences relating to SAG0475

ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
ANASWDMYKNFEVVRGDEFIDTFESLRGE

SEQ ID NO. 6713

STRAIN H36B frame: 1

GRVMKTIITTFENKQVVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGIKVVC
GSHPLELLEDDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITG
SNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRQLGKLVHGISFYNDKSTNI

SEQ ID NO. 6714

STRAIN 18RS21 frame: 1

GRVMKTIITTFENKQVVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGIKVVC
GSHPLELLEDDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITG
SNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRQLGKLVHGISFYNDKSTNI

SEQ ID NO. 6715

STRAIN M732 frame: 1

GRVMKTIITTFENKQVVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGIKVVC
GSHPLELLEDDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITG
SNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRQLGKLVHGISFYNDKSTNI

SEQ ID NO. 6716

STRAIN COH1 frame: 1

GRVMKTIITTFENKQVVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGIKVVC
GSHPLELLEDDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITG
SNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRQLGKLVHGISFYNDKSTNI

SEQ ID NO. 6717

STRAIN M781 frame: 1

GRVMKTIITTFENKQVVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGIKVVC
GSHPLELLEDDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITG
SNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRQLGKLVHGISFYNDKSTNI

SEQ ID NO. 6718

STRAIN CJB110 frame: 1

GRVMKTIITTFENKQVVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGIKVVC
GSHPLELLEDDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITG
SNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEEYVAAKWNIQNMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRQLGKLVHGISFYNDKSTNI

SEQ ID NO. 6719

STRAIN 1169NT frame: 3

ITTFENKQVVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGIKVVC
GSHPLELLEDDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITG
SNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
QVIRETLSNFGGVKHLRQLGKLVHGISFYNDKSTNI

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6720

STRAIN JM9130013 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPFDENPTAQSLLLEEGI
KVVCGSHPLELLEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQIIGI
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGVSFEDYVAAKWNINQMSSSDFLVLFNFNQGISKELAKTTK
ATIIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGKVRHLQSLGKLVHGISFYNDKSKSTNIALATQKALSGFDNTKVLIIAGGLD
RSNEFDELI PDI TGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6721

STRAIN 2603 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAI VTVNDGKPFDENPTAQSLLLEEGI
KVVCGSHPLELLEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQIIGI
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFFQLMGVK
EFRPHIAVITNLMPTHLDYHGVSFEDYVAAKWNINQMSSSDFLVLFNFNQGISKELAKTTK
ATIIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGKVRHLQSLGKLVHGISFYNDKSKSTNIALATQKALSGFDNTKVLIIAGGLD
RGNEFDELI PDI TGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25243.2{*} April 29, 2002 02:20 ..

msa25243.2{305_18RS21} 1 50
msa25243.2{305_2603} grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_JM9130013} grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_COH1} grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_M732} grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_M781} grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_1169NT} -----ITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_A909} -----ITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_CJB110} -----ITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_090} -----ITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
msa25243.2{305_H36B} grvmktITTF ENKKVLVLGL ARSGEAAARL LAKLGAI VTV NDGKPFDENP
Consensus -----**** *****

msa25243.2{305_18RS21} 51 100
msa25243.2{305_2603} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_JM9130013} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_COH1} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_M732} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_M781} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_1169NT} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_A909} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_CJB110} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_090} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
msa25243.2{305_H36B} TAQSLLEEGI KVVCGSHPLE LLEDFCYMI KNPGI PYNPNP MVKKALEKQI
Consensus *****

msa25243.2{305_18RS21} 101 150
msa25243.2{305_2603} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_JM9130013} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_COH1} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M732} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M781} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_1169NT} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_A909} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_CJB110} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_090} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_H36B} PVLTEVELAY LVSESQIIGI TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
Consensus *****

msa25243.2{305_18RS21} 151 200
msa25243.2{305_2603} GFPASEVVQA AnDKD tLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_JM9130013} GFPASEVVQA AnDKD tLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_COH1} GFPASEVVQA AdDKD iLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M732} GFPASEVVQA AdDKD iLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M781} GFPASEVVQA AdDKD iLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_1169NT} GFPASEVVQA AdDKD iLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_A909} GFPASEVVQA AnDKD tLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_CJB110} GFPASEVVQA AdDKD iLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_090} GFPASEVVQA AdDKD iLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_H36B} GFPASEVVQA AnDKD tLVME LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
Consensus *****

Table 67: Comparative Sequences relating to SAG0475

		201			250	
msa25243.2{305_18RS21}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_2603}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_JM9130013}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_COH1}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_M732}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_M781}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_1169NT}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_A909}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_CJB110}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_090}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
msa25243.2{305_H36B}		GSFEdYVAAK	WNIQNMSSS	DFLVLNFNQG	ISKELAKTTK	ATIVPFSTTE
Consensus		****-****	*****	*****	*****	*****
		251			300	
msa25243.2{305_18RS21}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_2603}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_JM9130013}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_COH1}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_M732}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_M781}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_1169NT}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_A909}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_CJB110}		KVDGAYVQDK	QLFYKGENIM	lvDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_090}		KVDGAYVQDK	QLFYKGENIM	lvDDIGVPGS	HNveNALATI	AVAKLAGISN
msa25243.2{305_H36B}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNveNALATI	AVAKLAGISN
Consensus		*****	*****	-*****	****-*****	*****
		301			350	
msa25243.2{305_18RS21}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_2603}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_JM9130013}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_COH1}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_M732}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_M781}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_1169NT}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_A909}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_CJB110}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_090}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
msa25243.2{305_H36B}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt
Consensus		*****	*****	*****	***-----	-----
		351			400	
msa25243.2{305_18RS21}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_2603}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_JM9130013}		kvliaggld	rsnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_COH1}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_M732}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_M781}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_1169NT}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_A909}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_CJB110}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_090}		kvliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys
msa25243.2{305_H36B}		-----	-----	-----	-----	-----
Consensus		-----	-----	-----	-----	-----
		401			450	
msa25243.2{305_18RS21}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_2603}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_JM9130013}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_COH1}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_M732}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_M781}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_1169NT}		naldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_A909}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_CJB110}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_090}		daldvrdavh	kayevaqqgd	villspanas	wdmyknfevr	gdefidtfes
msa25243.2{305_H36B}		-----	-----	-----	-----	-----
Consensus		-----	-----	-----	-----	-----
		451				
msa25243.2{305_18RS21}		lrge				
msa25243.2{305_2603}		lrge				
msa25243.2{305_JM9130013}		lrge				
msa25243.2{305_COH1}		----				
msa25243.2{305_M732}		lrge				
msa25243.2{305_M781}		lrge				
msa25243.2{305_1169NT}		----				
msa25243.2{305_A909}		lrge				
msa25243.2{305_CJB110}		lrge				
msa25243.2{305_090}		lrge				
msa25243.2{305_H36B}		----				
Consensus		----				

Table 68: Comparative Sequences relating to SAG 0499

SEQ ID NO. 6801
 STRAIN 2603
 ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTTGATACACGAGAG
 CAAGCGAAACGTTGGTGTATGGCAGGAATGGTGTATTAACGTTATCAATGGAGAACGTTAT
 GATAAACCCAGGTGAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTA
 AATATGTTAGTAGAGGTGGATTGAATTTAGAAAAGCTTTACAAGTTTTGAAATTTCA
 GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTACTGATGTTATG
 CTACAATCAGGAGCGCGTTTTAGTTTACCGAGTAGATGTAGGAACAATCAATTAGTTTTGG
 AAGTTACGTCAGGATCATCGTGTCTGTTCTATGGAAACAATATAATTTAGGTATGCCCAA
 AAGAAGATTTCAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCT
 CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAGTAGTGGCA
 TTAATTAACCAATTTGAAGCAGGTCTGAGCAAATTTGGTAAAATGTTATGTTCAAA
 GACAAGTTGGTTTCATGAAAAGGTTTGCACAACAGTGACCAATTTACGAAAAGATTATGGA
 TATACGGTTAAACATCTTGATTTTTCGCCCATTCAGGTGGACATGGAAATATTGAGTTT
 TTAATGCATTTGCAAAGTGTCAAGATCCCAAATCTTGTGCTTGACCAATACAGAT
 GTTATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6802
 STRAIN 090
 GCTAAAGAGAGGGTAGATGTTCTTGCCT
 ATAAAAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTTGGTGTATG
 GCAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACCCAGG
 TGAAGAGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAA
 AATATGTTAGTAGAGGTGGATTGAAATTTAGAAAAGCTTTACAAGTTTTT
 GAAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
 TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTGTAGTTTACGCAG
 TAGATGTAGGAACAATCAATTAGTTTGAAGTTACGTCAGGATCATCGT
 GTTCTGTTCTATGGAAACAATATAATTTAGGTATGCCCAAAAAGAGATTT
 CAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAA
 GTAGTGGCATTAAATTAACCAATTTGAAGCAGGTCTGAGCAAATTTGG
 TAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
 CAGTGACCAATTTACGAAAAGATTATGGATATACGGTTAAACATCTTGAT
 TTTTCGCCCATTTCAAGGTGGACATGGAATATTGAGTTTTTAATGCATTT
 GCAAAGTGTCAAGATCCCAAATCTTGTGCTTGACCAATACAGATG
 TTATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6803
 STRAIN A909
 GCTAAAGAGAGGGTAGATGTTCTTGCCTA
 TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTTGGTGTATGG
 CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACCCAGGT
 GAAAAGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTTAGAAAAGCTTTACAAGTTTTT
 AAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTGTAGTTTACGCAGT
 AGATGTAGGAACAATCAATTAGTTTGAAGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTAGGTATGCCCAAAAAGAGATTT
 AAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCAATTTGAAGCAGGTCTGAGCAAATTTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAA
 AGTGACCAATTTACGAAAAGATTATGGATATACGGTTAAACATCTTGAT
 TTTTCGCCCATTTCAAGGTGGACATGGAATATTGAGTTTTTAATGCATTT
 CAAAAGTGTCAAGATCCCAAATCTTGTGCTTGACCAATACAGATGT
 TATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6804
 STRAIN H36B
 GCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGG
 GACTTTTTGATACACGAGAGCAAGCGAAACGTTGGTGTATGGCAGGAATG
 GTGATTAACTTATCAATGGAGAACGTTATGATAAACCCAGGTGAAAAGGT
 TGCAAGCATACTGAATTAATACTAAAAGGTGAAAACTAAAATATGTTA
 GTAGAGGTGGATTGAAATTTAGAAAAGCTTTACAAGTTTTTGAATTTCA
 GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTAC
 TGATGTTATGCTACAATCAGGAGCGCGTTTGTAGTTTACGCAGTAGATGTAG
 GAACAATCAATTAGTTTGAAGTTACGTCAGGATCATCGTGTCTGTTCT
 ATGCAACAATATAATTTAGGTATGCCCAAAAAGAGATTTCAAGGAGG
 ACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCTTAATTTGA
 TTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAGTAGTGGCA
 TTAATTAACCAATTTGAAGCAGGTCTGAGCAAATTTGTAATAAATGG
 TATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAACAGTGACCA
 ATTTACGAAAAGATTATGGATATACGGTTAAACATCTTGATTTTTCGCC
 ATTTCAAGGTGGACATGGAATAATTGAGTTTTTAATGCATTTGCAAAAAG
 TCAAGATCCCAAATCTTGTGCTTGACCAATACAGATGTTATAGAAA
 AAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6805
 STRAIN 18RS21
 GCTAAAGAGAGGGTAGATGTTCTTGCCTA
 TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTTGGTGTATGG
 CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACCCAGGT

Table 68: Comparative Sequences relating to SAG 0499

GAAAAGGTTGCAGACGATACTGAATTA AAACTAAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAGCTTTACAAGTTTMTG
AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGTG
TTCGTTCTATGGAACAATAAATTTAGGTTATGCCAAAAGAAGATTTC
AAGGAGGACTGCCTGAAATTTGCATCGATAGATGTCATTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAAATTTAGTGGATGGTGGACAAG
TAGTGGCATTAAATTA AACCAAAATTTGAAGCAGGTCGTGAGCAAATGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTT CATGAAAAGGTTTGGACAAC
AGTGACCAATTTCCAGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCATTCAAGGTGGACATGGAATAATGAGTTT TTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATA CAAGATGT
TATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6806

STRAIN M732

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAAACGTGGTGTATGG
CAGGACTGGTGATTAACGTTATCAATGGGAGAACGTTATGATAAACCCAGG
GAAAAGGTTGCAGACGATACTGAATTA AAACTAAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAGCTTTACAAGTTTMTG
AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGTG
TTCGTTCTATGGAACAATAAATTTAGGTTATGCCAAAAGAAGATTTC
AAGGAGGACTGCCTGAAATTTGCATCGATAGATGTCATTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAAATTTAGTGGATGGTGGACAAG
TAGTGGCATTAAATTA AACCAAAATTTGAAGCAGGTCGTGAGCAAATGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTT CATGAAAAGGTTTGGACAAC
AGTGACCAATTTCCAGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCATTCAAGGTGGACATGGAATAATGAGTTT TTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATA CAAGATGT
TATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6807

STRAIN COH1

GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAAACGTGGTGTATG
GCAGGACTGGTGATTAACGTTATCAATGGGAGAACGTTATGATAAACCCAGG
CGAAAAGGTTGCAGACGATACTGAATTA AAACTAAAAGGTGAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAGCTTTACAAGTTTMTG
GAAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGT
GTTTCGTTCTATGGAACAATAAATTTAGGTTATGCCAAAAGAAGATTTC
CAAGGAGGACTGCCTGAAATTTGCATCGATAGATGTCATTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAAATTTAGTGGATGGTGGACAA
GTAGTGGCATTAAATTA AACCAAAATTTGAAGCAGGTCGTGAGCAAATGG
TAAAATGGTATTGTCAAAGACAAGTTGGTT CATGAAAAGGTTTGGACAA
CAGTGACCAATTTCCAGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTCGCCATTCAAGGTGGACATGGAATAATGAGTTT TTAATGCATTTG
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATA CAAGATG
TTATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6808

STRAIN M781

GCTAAAGAGAGGGTAGATGTTCTTGCCT
ATAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAAACGTGGTGTATG
GCAGGACTGGTGATTAACGTTATCAATGGGAGAACGTTATGATAAACCCAGG
CGAAAAGGTTGCAGACGATACTGAATTA AAACTAAAAGGTGAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAGCTTTACAAGTTTMTG
GAAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGT
GTTTCGTTCTATGGAACAATAAATTTAGGTTATGCCAAAAGAAGATTTC
CAAGGAGGACTGCCTGAAATTTGCATCGATAGATGTCATTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAAATTTAGTGGATGGTGGACAA
GTAGTGGCATTAAATTA AACCAAAATTTGAAGCAGGTCGTGAGCAAATGG
TAAAATGGTATTGTCAAAGACAAGTTGGTT CATGAAAAGGTTTGGACAA
CAGTGACCAATTTCCAGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTCGCCATTCAAGGTGGACATGGAATAATGAGTTT TTAATGCATTTG
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATA CAAGATG
TTATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6809

STRAIN CJB110

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAAACGTGGTGTATGG
CAGGAAATGGTGATTAACGTTATCAATGGGAGAACGTTATGATAAACCCAGT
GAAAAGGTTGCAGACGATACTGAATTA AAACTAAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAGCTTTACAAGTTTMTG
AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT

Table 68: Comparative Sequences relating to SAG 0499

GGTTTTACTGATGTTATGCTACAATCAGGAGCGGTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATAAATTTAGGTATGCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCCTATTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGACAAG
TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAGGTTGGACATGGAAATATTGAGTTTTAATGCATTGG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6810

STRAIN 1169NT

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGACTGGTGATTACGTTATCAATGGAGAACGTTATGATAAACCCAGGC
GAAAAGGTTGCAGACGATACTGAATTAAACTAAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG
AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATAAATTTAGGTATGCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCCTATTATCTCTCT
TAATTTGATTTTGCAGCTCTAAAAGAAATTTTAGTGGATGGTGACAAG
TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAGGTTGGACATGGAAATATTGAGTTTTAATGCATTGG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6811

STRAIN JM9130013

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACCCAGGT
GAAAAGGTTGCAGACGATACTGAATTAAACTAAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG
AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCCCTCTACGGGT
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAGT
AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG
TTCGTTCTATGGAACAATAAATTTAGGTATGCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCCTATTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGACAAG
TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
TTTCGCCCATTCAGGTTGGACATGGAAATATTGAGTTTTAATGCATTGG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

PRETTY of: /biotmp/msa236683.2{*} May 14, 2003 02:57 ..

1 50
msa236683.2{310_090} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_18RS21} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_2603} atgGCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_A909} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_CJB110} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_H36B} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_JM9130013} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_COH1} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_M732} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_M781} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_1169NT} ---GCTAAAG AGAGGGTAGA TGTTCTTGCC TATAAACAGG GACTTTTTGA
Consensus *****

51 100
msa236683.2{310_090} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_18RS21} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_2603} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_A909} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_CJB110} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_H36B} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_JM9130013} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_COH1} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_M732} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_M781} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
msa236683.2{310_1169NT} TACACGAGAG CAAGCGAAAC GTGGTGTTAT GGCAGGAaTG GTGATTAACG
Consensus *****

Table 68: Comparative Sequences relating to SAG 0499

	101		150
msa236683.2{310_090}	TTATCAATGG AGAACGTTAT GATAAACCCAG GtGAAAAGGT TGCAGACGAT		
msa236683.2{310_18RS21}	TTATCAATGG AGAACGTTAT GATAAACCCAG GtGAAAAGGT TGCAGACGAT		
msa236683.2{310_2603}	TTATCAATGG AGAACGTTAT GATAAACCCAG GtGAAAAGGT TGCAGACGAT		
msa236683.2{310_A909}	TTATCAATGG AGAACGTTAT GATAAACCCAG GtGAAAAGGT TGCAGACGAT		
msa236683.2{310_CJB110}	TTATCAATGG AGAACGTTAT GATAAACCCAG GtGAAAAGGT TGCAGACGAT		
msa236683.2{310_H36B}	TTATCAATGG AGAACGTTAT GATAAACCCAG GtGAAAAGGT TGCAGACGAT		
msa236683.2{310_JM9130013}	TTATCAATGG AGAACGTTAT GATAAACCCAG GtGAAAAGGT TGCAGACGAT		
msa236683.2{310_COH1}	TTATCAATGG AGAACGTTAT GATAAACCCAG GcGAAAAGGT TGCAGACGAT		
msa236683.2{310_M732}	TTATCAATGG AGAACGTTAT GATAAACCCAG GcGAAAAGGT TGCAGACGAT		
msa236683.2{310_M781}	TTATCAATGG AGAACGTTAT GATAAACCCAG GcGAAAAGGT TGCAGACGAT		
msa236683.2{310_1169NT}	TTATCAATGG AGAACGTTAT GATAAACCCAG GcGAAAAGGT TGCAGACGAT		
Consensus	*****	*****	*-*****
	151		200
msa236683.2{310_090}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_18RS21}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_2603}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_A909}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_CJB110}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_H36B}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_JM9130013}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_COH1}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_M732}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_M781}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
msa236683.2{310_1169NT}	ACTGAATTAA AACTAAAAGG TGAAAAACTA AAATATGTTA GTAGAGGTGG		
Consensus	*****	*****	*****
	201		250
msa236683.2{310_090}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_18RS21}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_2603}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_A909}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_CJB110}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_H36B}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_JM9130013}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_COH1}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_M732}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_M781}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
msa236683.2{310_1169NT}	ATTGAAATTA GAAAAGCCTT TACAAGTTTT TGAAATTTCA GTTGCAGATA		
Consensus	*****	*****	*****
	251		300
msa236683.2{310_090}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_18RS21}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_2603}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_A909}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_CJB110}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_H36B}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_JM9130013}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_COH1}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_M732}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_M781}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
msa236683.2{310_1169NT}	AGCTAACTAT AGATATTGGC GCCTCTACGG GTGGTTTTAC TGATGTTATG		
Consensus	*****	*****	*****
	301		350
msa236683.2{310_090}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_18RS21}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_2603}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_A909}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_CJB110}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_H36B}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_JM9130013}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_COH1}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_M732}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_M781}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
msa236683.2{310_1169NT}	CTACAATCAG GAGCGCGTTT AGTTTACGCA GTAGATGTAG GAACAAATCA		
Consensus	*****	*****	*****
	351		400
msa236683.2{310_090}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_18RS21}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_2603}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_A909}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_CJB110}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_H36B}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_JM9130013}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_COH1}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_M732}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_M781}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
msa236683.2{310_1169NT}	ATTAGTTTGG AAGTTACGTC AGGATCATCG TGTTCTGTTCT ATGGAACAAAT		
Consensus	*****	*****	*****

Table 68: Comparative Sequences relating to SAG 0499

	401				450
msa236683.2{310_090}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_18RS21}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_2603}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_A909}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_CJB110}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_H36B}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_JM9130013}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_COH1}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_M732}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_M781}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_1169NT}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa236683.2{310_090}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_18RS21}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_2603}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_A909}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_CJB110}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_H36B}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_JM9130013}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_COH1}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_M732}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_M781}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
msa236683.2{310_1169NT}	TTTGCATCGA	TAGATGTCTC	ATTTATCTCT	CITTAATTGA	TTTTaCCAGC
Consensus	*****	*****	*****	*****	*****
	501				550
msa236683.2{310_090}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_18RS21}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_2603}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_A909}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_CJB110}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_H36B}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_JM9130013}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_COH1}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_M732}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_M781}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
msa236683.2{310_1169NT}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTA AAC
Consensus	*****	*****	*****	*****	*****
	551				600
msa236683.2{310_090}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_18RS21}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_2603}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_A909}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_CJB110}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_H36B}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_JM9130013}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_COH1}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_M732}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_M781}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
msa236683.2{310_1169NT}	CACAATTGA	AGCAGGTCGT	GAGCAAATG	GTAAAATGG	TATTGTCAAA
Consensus	*****	*****	*****	*****	*****
	601				650
msa236683.2{310_090}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_18RS21}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_2603}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_A909}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_CJB110}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_H36B}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_JM9130013}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_COH1}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_M732}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_M781}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
msa236683.2{310_1169NT}	GACAAGTTGG	TTCATGAAAA	GGTTTTGACA	ACAGTGACCA	ATTTACCGAA
Consensus	*****	*****	*****	*****	*****
	651				700
msa236683.2{310_090}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_18RS21}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_2603}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_A909}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_CJB110}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_H36B}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_JM9130013}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_COH1}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_M732}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_M781}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG
msa236683.2{310_1169NT}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCC	aTTCaAGGTG

Table 68: Comparative Sequences relating to SAG 0499

Consensus	*****	*****	*****	*****	*****
	701				750
msa236683.2{310_090}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_18RS21}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_2603}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_A909}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_CJB110}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_H36B}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_JM9130013}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_COH1}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_M732}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_M781}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
msa236683.2{310_1169NT}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAAGTG	TCAAGATCCA
Consensus	*****	*****	*****	*****	*****
	751				800
msa236683.2{310_090}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_18RS21}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_2603}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_A909}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_CJB110}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_H36B}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_JM9130013}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_COH1}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_M732}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_M781}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
msa236683.2{310_1169NT}	CAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA
Consensus	*****	*****	*****	*****	*****
	801				825
msa236683.2{310_090}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_18RS21}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_2603}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_A909}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_CJB110}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_H36B}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_JM9130013}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_COH1}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_M732}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_M781}	GGAATTTAAG	AAAAATGAAG	AAGAG		
msa236683.2{310_1169NT}	GGAATTTAAG	AAAAATGAAG	AAGAG		
Consensus	*****	*****	*****		

SEQ ID NO. 6812

STRAIN 2603 frame: 1

MAKERVDVLA... YVSRGGLKLEKALQVFEI... MHLQKCQDPQNLVLDQIQDVI...

SEQ ID NO. 6813

STRAIN 090 frame: 1

AKERVDVLA... YVSRGGLKLEKALQVFEI... MHLQKCQDPQNLVLDQIQDVI...

SEQ ID NO. 6814

STRAIN A909 frame: 1

AKERVDVLA... YVSRGGLKLEKALQVFEI... MHLQKCQDPQNLVLDQIQDVI...

SEQ ID NO. 6815

STRAIN 18RS21 frame: 1

AKERVDVLA... YVSRGGLKLEKALQVFEI... MHLQKCQDPQNLVLDQIQDVI...

SEQ ID NO. 6816

STRAIN M732 frame: 1

AKERVDVLA... YVSRGGLKLEKALQVFEI... LRDHHRVRSMEQYNFRYAQKEDF...

Table 68: Comparative Sequences relating to SAG 0499

IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNI EFL
MHLQKCQDPQNLVLDQIQDVI EKAHKEFKKNEEE

SEQ ID NO. 6817

STRAIN COH1 frame: 1

AKERVDVLA YKQGLFD TREQAKRGVMAGLVIN VINGERYDKPGEKVADD TELKLGK EKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVG TNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDV SFI SLNLLPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNI EFL
MHLQKCQDPQNLVLDQIQDVI EKAHKEFKKNEEE

SEQ ID NO. 6818

STRAIN M781 frame: 1

AKERVDVLA YKQGLFD TREQAKRGVMAGLVIN VINGERYDKPGEKVADD TELKLGK EKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVG TNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDV SFI SLNLLPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNI EFL
MHLQKCQDPQNLVLDQIQDVI EKAHKEFKKNEEE

SEQ ID NO. 6819

STRAIN CJB110 frame: 1

AKERVDVLA YKQGLFD TREQAKRGVMAGLVIN VINGERYDKPGEKVADD TELKLGK EKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVG TNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDV SFI SLNLLPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNI EFL
MHLQKCQDPQNLVLDQIQDVI EKAHKEFKKNEEE

SEQ ID NO. 6820

STRAIN 1169NT frame: 1

AKERVDVLA YKQGLFD TREQAKRGVMAGLVIN VINGERYDKPGEKVADD TELKLGK EKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVG TNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDV SFI SLNLLPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNI EFL
MHLQKCQDPQNLVLDQIQDVI EKAHKEFKKNEEE

SEQ ID NO. 6821

STRAIN JM9130013 frame: 1

AKERVDVLA YKQGLFD TREQAKRGVMAGLVIN VINGERYDKPGEKVADD TELKLGK EKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVG TNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDV SFI SLNLLPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNI EFL
MHLQKCQDPQNLVLDQIQDVI EKAHKEFKKNEEE

SEQ ID NO. 6822

STRAIN H36B frame: 1

AKERVDVLA YKQGLFD TREQAKRGVMAGLVIN VINGERYDKPGEKVADD TELKLGK EKLK
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVG TNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDV SFI SLNLLPALKEILVDGGQVVAL
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNI EFL
MHLQKCQDPQNLVLDQIQDVI EKAHKEFKKNEEE

PRETTY of: /biotmp/msa236800.2{*} May 14, 2003 02:58 ..

1 50
msa236800.2{310_090} -AKERVDVLA YKQGLFD TRE QAKRGVMAGm VIN VINGERY DKPGEKVADD
msa236800.2{310_18RS21} -AKERVDVLA YKQGLFD TRE QAKRGVMAGm VIN VINGERY DKPGEKVADD
msa236800.2{310_2603} mAKERVDVLA YKQGLFD TRE QAKRGVMAGm VIN VINGERY DKPGEKVADD
msa236800.2{310_A909} -AKERVDVLA YKQGLFD TRE QAKRGVMAGm VIN VINGERY DKPGEKVADD
msa236800.2{310_CJB110} -AKERVDVLA YKQGLFD TRE QAKRGVMAGm VIN VINGERY DKPGEKVADD
msa236800.2{310_H36B} -AKERVDVLA YKQGLFD TRE QAKRGVMAGm VIN VINGERY DKPGEKVADD
msa236800.2{310_JM9130013} -AKERVDVLA YKQGLFD TRE QAKRGVMAGm VIN VINGERY DKPGEKVADD
msa236800.2{310_COH1} -AKERVDVLA YKQGLFD TRE QAKRGVMAG1 VIN VINGERY DKPGEKVADD
msa236800.2{310_M732} -AKERVDVLA YKQGLFD TRE QAKRGVMAG1 VIN VINGERY DKPGEKVADD
msa236800.2{310_M781} -AKERVDVLA YKQGLFD TRE QAKRGVMAG1 VIN VINGERY DKPGEKVADD
msa236800.2{310_1169NT} -AKERVDVLA YKQGLFD TRE QAKRGVMAG1 VIN VINGERY DKPGEKVADD
Consensus *****

51 100
msa236800.2{310_090} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_18RS21} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_2603} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_A909} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_CJB110} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_H36B} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_JM9130013} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_COH1} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M732} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M781} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_1169NT} TELKLGK EKLK KYVSRGGLKL EKALQVFEIS VADKLTIDIG ASTGGFTDVM
Consensus *****

101

150

Table 68: Comparative Sequences relating to SAG 0499

msa236800.2{310_090}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_18RS21}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_2603}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_A909}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_CJB110}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_H36B}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_JM9130013}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_COH1}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_M732}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_M781}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_1169NT}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
Consensus	*****	*****	*****	*****	*****
msa236800.2{310_090}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_18RS21}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_2603}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_A909}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_CJB110}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_H36B}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_JM9130013}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_COH1}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M732}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M781}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_1169NT}	FASIDVSPIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
Consensus	*****	*****	*****	*****	*****
msa236800.2{310_090}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_18RS21}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_2603}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_A909}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_CJB110}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_H36B}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_JM9130013}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_COH1}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_M732}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_M781}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNI EF	LMHLQKCQDP
msa236800.2{310_1169NT}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNI EF	LMHLQKCQDP
Consensus	*****	*****	*****	*****	*****
msa236800.2{310_090}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_18RS21}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_2603}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_A909}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_CJB110}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_H36B}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_JM9130013}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_COH1}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M732}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M781}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_1169NT}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
Consensus	*****	*****	****		

Table 69: Comparative Sequences relating to SAG0032

SEQ ID NO. 6901
 STRAIN 2603
 ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGT
 GTTCAAGCACAAAGAAACAGATACGACGTGGACAGCACGTA CTGTTTCAGAGGTAAGGCT
 GATTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACTAAGC
 GTTATTTTCAGAAGCAATGTCAATTGATATGAATGCTTAGCAAAAATAAATAACATTGCA
 GATATCAATCTTATTATCCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCAT
 ACTGCCACTTCAATGAAAATAGAAACCCAGCAACAAATGCTGCTGGTCAAAACACAGCT
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTCTCTCAATACA
 ATTTCCGGAAGGTATGACACCAGAAGCAGCAACACGATTGTTCCGCCAATGAAGACATAT
 TCTTCTGCGCCAGCTTTGAAATCAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAA
 GCAGCAGCTAATGAACAGGTATCACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCA
 GCAGCTAAGAGGAAGTTAAACCAACTCAGACGCTCAGTCAGTCAGTCAACACACAGTATCA
 CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCCGGTAAGA
 GTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCTAAAGTAGAACTGGTGCA
 TCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTCACCAGCTACAGAC
 AGTAAAGTTACAAGCGACTGAAAGTTAAGAGCGTTCGGGTAGCACAAAAGCTCCAACAGCA
 ACACCGGTAGCAACACCGCTTCAACAACAATAATGCAGTAGCTGCACATCTGAAAATGCA
 GGGCTCCAACCTCATGTGTCAGCTTATAAAGAAAAGTAGCGTCAACTTTAGGAGTTAAT
 GAATTCAGTACATACCGTGGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGAC
 TTTATTTAGGTTACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTCTACACAAAAT
 ATGGCAGCAAATAACACTTTCATATGTTATCTGGCAACAAGTTTACTCAAATACAAAC
 AGTATTTATGGACTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 AACCACTATGACCAGTTCACGTATCATTTAAACAATAATATAAAAAAGGAAGCTATTTG
 GCTTCTTTTATATGCTTGAATAGACTTCAAGGTTCTTATATAATTTTATTA

SEQ ID NO. 6902
 STRAIN 090
 TGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTT
 CAATGAAAATAGAAAACACCAGCAACAATGCTGCTGGTCAAACACCAGCT
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTC
 TCTCAATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTG
 TTTCCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAAATCAAAGA
 GTATTAGCAACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAAACAGGT
 ATCAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAG
 AGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
 CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC
 GGTAAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTC
 CTAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTT
 CCTGTGACTACGACTTCAACAGCTACAGCAGTAAGTTACAAGCGACTGA
 AGTTAAGAGCGTTCGGGTAGCACAAAAGCTCCAACAGCAACCCGGTAG
 CACAACAGCTTCAACAACAATGCAAGTGTGCACATCTGAAAATGCA
 GGGCTCCAACCTCATGTGTCAGCTTATAAAGAAAAGTAGCGTCAACTTA
 TGGAGTTAATGAATTCAGTACATACCGTGCAGGTGATCCAGGTGATCATG
 GTAAGGTTTAGCAGTCGACTTATTGTAGGTAAAAACCAAGCACTTGGT
 AATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTT
 ATATGTTATCTGGCAACAAGTTTACTCAAATACAAATAGTATTATG
 GACCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 AACCACTATGACCAGTTCACGTATCATTTAAACAATAATATAAAAAAGG
 AAGCTATTTGGCTTCTTTTATATGCTTGAATAGACTTCAAGGTTCT
 TATATAATTTTATTA

SEQ ID NO. 6903
 STRAIN A909
 CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAA
 ATATGGTGATACACTAAGCGTTATTTCAGAAGCAATGTCAATTGATATGA
 ATGCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCT
 GAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCTACTTC
 AATGAAAATAGAAAACACCAGCAACAATGCTGCTGGTCAAACAACAGCTA
 CTGTGATTTGAAAACCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTCT
 CTCATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTTGT
 TTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAAATCAAAGAAG
 TATTAGCACAAAGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAAACAGGTA
 TCAACAGCTCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGA
 GGAAGTTAAACCAaCTCagACGTCAgTCAGTCAGTCAACAACAGTATCAC
 CagCTTCTGTTGCCGCTGAAACACCAGCTCCAagTAGCTAAaGTAGCACC
 GTAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCC
 TAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTC
 CTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAA
 GTTAAGAGCGTTCGGGTAGCACAAAAGCTCCAACAGCAACCCGGTAGC
 ACAACAGCTTCAACAACAATAATGCAGTAGCTGCACATCTGAAAATGCAA
 GGCTCCAACCTCATGTGTCAGCTTATAAAGAAAAGTAGCGTCAACTTAT
 GGAGTTAATGAATTCAGTACATACCGTGGGGAGATCCAGGTGATCATGG
 TAAAGGTTTAGCAGTTGACTTTATTGTAGGTA AAAACCAAGCACTTGGTA
 ATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAATAACATTTCA
 TATGTTATCTGGCAACAAGTTTACTCAAATACAAATAGTATTATG
 ACCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 ACCaCTATGACCAGTTCACGTATCATTTAAACAATAATATAAAAAAGGA
 AGCTaTTGGCTTCTTTTATATGCTTGAATAGACTTCAAGGTTCTT
 ATATAATTTTATTA

SEQ ID NO. 6904
 STRAIN H36B

Table 69: Comparative Sequences relating to SAG0032

CTGATTGGTAAAGCAAGACAATAAATCATCATATAcTGTGAAATA
 TGGTGATACAcTAAGCGTTATTTTCAGAAAGCAATGTCaATTGATATGAATG
 TCTTAGCAAAAATTAAATACATTGCAGATATCAATCTTATTTATCCTGAG
 ACAACaCTGaCAGTAaCTTACGATCAGAAGAGTCATACTGCTACTTCAAT
 GAAAAATAGAAACACCAGCAACAATGCTGCTGGTCAAACAACAGCTACTG
 TCGATTGGAAAACCAATCAAGTTTCGTTGTCAGACCAAAAAGTTCTCTC
 AATACAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTC
 GCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAAGAGTAT
 TAGCACAAGGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCA
 CCAGCTCCTGTGAAGTTCGATTACTTCAAGAGTTCAGCAGCTAAAGAGGA
 AGTTAAACCAACTCAGACCTCAGTCAGTCAGTCAACAACAGTATCACCAG
 CTTCTGTTGCGCTGAAAACACCAGCTCCAGTAGcTAAAGTAGCACCGGTA
 AGAACTGTAGCAGCCCcTAGAGTGGCAAGTGTAAAGTAGTCACTCcTAA
 AGTAGAAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTG
 TGACTACGACTTCAACAGCTACAGACAGTAAGTTACAGCGACTGAAGTT
 AAGAGCGTTCGGGTAGCAAAAAGCTCCAACAGCAACCCGGTAGCACA
 ACCAGCTTCAACAACAATGTCAGTAGCTGCACATCCTGAAAAATGCAAGGC
 TCCAACCTCATGTTGCAGCTTATAAAGAAAAGTAGCGTCAACTTATGGA
 GTTAAATGAATTCAGTACATAACCGTGGGGAGATCCAGGTGATCATGGTAA
 AGGTTTAGCAGTTGACTTTATTGTAGGTAAAACCAAGCACTTGGTAAATG
 AAGTTGCACAGTACTCTACACAAAATcATGGCAGCAAAATAACATTTTATAT
 GTTATCTGGCaACAAGTTTACTCAAATACAAATAGTATTTATGGACC
 TGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAAC
 ACTATGACCAGTTCAGTATCATTTAACAAATAATATAAAAAGGAAGC
 TATTTGGCTTCTTTTATATGCCTTGCAATAGAcTTCAAGGTTCTTATA
 TAATTTTATTA

SEQ ID NO. 6905
 STRAIN 18RS21

CTGATTGGTAAAGCAAGACAAT
 AAATCATCATATACCTGTGAAATATGGTGATACAcTAAGcGTTATTTTCAGA
 AGCAATGTCAATTGATATGAATGCTTTCAGCAAAAaTAAATAACATTGCAG
 ATATCAATCTTATTTATCCTGAGACAAcCTGaCAGTAACCTTACGATCAG
 AAGAGTCATACTGCCCaCTTCAATGAAAATAGAAAACCAGCAaCAAAATGC
 TGCTGGTCAaACAaCAGCTACTGTGGATTTGAAAACCAATCaAGTTTCTG
 TTGCAGACCAAAAAGTTTCTCTCAATACAATTTCCGGAAGGTATGACACCA
 GAAGCAGCAACAACGATTGTTTCGCCAATGAAGACaTATTCTTCTGCGCC
 AGCTTTGAAaTCAAAAGAAGTATTAGCACAAAGAGCAAGCTGTTAGTCAAG
 CAGCAGCTAATGAAcAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCA
 GAAGTTCCAGCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAG
 TCAGTCAACAACAGTATCACCAGCTTCTGTTGCGCTGAAAACACCAGCTC
 CAGTAGCTAAAGTAGCACCGGTAAAGAACTGTAGCAGCCCTAGAGTGGCA
 AGTGTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGATCACCAGAGCA
 TGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTACCAGCTACAGACA
 GTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCGGTAGCACAAAAGCT
 CCAACAGCAACACCAGGTAGCACAAACCAGCTTCAACAACAATGCAAGTAGC
 TGCACATCCTGAAAATGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAG
 AAAAAAGTAGCGTCAACTTATGGAGTTAATGAATTCAAGTACATACCGTGGC
 GGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGG
 TACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTcTACACAAAATA
 TGGCAGCAAAATAACATTTTATATGTTATCTGGCAACAAGTTTACTTCA
 AATAACAACAGTATTTATGGACCTGCTAATACTTGGAAATGCAATGCCAGA
 TCGTGGTGGCGTTACTGCCAACCACTATGACCAGCTTACGATCATTTA
 ACAAAATAATATAAAAAGGAAGCTATTGGCTTCTTTTATATGCCTTG
 AATAGACTTTCAGGTTCTTATATAATTTTATTA

SEQ ID NO. 6906
 STRAIN COH1

CTGATT
 GGTAAGCAAGACAATAAATCATCATATACCTGTGAAATATGGTGATACAC
 TAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAA
 ATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACTGAC
 AGTAACCTACGATCAGAAGAGTCATACTGCCACTTCAATGAAAATAGAAA
 CACCAGCAACAATGCTGCTGGTCAAACAACAGcTACTGTGATTTGAAA
 ACCAATCAAGTTTGTGTCAGACCAAAAAGTTTCTCTCAATACAATTT
 GGAAGGTATGACACCAGaaGCAGCAACAACGATTGTTTCGCCAATGAAGA
 CaTATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAAGAG
 CAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAGCTCCTGT
 GAAGTCGATTACTTCAAGAGTTCAGCAGCTAAAGAGGAAGTTAAACCAA
 CTCAGACGTCAGTCAGTCAAGTAAACAACAGTATCACCAGCTTCTGTTGCC
 GCTGAAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAAGAACTGTAGC
 AGCCCCTAGAGTGGCAAGTGCcTAAAGTAGTCACTCcTAAAGTAGAAAATG
 GTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACT
 TCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTC
 GGTAGCACAAAAGCTCCAACAGCAACACCAGGTAGCACAAACCAGCTTCAA
 CAACAATGCAAGTAGCTGCACATCCTGAAAATGCAGGGCTCCAACCTCAT
 GTTGCAGCTTATAAAGAAAAGTAGCGTCAACTTATGGAGTTAATGAATT
 CAGTACATACCGTGGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAG
 TTGACTTTATTGTAGGTAAAACCAAGCACTTGGTAATGAAGTTGCACAG
 TaCTTACACAAAATATGGCAGCAAAATAACATTTTATATGTTATCTGGCA
 ACAAAAGTTTATTCAAATACAATAGTATTTATGGACCTGCTAATACTT
 GGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATGACCAC
 GTTCCAGTATCATTTAACAAATAATATAAAAAGGAAGCTATTGGCTTCT

Table 69: Comparative Sequences relating to SAG0032

TTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATT
A

SEQ ID NO. 6907

STRAIN M732

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
GATACAnTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTT
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTATCTCTGAGACAA
CACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA
ATAGAAAACACAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA
TTTGA AAAACCAATCAAGTTTTTGTTCAGACCAAAAAGTTTCTCTCAATA
CAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
ATGAAGACATATTTCTCTGCGCCAGCTTTGAAATCAAAGAAGTATTAGC
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG
CTCCTGTGAAGTcGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT
AAACCACTCAGACGTCAGTCAGTCAGTTAACACAGTATCACCAGCTTC
TGTTGCCGCTGAAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA
CTGTAGCAGCCCCTAGAGTGGCAAGTGTCAAAGTAGTCACTCCTAAAGTA
GAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTCTGTGAC
TACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGA
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACA
GCTTCAAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
ACCTCATGTTGCAGCTTATAAAGAAAAGTAGCGTCAACTTATGGAGTTA
ATGAATTcAGTACATACCGTGGGGAGATCCAGGTGATCATGGTAAAGGT
TTAGCAGTTGACTTTAttgt aggt aaaaaccAAGCACTTGGTAAATGAAGT
TGCACAGTACTcTACACAAAATATGGCAGCAAATAACATTTcATATGTTA
TCTGGCAACAAAAGTTTTATTCAAATACAATAAGTATTATGGACCTGCT
AATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA
TGACCAGGTTcAGTATCATTTAACAAAATAATATAAAAAGGAAGCTATT
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT
TTTTATTA

SEQ ID NO. 6908

STRAIN M781

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
GATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTT
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTATCTCTGAGACAA
CACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA
ATAGAAAACACAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA
TTTGA AAAACCAATCAAGTTTTTGTTCAGACCAAAAAGTTTCTCTCAATA
CAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
ATGAAGACATATTTCTCTGCGCCAGCTTTGAAATCAAAGAAGTATTAGC
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG
CTCCTGTGAAGTcGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT
AAACCACTCAGACGTCAGTCAGTCAGTTAACACAGTATCACCAGCTTC
TGTTGCCGCTGAAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA
CTGTAGCAGCCCCTAGAGTGGCAAGTGTCAAAGTAGTCACTCCTAAAGTA
GAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTCTGTGAC
TACGACTTCACCAGCTACAGACAGTaaGTTACAAGCGACTGAAGTTAAGA
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACA
GCTTCAAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
ACCTCATGTTGCAGCTTATAAAGAAAAGTAGCGTCAACTTATGGAGTTA
ATGAATTcAGTACATACCGTGGGGAGATCCAGGTGATCATGGTAAAGGT
TTAGCAGTTGACTTTATTGTAGGTA AAAAACAAGCACTTGGTAAATGAAGT
TGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTcATATGTTA
TCTGGCAACAAAAGTTTTATTCAAATACAATAAGTATTATGGACCTGCT
AATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA
TGACCAGGTTcAGTATCATTTAACAAAATAATATAAAAAGGAAGCTATT
TGGCTTCTTTTTTATATGCCTTGAATAgACTTTCAAGGTTCTTATATAAT
TTTTATTA

SEQ ID NO. 6909

STRAIN CJB110

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAA
TATGGTGATACCTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAA
TGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTATCTCTG
AGACAACACTGCAGTAACCTACGATCAGAAGAGTCATACTGCCACTTCA
ATGAAAATAGAAAACACAGCAACAAATGCTGCTGGTCAAACAACAGCTAC
TGTGGATTTGAAAACCAATCAAGTTTcTGTTCAGACCAAAAAGTTTCTC
TCAATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTT
TCGCCAATGAAGACATATTTCTCTGCGCCAGCTTTGAAATCAAAGAAGT
ATTAGCAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTAT
CAACAGCTCCTGTGAAGTcGATTACTTCAGAAGTTCCAGCAGCTAAAGAG
GAAGTTAAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACC
AGCTTCTGTGGCCGCTGAAAACACCAGCTCCAGTAGCTAAAGTAGCACCGG
TAAgaAACTGTAGCAGCCCCTAGAGTGGCAAGTGTFAAGTAGTCACTCTC
AAAGTAGAAAACCTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCC
TGTGACTACGACTTCAACAGcTACAGACAGTaaGTTaCAAGCGACTGAAG
TTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCA
CAACAGCTTCAAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGG
GCTCCAACCTCATGTGcAGCTTATaAAGAAAAGTAGCGTCAACTTATG
GAGTTAATGAATTCAGTACATaCCGTGCAGGTGATCCAgGTGATCATGGT
AAAGGTTTAGCAGTcGACTTTATTGTAgTAAAAACCAAGCACTTGGTAA

Table 69: Comparative Sequences relating to SAG0032

TGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCAT
ATGTTTATCTGGCAACAAAAGTTTTACTCAAATACAAATAGTATTTATGGA
CCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAA
CCATTATGACCATGTTACAGTATCATTTAAACAATAATATAAAAAAGGAA
GCTATTTGGCTTCTTTTATATATGCCTTGAATAGACTTCAAGGTTCCTTA
TATAATTTTTATTA

SEQ ID NO. 6910

STRAIN 1169NT

CTGATTTG
GTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACT
AAGCGTTATTTTCAGAACCAATGTCAATTGATATGAATGTCTTAGCAAAAA
TTAATAACATTGCGAGATATCAATCTTATTATCCTGAGACAACACTGACA
GTAACCTTACGATCAGAGAGTCTACTGCCACTTCAATGAAAATAGAAAC
ACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTGGATTTGAAAA
CCAATCAAGTTTCTGTGACAGCAAAAAAGTTTCTCTCAATCAAAATTCG
GAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCAATGAAGAC
ATATTTCTTCTGCGCCAGCTTTGAAATCAAAGAAGTATTAGCACAAGAGC
AAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTG
AAGTCGATTACTTCAgAAGTTCAGCAGCTAAAGAGGAAGTTAGACCAaC
TcAGACGTCAGTCACTCACTCAACACAGTATCACCAGCTTCTGTGCGCG
CTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCCGGTAAGAAGTGTAGCA
GCCCCAGCCCTAGAGTGGCAAGTCTAAAGTACTCACTCTTAAAGTAGA
AACTGGTGATCACCAGAGCATGTACCAGCTCCAGCAGTTCTCTGTGACTA
CGACTTCAACAGCTACaGACAAaTaAGTTACAAGCGACTGAAGTTAAgAGC
GTCCGGTgGCACAAAAGCTTCAACAGCAACACCCGGTAgGCACAAACCAGC
TTcAAACAACAAATGCGAGTAgTGACATCCTGAAAATGCAGGACTCCAAC
CTCATGTTGCAGCTTATAAAGAAAAGTAGCGTCAACTTATGGAGTTAAT
GAATTCAGTACATaCCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTT
AGCAGTTGACTTTATTGTAgGTAAAAACCAAGCACTTGGTAATGAAGTTG
CACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCATATGTTATC
TGGCAACAAAAGTTTACTCAAATACAAATAGTATTTATGGACCTGCTAA
TACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATG
ACCAGCTTCAAGTATCATTTAAACAATAATATAAAAAAGGAAGCTATTTG
GCTTCTTTTATATATGCCTTGAATAGACTTCAAGGTCTTATATAATTT
TTATTA

SEQ ID NO. 6911

STRAIN JM9130013

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACT
GTGAAATATGGTGATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGA
TATGAATGCTTAGCAAAAAATAAATAACATTGCAGATATCAATCTTATTT
ATCCTGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACCTGCC
ACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAAC
AGCTACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACCAAAAAAG
TTTCTCTCAATCAAAATTCGGAAGGTATGACACCAGAAGCAGCAACCAAG
ATTGTTTCGCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAA
AGAAGTATFAGCACAAGAGCAAGCTGTAGTCAAGCAGCAGCTAATGAAC
AGGTATCACCAGCTCCTGTGAAGTTCGATTACTTCAAGAAGTTCAGCAGCT
AAAGAGGAAGTTAAACCAACTCAGACGTCAGTCACTCAACCAACAGT
ATCACCAgCTTCTGTTGCGCGTGAACACCAGCTCCAGTAGCTAAAGTAG
CACCCGGTAAGAAGTGTAGCAGCCCTAgAGTGGCAAGTGTAAAGTAGTC
ACTCTAAAGTAGAAAAGTGGTGCATCACCAGAGCATGTATCAGCTCCAGC
AGTTCTGTGACTACGACTTCAACAGCTACAGaCAGTAAGTTACAAGCGA
cTGAAGTTAAGAGCGTTCCGGTAGCACA AAAAGCTTCAACAGCAACACCG
GTAGCaAACCCAGCTTCAACAACAATGCAGTAGCTGCACATCTGAAA
TGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAGTAGCGTCAA
CTTATGGAGTTAATGAATTCAGTACATACCGTGGGGAGATCCAGGTGAT
CATGGTAAAGGTTAGCAGTTGACTTTATTGTAGGTACTAATCAAGCACT
TGGTAATAAAGTTGCAGTACTCTACACAAAATATGGCAGCAAATAACA
TTTTCATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAACAGTATT
TATGGACCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTAC
TGCCAACCACTATGACCAGCTTCAAGTATCATTTAAACAATAATATAAAA
AAGGAAGCTATTTGGCTTCTTTTATATATGCCTTGAATAGACTTCAAGG
TCTTATATAATTTTTATTA

PRETTY of: /biotmp/msa167919.2{*} March 11, 2003 08:55 ..

Table with 5 columns: sequence identifier, position 1, position 50, position 51, position 100. Rows include various strain identifiers like msa167919.2{322_COH1} and a consensus row with asterisks.

Table 69: Comparative Sequences relating to SAG0032

msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	agtcgcaagt	gttcaagcac	aagaacacaga	tacgacgtgg	acagcacgta
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
101					
msa167919.2{322_COH1}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_M781}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_M732}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_18RS21}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_2603}	ctgtttcaga	ggtaaaggct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_JM9130013}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_A909}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_H36B}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_1169NT}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
Consensus	*****	*****-	-----	-----	-----
151					
msa167919.2{322_COH1}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_M781}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_M732}	tatactgtga	aatatggtga	tacantaagc	gttatttcag	aagcaatgtc
msa167919.2{322_18RS21}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_2603}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_JM9130013}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_A909}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_H36B}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_1169NT}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
Consensus	-----	-----	-----	-----	-----
201					
msa167919.2{322_COH1}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_M781}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_M732}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_18RS21}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_2603}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_JM9130013}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_A909}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_H36B}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_1169NT}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
Consensus	-----	-----	-----	-----	-----
251					
msa167919.2{322_COH1}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_M781}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_M732}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_18RS21}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_2603}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_JM9130013}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_A909}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_H36B}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_1169NT}	ttatztatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
Consensus	-----	*****	*****	*****	*****
301					
msa167919.2{322_COH1}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M781}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M732}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_18RS21}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_2603}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_JM9130013}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_090}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_CJB110}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_A909}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_H36B}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_1169NT}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
Consensus	*****	*****	*****	*****	*****

Table 69: Comparative Sequences relating to SAG0032

	351				400
msa167919.2{322_COH1}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_M781}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_M732}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTtT	GTTGCAGACC
msa167919.2{322_18RS21}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTcT	GTTGCAGACC
msa167919.2{322_2603}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTcT	GTTGCAGACC
msa167919.2{322_JM9130013}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTcT	GTTGCAGACC
msa167919.2{322_090}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTcT	GTTGCAGACC
msa167919.2{322_CJB110}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTcT	GTTGCAGACC
msa167919.2{322_A909}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTcT	GTTGCAGACC
msa167919.2{322_H36B}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA	TCAAGTTTcT	GTTGCAGACC
msa167919.2{322_1169NT}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA	TCAAGTTTcT	GTTGCAGACC
Consensus	*****	*****	*****	*****	*****
	401				450
msa167919.2{322_COH1}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_M781}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_M732}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_18RS21}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_2603}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_JM9130013}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_090}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_CJB110}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_A909}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_H36B}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
msa167919.2{322_1169NT}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG	GTATGACACC	AGAAGCAGCA
Consensus	*****	*****	*****	*****	*****
	451				500
msa167919.2{322_COH1}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_M781}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_M732}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_18RS21}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_2603}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_JM9130013}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_090}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_CJB110}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_A909}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_H36B}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
msa167919.2{322_1169NT}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT	TCTTCTGCGC	CAGCTTTGAA
Consensus	*****	*****	*****	*****	*****
	501				550
msa167919.2{322_COH1}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GtAGCAGCTA
msa167919.2{322_M781}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GtAGCAGCTA
msa167919.2{322_M732}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GtAGCAGCTA
msa167919.2{322_18RS21}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_2603}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_JM9130013}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_090}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_CJB110}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_A909}	ATCAAAGAA	GTATTAGCAC	AAGgGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_H36B}	ATCAAAGAA	GTATTAGCAC	AAGgGCAAGC	TGTTAGTCAA	GcAGCAGCTA
msa167919.2{322_1169NT}	ATCAAAGAA	GTATTAGCAC	AAGaGCAAGC	TGTTAGTCAA	GcAGCAGCTA
Consensus	*****	*****	***-*****	*****	*-*****
	551				600
msa167919.2{322_COH1}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_M781}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_M732}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_18RS21}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_2603}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_JM9130013}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_090}	ATGAACAGGT	ATCaaCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_CJB110}	ATGAACAGGT	ATCaaCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_A909}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_H36B}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
msa167919.2{322_1169NT}	ATGAACAGGT	ATCacCAGCT	CCTGTGAAGT	CGATTACTTC	AGAAGTTCCA
Consensus	*****	****-*****	*****	*****	*****
	601				650
msa167919.2{322_COH1}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_M781}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_M732}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_18RS21}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_2603}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_JM9130013}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_090}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_CJB110}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_A909}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_H36B}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
msa167919.2{322_1169NT}	GCAGCTAAAG	AGGAAGTTAg	ACCAACTCAG	ACGTCAGTCA	GTCAGTcAAC
Consensus	*****	*****	*****	*****	*****-***

Table 69: Comparative Sequences relating to SAG0032

	651				700
msa167919.2{322_COH1}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M781}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M732}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_18RS21}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_2603}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_JM9130013}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_090}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_CJB110}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_A909}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_H36B}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_1169NT}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
	Consensus	*****	*****	*****	*****
	701				750
msa167919.2{322_COH1}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M781}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M732}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_18RS21}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_2603}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_JM9130013}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_090}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_CJB110}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_A909}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_H36B}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_1169NT}	AAGTAGCACC	GGTAAGAACT	GTAGcagccc	CAGCCCCTAG	AGTGGCAAGT
	Consensus	*****	****-----	*****	*****
	751				800
msa167919.2{322_COH1}	GcTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M781}	GcTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M732}	GcTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_18RS21}	GtTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_2603}	GtTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_JM9130013}	GtTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_090}	GtTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_CJB110}	GtTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_A909}	GtTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_H36B}	GtTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_1169NT}	GcTAAAGTAG	TCACTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
	Consensus	*-*****	*****	*****	*****
	801				850
msa167919.2{322_COH1}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M781}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M732}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_18RS21}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_2603}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_JM9130013}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_090}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_CJB110}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_A909}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_H36B}	AtCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_1169NT}	AcCAGCTCCA	GCAGTTCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
	Consensus	*-*****	*****	****-*****	*****-*
	851				900
msa167919.2{322_COH1}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M781}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M732}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_18RS21}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_2603}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_JM9130013}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_090}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_CJB110}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_A909}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_H36B}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_1169NT}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
	Consensus	*****	*****	****-*****	*****
	901				950
msa167919.2{322_COH1}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_M781}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_M732}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_18RS21}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_2603}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_JM9130013}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_090}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_CJB110}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_A909}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_H36B}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC
msa167919.2{322_1169NT}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAATG	CAGTAGCTGC

Table 69: Comparative Sequences relating to SAG0032

Consensus	*****	*****	*****	*****	*****
	951				1000
msa167919.2{322_COH1}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M781}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M732}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_18RS21}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_2603}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_JM9130013}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_090}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_CJB110}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_A909}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_H36B}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_1169NT}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
Consensus	*****	*****-*-*	*****	*****	*****
	1001				1050
msa167919.2{322_COH1}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_M781}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_M732}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_18RS21}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_2603}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_JM9130013}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_090}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_CJB110}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_A909}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_H36B}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
msa167919.2{322_1169NT}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgA
Consensus	*****	*****	*****	*****	*****-*-*
	1051				1100
msa167919.2{322_COH1}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M781}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M732}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_18RS21}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_2603}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_JM9130013}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_090}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_CJB110}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_A909}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_H36B}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_1169NT}	GATCCAGGTG	ATCATGGTAA	AGGTTAGCA	GTtGACTTTA	TTGTAGGTAA
Consensus	*****	*****	*****	**-*****	*****-
	1101				1150
msa167919.2{322_COH1}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_M781}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_M732}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_18RS21}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_2603}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_JM9130013}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_090}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_CJB110}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_A909}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_H36B}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTAActTACA	CAAAtATGG
msa167919.2{322_1169NT}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTAActTACA	CAAAtATGG
Consensus	-*-*****	*****-	*****	*****	*****
	1151				1200
msa167919.2{322_COH1}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_M781}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_M732}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_18RS21}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_2603}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_JM9130013}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_090}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_CJB110}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_A909}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_H36B}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_1169NT}	CAGCAAATAA	CATTTcATAT	GTTATcTGGC	AACAAAAGTT	TTAcTCAAAT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa167919.2{322_COH1}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M781}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M732}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_18RS21}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_2603}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_JM9130013}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_090}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_CJB110}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_A909}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_H36B}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG

Table 69: Comparative Sequences relating to SAG0032

msa167919.2{322_1169NT}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
Consensus	*****	*****	*****	*****	*****
	1251				1300
msa167919.2{322_COH1}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_M781}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_M732}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_18RS21}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_2603}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_JM9130013}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_090}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_CJB110}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_A909}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_H36B}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msa167919.2{322_1169NT}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
Consensus	*****	*****	*-*****	-*****	*****
	1301				1350
msa167919.2{322_COH1}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_M781}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_M732}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_18RS21}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_2603}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_JM9130013}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_090}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_CJB110}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_A909}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_H36B}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
msa167919.2{322_1169NT}	AATAATATAA	AAAAGGAAGC	TATTTGGCCT	CITTTTTATA	TGCCTTGaat
Consensus	*****	*****	*****	*****	*****_**
	1351				1382
msa167919.2{322_COH1}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_M781}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_M732}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_18RS21}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_2603}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_JM9130013}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_090}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_CJB110}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_A909}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_H36B}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
msa167919.2{322_1169NT}	AGACTTCAA	GGTCTTATA	TAATTTTAT	TA	
Consensus	*****	*****	*****	**	

SEQ ID NO. 6912

STRAIN 2603 frame: 1

MNKKVLLSTMAASLLSVASVQAQETDITWTARTVSEVKADLVKQDNKSSYTVKYGDTLS
VSEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSHATSMKIEPATNAAGQTTA
TVDLKTNQVSVADQKVS LNTI SEGMP EAATTI VSPMKTYSSAPALKSKEVLAQEQAQV
AAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVQSSTTVSPASVAEETPAPVAKVAPVRT
VAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKSVPVQAQKAPTA
TPVAQPASTTNAVAHAPENAGLQPHVAAYKEKVA STYGVNEFSTYRAGDPGDHGKGLAVD
FIVGKNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTA
NHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNYF

SEQ ID NO. 6913

STRAIN 090 frame: 2

ETTLTVTYDQKSHATSMKIEPATNAAGQTPATVLDLKNQVSVADQKVS LNTI SEGMP
EAATTI VSPMKTYSSAPALKSKEVLAQEQAQVAAANEQVSTAPVKSITSEVPAAKEEVK
PTQTSVQSSTTVSPASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVS
PAVPVTTTSTATDSKLQATEVKSVPVQAQKAPATPVAQPASTTNAVAHAPENAGLQPHVA
AYKEKVA STYGVNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNIS
YVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYAL
NRLSRFLYNYF

SEQ ID NO. 6914

STRAIN A909 frame: 3

DLVKQDNKSSYTVKYGDTLSVI SEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIEPATNAAGQTTATVLDLKNQVSVADQKVS LNTI SEGMP EAATTI VSPMKTY
SSAPALKSKEVLAQQAQVAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD
SKLQATEVKSVPVQAQKAPATPVAQPASTTNAVAHAPENARLQPHVAAYKEKVA STYGVN
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNYF

SEQ ID NO. 6915

STRAIN H36B frame: 3

DLVKQDNKSSYTVKYGDTLSVI SEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIEPATNAAGQTTATVLDLKNQVSVADQKVS LNTI SEGMP EAATTI VSPMKTY
SSAPALKSKEVLAQQAQVAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD
SKLQATEVKSVPVQAQKAPATPVAQPASTTNAVAHAPENARLQPHVAAYKEKVA STYGVN

Table 69: Comparative Sequences relating to SAG0032

EFSTYRAGDPGDHGGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHHVHSFNK.YKKGSYLASFLYALNRLSRFLYNYF

SEQ ID NO. 6916

STRAIN 18RS21 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLISEGMPPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSIITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHHVHSFNK.YKKGSYLASFLYALNRLSRFLYNYF

SEQ ID NO. 6917

STRAIN M732 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLISEGMPPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSIITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHHVHSFNK.YKKGSYLASFLYALNRLSRFLYNYF

SEQ ID NO. 6918

STRAIN COH1 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLISEGMPPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSIITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHHVHSFNK.YKKGSYLASFLYALNRLSRFLYNYF

SEQ ID NO. 6919

STRAIN M781 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLISEGMPPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSIITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHHVHSFNK.YKKGSYLASFLYALNRLSRFLYNYF

SEQ ID NO. 6920

STRAIN CJB110 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLISEGMPPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSTAPVKSIITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTTPKVETGASPEHVSAPAVPVTTTSTATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHHVHSFNK.YKKGSYLASFLYALNRLSRFLYNYF

SEQ ID NO. 6921

STRAIN 1169NT frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLISEGMPPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSIITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTTPKVETGASPEHVPAPAVPVTTTSTA
TDNKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN
VNEFSTYRAGDPGDHGGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYSN
TNSIYGPANTWNAMPDRGGVTANHYDHHVHSFNK.YKKGSYLASFLYALNRLSRFLYNYF

SEQ ID NO. 6922

STRAIN JM9130013 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLISEGMPPEAATTIVSPMKTY
SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSIITSEVPAAKEEVKPTQTSVQSSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTTPKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHGGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHHVHSFNK.YKKGSYLASFLYALNRLSRFLYNYF

PRETTY of: /biotmp/msa237049.2{*} May 14, 2003 03:04 ..

Table with 2 columns: sequence identifiers (msa237049.2{322_COH1}, msa237049.2{322_M781}, etc.) and alignment markers (1, 50) with dashes indicating alignment positions.

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_CJB110}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_18RS21}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_2603}	mnkkvlltst	maasllsvas	vqagetdttw	tartvsevka	dlvkqdnkss
msa237049.2{322_JM9130013}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_1169NT}	-----	-----	-----	-----	dlvkqdnkss
Consensus	*****	*****	*****	*****	-----
51					
msa237049.2{322_COH1}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_M781}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_M732}	ytvkygdtxs	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_A909}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_H36B}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_090}	-----	-----	-----	-----ETT	LTVTYDQKSH
msa237049.2{322_CJB110}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_18RS21}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_2603}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_JM9130013}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_1169NT}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
Consensus	-----	-----	-----	-----***	*****
101					
msa237049.2{322_COH1}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_M781}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_M732}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_A909}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_H36B}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_090}	TATSMKIETP	ATNAAGQTTpA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_CJB110}	TATSMKIETP	ATNAAGQTTpA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_18RS21}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_2603}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_JM9130013}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
msa237049.2{322_1169NT}	TATSMKIETP	ATNAAGQTTA	TVDLKTNQVf	VADQKVS LNT	I SEG MTP EAA
Consensus	*****	*****	*****	*****	*****
151					
msa237049.2{322_COH1}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSI TSEVP
msa237049.2{322_M781}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSI TSEVP
msa237049.2{322_M732}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSI TSEVP
msa237049.2{322_A909}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	AAANEQVSpA	PVKSI TSEVP
msa237049.2{322_H36B}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	AAANEQVSpA	PVKSI TSEVP
msa237049.2{322_090}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVStA	PVKSI TSEVP
msa237049.2{322_CJB110}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVStA	PVKSI TSEVP
msa237049.2{322_18RS21}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSI TSEVP
msa237049.2{322_2603}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSI TSEVP
msa237049.2{322_JM9130013}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSI TSEVP
msa237049.2{322_1169NT}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSI TSEVP
Consensus	*****	*****	*****	*****	*****
201					
msa237049.2{322_COH1}	AAKEEVkPTQ	TSVsq1TTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_M781}	AAKEEVkPTQ	TSVsq1TTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_M732}	AAKEEVkPTQ	TSVsq1TTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_A909}	AAKEEVkPTQ	TSVsqeTTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_H36B}	AAKEEVkPTQ	TSVsqeTTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_090}	AAKEEVkPTQ	TSVsqeTTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_CJB110}	AAKEEVkPTQ	TSVsqeTTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_18RS21}	AAKEEVkPTQ	TSVsqeTTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_2603}	AAKEEVkPTQ	TSVsqeTTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_JM9130013}	AAKEEVkPTQ	TSVsqeTTVf	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_1169NT}	AAKEEVrPTQ	TSVsqeTTVf	PASVAAETPA	PVAKVAPVRT	VAapAPRVAS
Consensus	*****	*****	*****	*****	**..*****
251					
msa237049.2{322_COH1}	aKVVTpKVET	GASPEHVsAP	AVPVTITSpA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_M781}	aKVVTpKVET	GASPEHVsAP	AVPVTITSpA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_M732}	aKVVTpKVET	GASPEHVsAP	AVPVTITSpA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_A909}	vkVVTpKVET	GASPEHVsAP	AVPVTITStA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_H36B}	vkVVTpKVET	GASPEHVsAP	AVPVTITStA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_090}	vkVVTpKVET	GASPEHVsAP	AVPVTITStA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_CJB110}	vkVVTpKVET	GASPEHVsAP	AVPVTITStA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_18RS21}	vkVVTpKVET	GASPEHVsAP	AVPVTITSpA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_2603}	vkVVTpKVET	GASPEHVsAP	AVPVTITSpA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_JM9130013}	vkVVTpKVET	GASPEHVsAP	AVPVTITSpA	TDsKLQATEV	KSPVVAQKAP
msa237049.2{322_1169NT}	aKVVTpKVET	GASPEHVsAP	AVPVTITStA	TDnKLQATEV	KSPVVAQKAP
Consensus	*****	*****	*****	*****	*****
301					
msa237049.2{322_COH1}	TATpVAQPAS	TTNAVAAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_M781}	TATpVAQPAS	TTNAVAAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_M732}	TAsPVAQPAS	TTNAVAAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_A909}	TATpVAQPAS	TTNAVAAHPE	NarLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_H36B}	TATpVAQPAS	TTNAVAAHPE	NarLQPHVAA	YKEKVASTYG	VNEFSTYRAG

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_090}	TATPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_CJB110}	TATPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_18RS21}	TATPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_2603}	TATPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_JM9130013}	TATPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_1169NT}	TATPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
Consensus	***-*****	*****	***-*****	*****	*****
351					
msa237049.2{322_COH1}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_M781}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_M732}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_A909}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_H36B}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_090}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_CJB110}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_18RS21}	DPGDHGKGLA	VDFIVGtNQA	LGnkVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_2603}	DPGDHGKGLA	VDFIVGtNQA	LGnkVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_JM9130013}	DPGDHGKGLA	VDFIVGtNQA	LGnkVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_1169NT}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
Consensus	*****	*****-***	***-*****	*****	*****
401					
msa237049.2{322_COH1}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_M781}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_M732}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_A909}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALh
msa237049.2{322_H36B}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALh
msa237049.2{322_090}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_CJB110}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_18RS21}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_2603}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_JM9130013}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_1169NT}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
Consensus	*****	*****	*****	*****	*****
451 460					
msa237049.2{322_COH1}	RLSRFLYNFY				
msa237049.2{322_M781}	RLSRFLYNFY				
msa237049.2{322_M732}	RLSRFLYNFY				
msa237049.2{322_A909}	RLSRFLYNFY				
msa237049.2{322_H36B}	RLSRFLYNFY				
msa237049.2{322_090}	RLSRFLYNFY				
msa237049.2{322_CJB110}	RLSRFLYNFY				
msa237049.2{322_18RS21}	RLSRFLYNFY				
msa237049.2{322_2603}	RLSRFLYNFY				
msa237049.2{322_JM9130013}	RLSRFLYNFY				
msa237049.2{322_1169NT}	RLSRFLYNFY				
Consensus	*****				

Table 70: Comparative Sequences relating to SAG 1280

SEQ ID. NO. 7001
 STRAIN 2603
 ATGGGGAGGAAAATGAATCAAGAAGTCTTACTACAATGATGAGAGCCACTATTCCCTC
 GTGATAGAGCCTTGCTTGAGGCATTTTATATATACCAAGCAGAGCATTTTGATGAGGAGT
 GGGATAGTCTTATTATCAGTATTATGACCAATAGGCAAGAAAATAAATAGTCTGTTCAAG
 TACTTCACTTTGAGACAGATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATACTGCTC
 ATGATCTATTGACCTATACACAAGTTTTCCGCCAAAGTGGTCTTCAAAAACIAGATAAAC
 TATCGCCGTCTGAAAAAACTTGGTGTAGAAAGTGGCCTTGTTCATCTCGGCCACTCGTT
 TCAATTTATGGATTCCAATGGACACTACCAAAACCATATCGCCGGATTCACTCTTACAAA
 AGAGTAGGGGAGCTAATTTGGTCAATGTGTATCGTGTGGCTAATAAATTTAGCGGATCGTA
 TTAGTCCGATATTGAACAGTTTTCTTAACTTACGAGCCTGAGCTTGAAACTAGAGCTG
 ATGAAACTGTTCTAGAAAAATGAAGAACTGTTGATGAGCACAAAAAAGTGTTCATCAAG
 CAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTTGGATGTAGATTGTCTC
 AACTAGATGTTCAAATAGGAAAAACAGTCACTGCCAGCTTATGAAGAGTTATCCTTAC
 GACGTAATTTGAGATTCTAACATATTTTACCAAATTCGAAATGAACTGCCAAAGTCC
 CAAGTTTTTAGACGAGGTGATTTTGGACACAGAGATGAAATGACACCAGTCTTTGATGGCG
 AGGAAATTACTTACTTACTTCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAAACGAACTGA
 CTACAGTCCGAAGAAAGGAATTAGAAAAAATTTGGACAAGCCATTAGGATAGAAAAATCAAG
 AAAAAATTGACTCAGCTAGGGATTGATTTATCTCAGTTTGAACCCAGACCGAGTCCGGTATT
 TATTGGATGACAGCGTCTGTTTTCGTTTAAAAAATGCAGACCTTGTCTTACTAGGTGGTT
 ATCCCAAAGCCTCGTAACTCAACTAGCCCTTGGACAGAACTACTCCAAATGGGACTAA
 GTCATGAAAAAGTTGAATTTTCTTTGGTAGCCAGCTTCCCAATGAAAGAGCTGCGACAAG
 TTGCCCTACGCCTTTTTATACCAAGAACTCAGCAGAGAAGATGCGGAGCAATTTGAAAAAG
 ATAAAGGTAATCAGCCAGATTTAACTCTCAGAGATTGAAAAGCAAGCTAGAGAAAGCTG
 AGGAAAAGAAAGTAGTTGATGAAGAAATTCGCGGAAAATCCACTGGTTTCCAGAGATTGG
 ACACTTATCTCTGCGGGTCACTGGTTTCTATAAGGGACAGGACTTTGAGGTCAATGTCGG
 TCAGCGATGCTCGAATGAACGGTTTGAATTCGGATTGAGTTAGTCAATGACTTTTCGGATA
 TCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGAAAGTCACTCAGGCACTTC
 ATCAGCCAAAGGCAGAACCAAAAACAGAGTTAGAAGAAGCGGACCAAGAATTAACCTAT
 TCTCAATTTTCGGAAGAGGAGCCAGTTTCAAGATTGGACTATTGGAAACAGATGATTCAG
 AAAATGGTCAATACCATGATCTTGAAGAAAACAGATAATCAAATTCCTGAAGAGGAAG
 TCGTCGAAACAAATTCAGAGATTCCAGTAAACGGACTTTTATTTTCCAGAAGATTGACGG
 ACTTTTTATCTAAGACTGCTAGAGATAAGGTTGAGACAAAATTTGCGCCATTCGTTTGG
 TAAAAAATCTAGAAAGTAGAGCACCGCAATGCTTCACCAAGTGAACAAGAACTCCTTGCCA
 AGTATGTAGGCTGGGGTGGACTAGCCAAATGAATTTTGGATGACTATAATCCAAAATTTT
 CTAAGGAACGAGAAGAACTGAAGAGCCTAGTCAAGATAAAGAGTATTTCGGATATGAAAC
 AGTCTCTCCCTGACAGCCTATTACACAGACCCTCCCTGATCCGTCAGATGTGGGATAAGT
 TGGAAAAGAGATGGCTTTACAGGTGGCAAAAATCCTAGATCCTCCATGGGAACAGGGAATT
 TCTTTGCGGCTATGCCAAAACACTTAAGAGAAAAGAGTGAAGTGTATGGCTAGAGTTAG
 ATACTATTACAGGAGCTATTGCCCCAACCTTCATCCCAATAGTCATATTGAAATTAAGG
 GATTTGAGACGGTGGCTTTTAAACGACAATAGTTTGTATTGGTGAATTCAAATGTGCCCT
 TTGCCAATATACGAAATTCGGGATAATAGGTACGATAGGCCTTACATGATTCATGACTACT
 TTGTCAAAAAGTCACTTGTATTGCTTATGATGGTGGACAAAGTACGGATATCTCTCTCCA
 CAGGAATCTATGGATAAGCGAACAGAAAACATCTTACAAGATATTTCGTGAGCAACTGAAAT
 TTCTTGGTGGGGTTCCGACTTCCCTGACTCTGCCCTTAAAGGCCATTGACGGAACGAGTCA
 CAACGGATATGTTATCTTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAG
 CCTTTTCAGGTTCCATTCGCTATGACAAGGATAGTTCGCAATTTGGCTCAATCCTTATTTTG
 ATGGAGAATACAATAGAGTCAAGGTGCTAGGAACCTACGAGGTGAGGAATTTAAACGGAGAA
 CACTTCTGTTTAAAGGGACTAGTGTACTGATTGCAAGTGTGAAACAGCTCTAAATC
 ACGTTAAGGCCCAAGAGACTTATGATAGAAATGAGGTCACTTAAACCCAGATGTGTTGA
 CCAAAACAAAGTCAATGACTCCATTCCAGCTGAAATGAGGGAATAATCTAGGTCAATACA
 GTTTTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTTCGAGTCGGAA
 CCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAGGGCAACTTCAAAGCATGGGACA
 CCAAACTTCTCAAAGCAGATTGATCGCTTAAATGCCCTTAGAAGTACTGATAACACTG
 CTCTGGATGCTATGTGACCGATGATGCAGCCAAACGTTGGTCAAGTTAAGGGGTATTATA
 AAAAGACAGTTTTCTATGAAGCTCCATTGTCTTATAAAGAAGTGGCACGATCAAAAGGAA
 TGGTGCATATTTCGCAATGCCATCAAGAAAGTATTGCCATTCAACGCTATTATGACTATG
 ATAAGGAGACCTTTAAACCACTTGTAGGCAAACTCAATCGTACCTATGATAGCTTTGTCA
 AACACTATGGGTATTGAAATAGTCTGTGAACCGCAATCTTTTGTATAGTGTATGATAAGT
 ATTCGCTTCTTGTAGTTTGGAAAGATGAAAGTCTGGATCCAAGTGGAAAGTCTGTTATCT
 ATACTAAATCCCTTGCTTTGAGAAGGCTCTAGTGGTCTGAAAAAGAGGTTAAAAAGG
 TGCACTGCTCCCTGATGCCTTAAATTCGAGCTTGGCTGACGGAACGAGGTGTGATTTCC
 CTTATATGATGCTATCTATCAGGTTGAATCCGAGATGACCTTATTGAGGAGTTAGGCCG
 ACCTCATTATGCTGATCCTGAGAAGTATTGAAATGGAGAATTGACCTATGTTTCTCGCC
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